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197199

From: Whiteman, Brian
Sent: Tuesday, August 01, 2006 9:55 AM
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Subject: seq search

09966724

SEQ ID NO: 2

- 1) commercial databases
- 2) issued us patents and published us patent applications

oligo search SEQ ID NO: 2

- 1) commercial databases
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- limit length to oligos with 5-500 nucleotides of SEQ ID NO: 2
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Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner- Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

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78544

2-491 AA
NA

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

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Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

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_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

✓ Other CGP

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 12:43:11 ; Search time 615 Seconds
(without alignments)
7216.659 Million cell updates/sec

Title: US-09-966-724B-2

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2372	100.0	2372	2	US-07-903-103-1 Sequence 1, Appl1
2	2372	100.0	2372	2	US-08-044-619A-1 Sequence 1, Appl1
3	2372	100.0	2372	2	US-08-283-911-1 Sequence 1, Appl1
4	2372	100.0	2372	2	US-08-245-500A-2 Sequence 2, Appl1
5	2372	100.0	2372	2	US-08-390-546-2 Sequence 2, Appl1
6	2372	100.0	2372	2	US-08-390-479A-2 Sequence 2, Appl1
7	2372	100.0	2372	2	US-08-557-393-2 Sequence 2, Appl1
8	2372	100.0	2372	2	US-08-390-516C-2 Sequence 2, Appl1
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11	2372	100.0	2372	2	US-08-801-718-2 Sequence 2, Appl1
12	2372	100.0	2372	3	US-09-073-567-1 Sequence 1, Appl1
13	2372	100.0	2372	3	US-09-280-805-1 Sequence 1, Appl1
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44	812.2	34.2	966	3	US-09-167-322-7 Sequence 7, Appl1
45	652	27.5	652	3	US-09-510-252-3 Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-07-903-103-1
Sequence 1, Application US/07903103
Patent No. 5411860
GENERAL INFORMATION:
APPLICANT: VOGELSTEIN, BERT
APPLICANT: KINZLER, KENNETH
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G ST., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,103
FILING DATE: 19920623
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/867,840
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,40148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-07-903-103-1

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-08-044-619A-1

Sequence 1, Application US/08044619A

Patent No. 5420263

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY

APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G ST., N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/044.619A

FILING DATE: 07-APR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/903,103

FILING DATE: 23-JUN-1992

APPLICATION NUMBER: US 07/867,840

FILING DATE: 07-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107,40148

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

TELEX: 197430 BMB UT

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-044-619A-1

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB AAGAAACCCAGAGCAAGAAAGAGATGTGAATCTAGTTGGCCCTTAATGCTATTGAC 1620
QY 1621 CTGTGTGATTTGTCAGAGTGCACCTAAAAATGTTGCAATGTCATGAGCAAGAGAC 1680
DB CTGTGTGATTTGTCAGAGTGCACCTAAAAATGTTGCAATGTCATGAGCAAGAGAC 1680
QY 1681 ATCTTAGGCTGCTTTACATGTGCAAAAGAGCTAAAGAAAGAGATTAAGCCCTGCCAG 1740
DB ATCTTAGGCTGCTTTACATGTGCAAAAGAGCTAAAGAAAGAGATTAAGCCCTGCCAG 1740
QY 1741 TATGTAGCAACCAATTCAGAAATGTTGTGCTAATTTCCCTAGTTGACCTGTCTAT 1800
DB TATGTAGCAACCAATTCAGAAATGTTGTGCTAATTTCCCTAGTTGACCTGTCTAT 1800
QY 1801 AAGAGATTAATATATTTCTAATATATAACCTTAGAAATTTGAGACAACCTGAATTTAT 1860
DB AAGAGATTAATATATTTCTAATATATAACCTTAGAAATTTGAGACAACCTGAATTTAT 1860
QY 1861 CACATATATCAAGTGAAGAAAATGCTCAATTCACATGATTTCTTCTTTAGTATAT 1920
DB CACATATATCAAGTGAAGAAAATGCTCAATTCACATGATTTCTTCTTTAGTATAT 1920

QY 1921 TGACCTACTTGGTAGTGAATAGTGAATCTTACTATTAATTTGACTTGAATATAGCT 1980
DB TGACCTACTTGGTAGTGAATAGTGAATCTTACTATTAATTTGACTTGAATATAGCT 1980
QY 1981 CATCTTTACACCACTCTTAATTTTAATTAATTTCTACTGTCTTAAATGAGAATAC 2040
DB CATCTTTACACCACTCTTAATTTTAATTAATTTCTACTGTCTTAAATGAGAATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAAATATGATATAGCATTTTAAAGTAACTTATTTTGTG 2100
DB TTGGTTTTTTTTTTCTTAAATATGATATAGCATTTTAAAGTAACTTATTTTGTG 2100
QY 2101 AGACGAGTCTTGCTCTGTTAACCGAGCTGAGAGTGCAGTGGTGATCTTGCTCAGCA 2160
DB AGACGAGTCTTGCTCTGTTAACCGAGCTGAGAGTGCAGTGGTGATCTTGCTCAGCA 2160
QY 2161 AGCTGCTCCCTCCCGGGTTGCAACATTTCTCTGCTCAGCTCCCAATTAAGCTTGGCC 2220
DB AGCTGCTCCCTCCCGGGTTGCAACATTTCTCTGCTCAGCTCCCAATTAAGCTTGGCC 2220
QY 2221 TACAGTATCTGCACACACACCTGGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
DB TACAGTATCTGCACACACACCTGGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
QY 2281 ACCGTGTTAGCAGAGATGTCGATCTCTGACCTGTGATCCGCCACCTCGGCTTCC 2340
DB ACCGTGTTAGCAGAGATGTCGATCTCTGACCTGTGATCCGCCACCTCGGCTTCC 2340
QY 2341 CAAGTGTGGGATTTACAGCATGAGCCACCG 2372
DB CAAGTGTGGGATTTACAGCATGAGCCACCG 2372

RESULT 3
US-08-283-911-1
; Sequence 1, Application US/08283911
; Patent No. 5519118
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,911
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107,40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBWB DT
; INFORMATION FOR SEQ ID NO: 1:
;

SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-283-911-1

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTCTCGAAAGATGGA 60
DB 1 GCACCGCGGAGCTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTCTCGAAAGATGGA 60
QY 61 GCAGAAAGCCGAGCCCGAGGGGCGCCGGAACCTCTGACCGAGATCTCTGCTTTGG 120
DB 61 GCAGAAAGCCGAGCCCGAGGGGCGCCGGAACCTCTGACCGAGATCTCTGCTTTGG 120
QY 121 CAGCCGAGAGCAGCCGCTCCCGGATTAGTGTACGAGGCGCCAGTGGCCCTGGCCCG 180
DB 121 CAGCCGAGAGCAGCCGCTCCCGGATTAGTGTACGAGGCGCCAGTGGCCCTGGCCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGTGTCTTCCGAGTATGATGCCCGTG 240
DB 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGTGTCTTCCGAGTATGATGCCCGTG 240
QY 241 AAGGAACTGGGGAGCTTGGAGGAGCCCGGACTCCAGGCGGAAACCCCGAGTGTGA 300
DB 241 AAGGAACTGGGGAGCTTGGAGGAGCCCGGACTCCAGGCGGAAACCCCGAGTGTGA 300
QY 301 GGAGGAGGCAATGTGCAATACCAAGATGTCTACTGATGTGTGTGTAACCACT 360
DB 301 GGAGGAGGCAATGTGCAATACCAAGATGTCTACTGATGTGTGTGTAACCACT 360
QY 361 CACAGATTCAGCTTGGAAACAAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGT 420
DB 361 CACAGATTCAGCTTGGAAACAAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGT 420
QY 421 TATTTAAAGTCTGTGTGTGCAAAAAAGACACTTATATCTATGAAGAAGTTCTTTTATC 480
DB 421 TATTTAAAGTCTGTGTGTGCAAAAAAGACACTTATATCTATGAAGAAGTTCTTTTATC 480
QY 481 TTGGCCAGTATATATGATCTAAACGATTTATGATAGAGCAACAATATTTATTT 540
DB 481 TTGGCCAGTATATATGATCTAAACGATTTATGATAGAGCAACAATATTTATTT 540
QY 541 GTTCAATATCTTCTAGAGAGATTTGTGGCGTGCAGAGCTTCTGTGGAAGAGACACA 600
DB 541 GTTCAATATCTTCTAGAGAGATTTGTGGCGTGCAGAGCTTCTGTGGAAGAGACACA 600
QY 601 GGAATAATATATACCATGATCTCAAGGAACCTGTGTAGTCAATCAGCAGATCATCG 660
DB 601 GGAATAATATATACCATGATCTCAAGGAACCTGTGTAGTCAATCAGCAGATCATCG 660
QY 661 ACTCAGGTATCTGTGAGTGAAGACAGGTGTCACCTTGAAGTGGAGATGATCAAAAG 720
DB 661 ACTCAGGTATCTGTGAGTGAAGACAGGTGTCACCTTGAAGTGGAGATGATCAAAAG 720
QY 721 ACCTGTATCAAGAGCTTCAAGAAAGAACTTCACTTCACTTGTGTTTCTAGACAT 780
DB 721 ACCTGTATCAAGAGCTTCAAGAAAGAACTTCACTTCACTTGTGTTTCTAGACAT 780

QY 781 CTACCTCATCTGAAGAGAGCAATTAGTGAACAGAGAAATTCAGATGATATCTG 840
DB 781 CTACCTCATCTGAAGAGAGCAATTAGTGAACAGAGAAATTCAGATGATATCTG 840
QY 841 GTGAACGACAAAGAAACGCCCAAAATCTGATGATATTTCCCTTCTTGTGTAAGAAC 900
DB 841 GTGAACGACAAAGAAACGCCCAAAATCTGATGATATTTCCCTTCTTGTGTAAGAAC 900
QY 901 TGGCTCTGTGTGTAATGAAGATATGTTGTGAAGAAAGCAGTACAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTGTAATGAAGATATGTTGTGAAGAAAGCAGTACAGTGAATCTACAG 960
QY 961 GGAACCCATCGAATCCGGAATCTGTGAGTGTGTAGTGAACATTCAGAGTATGGTGG 1020
DB 961 GGAACCCATCGAATCCGGAATCTGTGAGTGTGTAGTGAACATTCAGAGTATGGTGG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAAGTGAATTTGAAGTGAATCTTCGACTCAG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTGTAAGTGAATTTGAAGTGAATCTTCGACTCAG 1080
QY 1081 AAGATTATAGCTTGTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGAGTATATC 1140
DB 1081 AAGATTATAGCTTGTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGAGTATATC 1140
QY 1141 AAGTTATCTGTATCAGGAGGAGAGTGTATCAGATTCATTGGAAGAACTCTGAAA 1200
DB 1141 AAGTTATCTGTATCAGGAGGAGAGTGTATCAGATTCATTGGAAGAACTCTGAAA 1200
QY 1201 TTTCTTACTGATCATTTAGGAAATGCACTTCATGCAATGAATGAATCCCGCTCCAT 1260
DB 1201 TTTCTTACTGATCATTTAGGAAATGCACTTCATGCAATGAATGAATCCCGCTCCAT 1260
QY 1261 CACATTGCAACAGATGTGTGGCCCTTGTGAGAAATTTGGCTTCTGTAAGATGAAGGAAAG 1320
DB 1261 CACATTGCAACAGATGTGTGGCCCTTGTGAGAAATTTGGCTTCTGTAAGATGAAGGAAAG 1320
QY 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAAATCTCAACAAGCTGAAGAGGCT 1380
DB 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAAATCTCAACAAGCTGAAGAGGCT 1380
QY 1381 TTGATGTCCTGATGTGAAGAAATCTATGTGAATGATCCAGAGGTCATGTGTGAG 1440
DB 1381 TTGATGTCCTGATGTGAAGAAATCTATGTGAATGATCCAGAGGTCATGTGTGAG 1440
QY 1441 AAAATGATGATATAATTTACAAAGCTTCACAATCAAGAAAGTGAAGCTATTCTCAG 1500
DB 1441 AAAATGATGATATAATTTACAAAGCTTCACAATCAAGAAAGTGAAGCTATTCTCAG 1500
QY 1501 CATCAACTTCTAGTACATTTATTTATGACAGCAAGAAAGATGTGAAGAGTTGAAAGG 1560
DB 1501 CATCAACTTCTAGTACATTTATTTATGACAGCAAGAAAGATGTGAAGAGTTGAAAGG 1560
QY 1561 AAGAAACCCAAAGCAAGAAAGAGTGTGGAATCTAGTTGGCCCTTAATGCAATTGAAC 1620
DB 1561 AAGAAACCCAAAGCAAGAAAGAGTGTGGAATCTAGTTGGCCCTTAATGCAATTGAAC 1620
QY 1621 CTTGTGTATTTGTCAAGGTCGACCTAAAATAGTTGCTTGTGCAATGCAAAACGAGAC 1680
DB 1621 CTTGTGTATTTGTCAAGGTCGACCTAAAATAGTTGCTTGTGCAATGCAAAACGAGAC 1680
QY 1681 ATCTTATGGCTGCTTTTATCATGTGCAAGAAAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
DB 1681 ATCTTATGGCTGCTTTTATCATGTGCAAGAAAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
QY 1741 TATGTAGCAACCAATTCAAAGATTTGCTAATCTTATTTCCCTAGTGAACCTGTCTAT 1800
DB 1741 TATGTAGCAACCAATTCAAAGATTTGCTAATCTTATTTCCCTAGTGAACCTGTCTAT 1800
QY 1801 AAGAGAAATATATTTCTAATATTAACCTTAGAAATTTGAGAAACCTGAAATTTAT 1860
DB 1801 AAGAGAAATATATTTCTAATATTAACCTTAGAAATTTGAGAAACCTGAAATTTAT 1860

QY 1861 CACATATATCAAGTGAAGAAAAATGCTCATATTCATAGATTTCTCTTTAGTATAT 1920
DB 1861 CACATATATCAAGTGAAGAAAAATGCTCATATTCATAGATTTCTCTTTAGTATAT 1920
QY 1921 TGACCTACTTTGGTATGTAATAGTAACTACTTAAATTTGCTGAATATGTACT 1980
DB 1921 TGACCTACTTTGGTATGTAATAGTAACTACTTAAATTTGCTGAATATGTACT 1980
QY 1981 CATCCTTACACCAACTCCTAATTTTAAATATTTCTCTCTTAAATGAGAATAC 2040
DB 1981 CATCCTTACACCAACTCCTAATTTTAAATATTTCTCTCTTAAATGAGAATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAAATATGTAATGACATTTAAATGTAATATTTTGTG 2100
DB 2041 TTGGTTTTTTTTTTCTTAAATATGTAATGACATTTAAATGTAATATTTTGTG 2100
QY 2101 AGACCGAGTCTTGTCTGTATACCCAGGCTGAGTGAAGTGGTATCTTGCTCATGCA 2160
DB 2101 AGACCGAGTCTTGTCTGTATACCCAGGCTGAGTGAAGTGGTATCTTGCTCATGCA 2160
QY 2161 AGCTTGCCTCCCGGGTTCGACACATTCCTGCTCAGCTCCCAATTAGTGGCC 2220
DB 2161 AGCTTGCCTCCCGGGTTCGACACATTCCTGCTCAGCTCCCAATTAGTGGCC 2220
QY 2221 TACAGTCACTGTCACACACACCTGGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
DB 2221 TACAGTCACTGTCACACACACCTGGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
QY 2281 ACCGTGTATGCCAGATGTCTGATCTCTGACCTCGTATCCGCCACTGCGCTTC 2340
DB 2281 ACCGTGTATGCCAGATGTCTGATCTCTGACCTCGTATCCGCCACTGCGCTTC 2340
QY 2341 CAAAGTGTGGGATTACAGGCGATGAGCCACCG 2372
DB 2341 CAAAGTGTGGGATTACAGGCGATGAGCCACCG 2372

RESULT 4

US-08-245-500A-2
Sequence 2, Application US/08245500A

Patent No. 5550023

GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE

APPLICANT: HILL, DAVID E.

APPLICANT: KINZLER, KENNETH W.

APPLICANT: VOGELSTEIN, BERT

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/245,500A

FILING DATE: 07-APR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107,42798

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-245-500A-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTCTTCTGGGGCTGTGTGGCCCTGTGTGTGGAAAGATGA 60
DB 1 GCACCGCGGAGCTTGGCTCTTCTGGGGCTGTGTGGCCCTGTGTGTGGAAAGATGA 60
QY 61 GCAGAAACCGAGCCGAGGGGGGCGGCGGACCCCTGACCGAGATCGTGCTTTCG 120
DB 61 GCAGAAACCGAGCCGAGGGGGGCGGCGGACCCCTGACCGAGATCGTGCTTTCG 120
QY 61 GCAGAAACCGAGCCGAGGGGGGCGGCGGACCCCTGACCGAGATCGTGCTTTCG 120
DB 61 GCAGAAACCGAGCCGAGGGGGGCGGCGGACCCCTGACCGAGATCGTGCTTTCG 120
QY 121 CAGCCAGAGACGCGTCCCTCCCGGATTAAGTGGCTACGAGCGCCAGTGCCTTGGCCG 180
DB 121 CAGCCAGAGACGCGTCCCTCCCGGATTAAGTGGCTACGAGCGCCAGTGCCTTGGCCG 180
QY 121 CAGCCAGAGACGCGTCCCTCCCGGATTAAGTGGCTACGAGCGCCAGTGCCTTGGCCG 180
DB 121 CAGCCAGAGACGCGTCCCTCCCGGATTAAGTGGCTACGAGCGCCAGTGCCTTGGCCG 180
QY 181 GAGAGTGAATGATATCCCGAGAGCCGAGGCGCTGCTTCCGCAATCATGTCCTCCGCTG 240
DB 181 GAGAGTGAATGATATCCCGAGAGCCGAGGCGCTGCTTCCGCAATCATGTCCTCCGCTG 240
QY 181 GAGAGTGAATGATATCCCGAGAGCCGAGGCGCTGCTTCCGCAATCATGTCCTCCGCTG 240
DB 181 GAGAGTGAATGATATCCCGAGAGCCGAGGCGCTGCTTCCGCAATCATGTCCTCCGCTG 240
QY 241 AAGGAACTGGGAGATCTTGAAGGGAACCCCGACTCCAGACCGGAAACCCCGAGATGTA 300
DB 241 AAGGAACTGGGAGATCTTGAAGGGAACCCCGACTCCAGACCGGAAACCCCGAGATGTA 300
QY 241 AAGGAACTGGGAGATCTTGAAGGGAACCCCGACTCCAGACCGGAAACCCCGAGATGTA 300
DB 241 AAGGAACTGGGAGATCTTGAAGGGAACCCCGACTCCAGACCGGAAACCCCGAGATGTA 300
QY 301 GGAGCAGGCAATATGCAATACCAATCATGTCTGTAAGTATGATGATGATGATGATGAT 360
DB 301 GGAGCAGGCAATATGCAATACCAATCATGTCTGTAAGTATGATGATGATGATGATGAT 360
QY 301 GGAGCAGGCAATATGCAATACCAATCATGTCTGTAAGTATGATGATGATGATGATGAT 360
DB 301 GGAGCAGGCAATATGCAATACCAATCATGTCTGTAAGTATGATGATGATGATGATGAT 360
QY 361 CACAGATTCAGCTTCGGAACAAGACCCCTGCTTGAACCAAGCCATTTGCTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGACCCCTGCTTGAACCAAGCCATTTGCTTGAAGT 420
QY 421 TATTAAGTCTGTGTGTCACAAAAGACACTTATGATGATGATGATGATGATGATGATGAT 480
DB 421 TATTAAGTCTGTGTGTCACAAAAGACACTTATGATGATGATGATGATGATGATGATGAT 480
QY 481 TTGGCCAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 TTGGCCAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 481 TTGGCCAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 TTGGCCAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 GTTCAATGATCTTGAAGATTTGTTGGCTGCAAGCTTCTGTGAAAGAGCACA 600
DB 541 GTTCAATGATCTTGAAGATTTGTTGGCTGCAAGCTTCTGTGAAAGAGCACA 600
QY 601 GGAATAATATATCAATGATCTTGAAGATTTGTTGGCTGCAAGCTTCTGTGAAAGAGCACA 660
DB 601 GGAATAATATATCAATGATCTTGAAGATTTGTTGGCTGCAAGCTTCTGTGAAAGAGCACA 660
QY 601 GGAATAATATATCAATGATCTTGAAGATTTGTTGGCTGCAAGCTTCTGTGAAAGAGCACA 660
DB 601 GGAATAATATATCAATGATCTTGAAGATTTGTTGGCTGCAAGCTTCTGTGAAAGAGCACA 660
QY 661 ACTCAGTACATCTGTGAGTGAAGACAGGTGCACTTGAAGTGAAGTGAATCAAAAG 720
DB 661 ACTCAGTACATCTGTGAGTGAAGACAGGTGCACTTGAAGTGAAGTGAATCAAAAG 720
QY 721 ACCTTGACAGAGCTTGAAGGAAAGAACTTCAATCTTCAATTTGTTTCAAGCAT 780
DB 721 ACCTTGACAGAGCTTGAAGGAAAGAACTTCAATCTTCAATTTGTTTCAAGCAT 780

Db	721	ACCTGTGACAAAGAGCTTCAGGAAGAAACCTTACCTTCAATTCCTCAATTTGGTTTCTAACCAT	780
QY	781	CTACCTCATCTTGAAAGAGAGCAATTAGTGAGACAGAGAAAAATTCAGATGAATATCTG	840
Db	781	CTACCTCATCTTGAAAGAGAGCAATTAGTGAGACAGAGAAAAATTCAGATGAATATCTG	840
QY	841	GTGAACGACAAAGAAAAAGCCCAATCTGATAGATATTTCCCTTTCCTTTGATGAAAGCC	900
Db	841	GTGAACGACAAAGAAAAAGCCCAATCTGATAGATATTTCCCTTTCCTTTGATGAAAGCC	900
QY	901	TGGCTCTGTGTATTAATGAAGGAGATATGTGTGAAAGAAAGACGTGACGTGAATCTACAG	960
Db	901	TGGCTCTGTGTATTAATGAAGGAGATATGTGTGAAAGAAAGACGTGACGTGAATCTACAG	960
QY	961	GGAGGCCATCGAATCCGATCTTGTAGTCTGTGTATGATGAACATTCAAGGTGAATGGTTGG	1020
Db	961	GGAGGCCATCGAATCCGATCTTGTAGTCTGTGTATGATGAACATTCAAGGTGAATGGTTGG	1020
QY	1021	ATCAGAGATTCAGATTCAGATTCAGTTAGTGTGAATTTGAGATTGAATCTCTCGACTCAG	1080
Db	1021	ATCAGAGATTCAGATTCAGATTCAGTTAGTGTGAATTTGAGATTGAATCTCTCGACTCAG	1080
QY	1081	AAGATTATAGCCTTAGTGAGAGAGACAAGAACTCGATGAATGAATGATGATGATATATC	1140
Db	1081	AAGATTATAGCCTTAGTGAGAGAGACAAGAACTCGATGAATGAATGATGATGATATATC	1140
QY	1141	AAGTTACTGTGTATCAGGCAGGGGAGAGTATACAGATTCATTTTGAAGAAATCCTGAAA	1200
Db	1141	AAGTTACTGTGTATCAGGCAGGGGAGAGTATACAGATTCATTTTGAAGAAATCCTGAAA	1200
QY	1201	TTTCCCTTAGCTGACTATTGGAATGACCTTCATGCAATGAAATGAAATCCCCCTTTCAT	1260
Db	1201	TTTCCCTTAGCTGACTATTGGAATGACCTTCATGCAATGAAATGAAATCCCCCTTTCAT	1260
QY	1261	CACANTGGAACAGATGTTGGGCCCTTCGTGGAATTTGGCTTCCTGAATGAAGGAAAG	1320
Db	1261	CACANTGGAACAGATGTTGGGCCCTTCGTGGAATTTGGCTTCCTGAATGAAGGAAAG	1320
QY	1321	ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATCTCAACAACAACCTGAAGAGGCT	1380
Db	1321	ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATCTCAACAACAACCTGAAGAGGCT	1380
QY	1381	TTGATGTTCTCGATTTGTAAAAAAACTATAGTGAATGATTCAGAGAGTCATGTGTTGAG	1440
Db	1381	TTGATGTTCTCGATTTGTAAAAAAACTATAGTGAATGATTCAGAGAGTCATGTGTTGAG	1440
QY	1441	AAATATGATGATTAATTAACAAGCTTCACAATCAACAAGAAAGTGAACATATTTCTCAG	1500
Db	1441	AAATATGATGATTAATTAACAAGCTTCACAATCAACAAGAAAGTGAACATATTTCTCAG	1500
QY	1501	CATCAACTCTAGTATGCAATTTATTTATACAGCCAAAGAAATGTGAAGATTTGAAGAG	1560
Db	1501	CATCAACTCTAGTATGCAATTTATTTATTTATAGACGCAAGAAAGATGTGAAGATTTGAAGAG	1560
QY	1561	AAGAAACCCAAAGACAAAGAGAGTGTGAATCTAGTTTGGCCCTTATATGCAATTTGAAC	1620
Db	1561	AAGAAACCCAAAGACAAAGAGAGTGTGAATCTAGTTTGGCCCTTATATGCAATTTGAAC	1620
QY	1621	CTTGTTGTATTTGTCAAGGTGCACTTAAAAATGTGTGATGTCCATGTGGCAAAACAGAGC	1680
Db	1621	CTTGTTGTATTTGTCAAGGTGCACTTAAAAATGTGTGATGTCCATGTGGCAAAACAGAGC	1680
QY	1681	ATCTTATAGGCTGTCTTCAATGTGCAATGATGTGTCTAATTTCCCTGATTTGACCTGTCTAT	1740
Db	1681	ATCTTATAGGCTGTCTTCAATGTGCAATGATGTGTCTAATTTCCCTGATTTGACCTGTCTAT	1740
QY	1741	TATGTAGACAAACCAATTCAAATGATTTGTCTAATTTATTTCCCTGATTTGACCTGTCTAT	1800
Db	1741	TATGTAGACAAACCAATTCAAATGATTTGTCTAATTTATTTCCCTGATTTGACCTGTCTAT	1800
QY	1801	AAGGAATTAATATATTTCTAATATATATAACCTAGGAATTTTATGACAACTGAATTTATTT	1860
Db	1801	AAGGAATTAATATATTTCTAATATATATAACCTAGGAATTTTATGACAACTGAATTTATTT	1860

QY	1661	TACGATATATCAAAATGAGAAAAATCCCAATTCACATAGAAATTCCTGCTTATATATAT	1920
Db	1661	CACATATATATCAAAATGAGAAAAATCCCAATTCACATAGAAATTCCTGCTTATATATAT	1920
QY	1921	TGACCTTACTTGTGTAGTGAATATGATATCTTATCTTAAATTTGACTTGAAATATGTAGCT	1980
Db	1921	TGACCTTACTTGTGTAGTGAATATGATATCTTATCTTAAATTTGACTTGAAATATGTAGCT	1980
QY	1981	CATCCTTTTACACCAACTCTTAATTTTAAATTAATTTTCTACTCTGTCTTAAATGAGAAATAC	2040
Db	1981	CATCCTTTTACACCAACTCTTAATTTTAAATTAATTTTCTACTCTGTCTTAAATGAGAAATAC	2040
QY	2041	TTGGTTTTTTTTTTCTTAAATATGTATATATGACATTTTAAATGTAACTTATATTTTTTTTG	2100
Db	2041	TTGGTTTTTTTTTTCTTAAATATGTATATATGACATTTTAAATGTAACTTATATTTTTTTTG	2100
QY	2101	AGACGAGTCTGTCTCTGTATACCCAGGCTGAGTGAAGTGAAGTGGTATCTTGGCTCACATGCA	2160
Db	2101	AGACGAGTCTGTCTCTGTATACCCAGGCTGAGTGAAGTGAAGTGGTATCTTGGCTCACATGCA	2160
QY	2161	AGCTCTGACCTCCCCGGGGTTGCAACAAATCTCCGCTCAAGCCTCCCAATTTAGCTTGACC	2220
Db	2161	AGCTCTGACCTCCCCGGGGTTGCAACAAATCTCTCGCTCAAGCCTCCCAATTTAGCTTGACC	2220
QY	2221	TACAGTCATCTGCACCAACACTGGCTAAATTTTTTTTGTACTTTTATGTAGAGACAGGGTTTC	2280
Db	2221	TACAGTCATCTGCACCAACAACCTGGCTAAATTTTTTTTGTACTTTTATGTAGAGACAGGGTTTC	2280
QY	2281	ACCGTGTTTAGCCAGAGATGTCTCTGATCTCTGACCTTGATCCGCCCACTCGGCTCC	2340
Db	2281	ACCGTGTTTAGCCAGAGATGTCTCTGATCTCTGACCTTGATCCGCCCACTCGGCTCC	2340
QY	2341	CAAAAGTCTGGGATTTACAGGCATGAGCACCG	2372
Db	2341	CAAAAGTCTGGGATTTACAGGCATGAGCACCG	2372

RESULT 5
US-08-390-546-2
Sequence 2, Application US/08390546
Patent No. 5606044
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: APPLICATION OF HUMAN MDM2 GENE IN
TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER RELEASABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390.546
FILING DATE: 07-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 11107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-546-2

Query Match 100.0%, Score 2372, DB 2, Length 2372;
Best Local Similarity 100.0%, Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCCGCGAGCTTGGCTCTTCTGGGGCTGTGTGGCTGTGTGGAAAGATGA 60
DB 1 GCACCCGCGAGCTTGGCTCTTCTGGGGCTGTGTGGCTGTGTGGAAAGATGA 60
QY 61 GCAGAAACCCGAGCCGAGGGGGGGCCGGAACCCCTGAGCCGAGATCCGTGCTTGG 120
DB 61 GCAGAAACCCGAGCCGAGGGGGGGCCGGAACCCCTGAGCCGAGATCCGTGCTTGG 120
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DB 121 CAGCCAGAGACACCGTCCCTCCCGGATTAAGTACGAGCCGAGTCCCTGGCCG 180
QY 121 CAGCCAGAGACACCGTCCCTCCCGGATTAAGTACGAGCCGAGTCCCTGGCCG 180
DB 121 CAGCCAGAGACACCGTCCCTCCCGGATTAAGTACGAGCCGAGTCCCTGGCCG 180
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QY 661 ACTCAGTACATCTGTGAGTGAACAGGTGCACTTGAAGGTGGAGATGATCAAAAG 720
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DB 1741 TATGTAGCAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
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Db 1801 AAGAGATTATATATTTCTAATAATTAACCTTAGAATTAGACACCTGAATTTATT 1860
QY 1861 CACATATATCAAGTAGAAGAAAATGCTCAATTCACATAGATTCTTCTCTTAGTAAT 1920
Db 1861 CACATATATCAAGTAGAAGAAAATGCTCAATTCACATAGATTCTTCTCTTAGTAAT 1920
QY 1921 TGAAGTCTTGTGTAGTGAATAGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Db 1921 TGAAGTCTTGTGTAGTGAATAGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
QY 1981 CATCTTTACACCACTCTTAATTTAATTAATTTACTCTCTTTAAATGAAGTAC 2040
Db 1981 CATCTTTACACCACTCTTAATTTAATTAATTTACTCTCTTTAAATGAAGTAC 2040
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Db 2041 TTGGTTTTTTTTTTCTTAATATATATATGACATTAATTAATTAATTTT 2100
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Db 2101 AGACCGAGTCTGCTCTGTTACCCAGCTGAGTGAAGTGAATCTTGCTCACTGCA 2160
QY 2161 AGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
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QY 2221 TACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Db 2221 TACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
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QY 2341 CAAAGTCTGAGATTAAGAGATGAGCCACCG 2372
Db 2341 CAAAGTCTGAGATTAAGAGATGAGCCACCG 2372

RESULT 6
US-08-390-479A-2
Sequence 2, Application US/08390479A
Patent No. 5618921
GENERAL INFORMATION:
APPLICANT: BURRILL, MARLEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,479A
FILING DATE: 02-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,48992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME: 12q12-14
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-479A-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 1 GGAAGCGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
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Db 61 GGAAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 120
QY 121 CAGCAGAGAGCAGCGTCTCCCGGATTAGGCGTACGAGCGGAGCGGAGCGGAGCGGAG 180
Db 121 CAGCAGAGAGCAGCGTCTCCCGGATTAGGCGTACGAGCGGAGCGGAGCGGAGCGGAG 180
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Db 181 GAGAGTGAATATATCCCGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 240
QY 241 AAGGAACTGGGAGATCTTGAAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGG 300
Db 241 AAGGAACTGGGAGATCTTGAAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGG 300
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QY 361 CACAGATTCAGCTTGGGAGCAAGAGACCTGCTGTAAGCAAAAGCCATTTGGAAGT 420
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Db 421 TATTAAGCTGTGTGTGCAAAAAGACCTTATATATATATATATATATATATATATAT 480
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QY 541 GTTCAATGATTTCTTGAAGATTTGTTGGCTGCAAGCTTCTGCTGTAAGAGCACA 600
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Db 601 GGAATAAT 660
QY 661 ACTCAGAT 720
Db 661 ACTCAGAT 720

QY 721 ACCTGTACAGAGCTTCAGAGAGAGAAACCTTCATCTTCACTTTGGTTTCTAGACCAT 780
Db 721 ACCTGTACAGAGCTTCAGAGAGAGAAACCTTCATCTTCACTTTGGTTTCTAGACCAT 780
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Db 781 CTACCTCATCTAGAGAGAGAGCAATTAGTGAACAAGAAATTCAGATGATATATCTG 840
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QY 901 TGAGCTGTGTGTATTAAGAGAGATATGTTGAAGAGAGAGTACAGATGATATACAG 960
Db 901 TGAGCTGTGTGTATTAAGAGAGATATGTTGAAGAGAGAGTACAGATGATATACAG 960
QY 961 GGAAGCCATCGAATCCGATCTTGATGCTGTGTGAAGTGAACATTCAGGTGATGTTGG 1020
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QY 1201 TTTCCCTTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
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QY 1261 CACATTGCAACAGATGTTGGGCTTCTGTGAAGATTTGGCTTCTGAAGATTAAGAGAG 1320
Db 1261 CACATTGCAACAGATGTTGGGCTTCTGTGAAGATTTGGCTTCTGAAGATTAAGAGAG 1320
QY 1321 ATTAAGGGGAGATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 ATTAAGGGGAGATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 TTGATGTTCTGATGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 TTGATGTTCTGATGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 AAAATGATGATTAATTAACAAGAGTTCACATCAACAAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 AAAATGATGATTAATTAACAAGAGTTCACATCAACAAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 CATCACTTCTAGTGAAG 1560
Db 1501 CATCACTTCTAGTGAAG 1560
QY 1561 AAGAAACCCAG 1620
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QY 1621 CTGTGTGTGATTTGTCAAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 1621 CTGTGTGTGATTTGTCAAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 ATCTTATGAGCTGCTTATCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
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QY 1741 TATGTAGCAACCAATTCAG 1800
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Db 1801 AAGAGATTAATTAATTTCTAATATTAACCTAGAGATTTAGACAACTGAATTTATTT 1860
QY 1861 CACATATATCAAG 1920
Db 1861 CACATATATCAAG 1920
QY 1921 TGACCTACTTGTGTAG 1980
Db 1921 TGACCTACTTGTGTAG 1980
QY 1981 CATCTTTACACCACTCTAATTTTAATTTTCTAATTTTCTAATTTTCTAATTTTCTAAT 2040
Db 1981 CATCTTTACACCACTCTAATTTTAAATTTTCTAATTTTCTAATTTTCTAATTTTCTAAT 2040
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Db 2041 TTGTTTTTTTTTTCTTAAAT 2100
QY 2101 AGACGAGTCTGTGCTGTGTACCAAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
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QY 2161 AGCTGTGCTTCTGCTCTGTGTACCAAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
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RESULT 7
US-08-557-393-2
; Sequence 2, Application US/08557393
; Patent No. 5702903
; GENERAL INFORMATION:
; APPLICANT: BURELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDX2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,500
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 HBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-557-393-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTCTTCTGGGCGCTGTGTGCGCTGTGTGTGCGAAAGATGGA 60
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DB 781 CTACCTCATCTTGAAAGAGAGCAATTAATGAGACAGAAAGAAATTCAGATTAATTCG 840
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DB 841 GTGAAGCAAAAGAAAGCCCAAAATCGATGATATTCCTTCCCTTCTTGAAGAGCC 900
QY 901 TGGCTCTGTGTGTAATGAAGAGATATGTTGTGAAGAGAGAGTGTGAGTGTGATCTACAG 960
DB 901 TGGCTCTGTGTGTAATGAAGAGATATGTTGTGAAGAGAGAGTGTGAGTGTGATCTACAG 960
QY 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTGTGTAAGTGAACATTCAGGTATGCTGG 1020
DB 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTGTGTAAGTGAACATTCAGGTATGCTGG 1020
QY 1021 ATCAGGATTCAGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 ATCAGGATTCAGTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AAGATTATAGCTTGTGTGAGAGAGCAAGAACTCTCAGATGAAGTGTGAGTGTATATC 1140
DB 1081 AAGATTATAGCTTGTGTGAGAGAGCAAGAACTCTCAGATGAAGTGTGAGTGTATATC 1140
QY 1141 AAGTTACTGTGTATCAGGAGGAGAGTGTATCAGATTCATTGTAAGAAATCTCTGAAA 1200
DB 1141 AAGTTACTGTGTATCAGGAGGAGAGTGTATCAGATTCATTGTAAGAAATCTCTGAAA 1200
QY 1201 TTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 TTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 CACATTGCAACAGATGTTGGGCTTCTGTGAGAAATGCGTTCCTGTGAGATTAAGAGGAAAG 1320
DB 1261 CACATTGCAACAGATGTTGGGCTTCTGTGAGAAATGCGTTCCTGTGAGATTAAGAGGAAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCAACCTGAAACCTCAACAGCTGAAGAGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCAACCTGAAACCTCAACAGCTGAAGAGGCT 1380
QY 1381 TTGATGTTCTGTATGTTGTAAGAAACCTATAGTGAATGATTCAGAGAGTCAATGTGTTGAG 1440
DB 1381 TTGATGTTCTGTATGTTGTAAGAAACCTATAGTGAATGATTCAGAGAGTCAATGTGTTGAG 1440
QY 1441 AAAATGATGATTAATTAACAAGGCTTCAACATCAAGAAAGTGAAGCTATTCACAG 1500
DB 1441 AAAATGATGATTAATTAACAAGGCTTCAACATCAAGAAAGTGAAGCTATTCACAG 1500
QY 1501 CATCACTTCTAGTGAATTAATTAATGAGAGCAAGAGATGTAAGAGTGTGAAGG 1560
DB 1501 CATCACTTCTAGTGAATTAATTAATGAGAGCAAGAGATGTAAGAGTGTGAAGG 1560
QY 1561 AAGAAACCCAGAGCAAGAGAGAGTGTGAATCTAGTGTGCTTGAATGCAATTGAAC 1620
DB 1561 AAGAAACCCAGAGCAAGAGAGAGTGTGAATCTAGTGTGCTTGAATGCAATTGAAC 1620
QY 1621 CTGTGTGATTTGTCAAGGTGCACTTAATAAATGTTGCTATTCATGCAAGCAAGAGC 1680
DB 1621 CTGTGTGATTTGTCAAGGTGCACTTAATAAATGTTGCTATTCATGCAAGCAAGAGC 1680
QY 1681 ATCTTATGAGCTGCTTATCAATGTGCAAGAGAGCTTAAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 ATCTTATGAGCTGCTTATCAATGTGCAAGAGAGCTTAAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 TATGTAGCAACCAATTCAAATGATGTTGTGCTAATTAATTTCCCTAGTGTGAGCTGTAT 1800

|||||
Db 1741 TATGAGCAACCAATTCAAATGATGTGCTAACTTATTTCCCTAGTGAACCTGTAT 1800
Qy 1801 AAGGAATATATATTTTAACTATATTAACCTAGGAATTTAGAACCTGAATTTAT 1860
Db 1801 AAGGAATATATATTTTAACTATATTAACCTAGGAATTTAGAACCTGAATTTAT 1860
Qy 1861 CACATATATCAAGAGAGAAAATGCTCAATTCACATGATTTCTCTTTAGATAT 1920
Db 1861 CACATATATCAAGAGAGAAAATGCTCAATTCACATGATTTCTCTTTAGATAT 1920
Qy 1921 TGACCTACTTTGATGGAATAGTAATTAATTAATTTGAATTTGAATTTAGT 1980
Db 1921 TGACCTACTTTGATGGAATAGTAATTAATTAATTTGAATTTGAATTTAGT 1980
Qy 1981 CATCTTTACCAACACTCTTAATTTAAATATTTCTCTCTGCTTAAAGAGATAC 2040
Db 1981 CATCTTTACCAACACTCTTAATTTAAATATTTCTCTCTGCTTAAAGAGATAC 2040
Qy 2041 TTGGTTTTTTTTTCTTAATATATATATGACATTTAATGTAATTTAATTTT 2100
Db 2041 TTGGTTTTTTTTTCTTAATATATATATGACATTTAATGTAATTTAATTTT 2100
Qy 2101 AGACCGAGTCTTGTCTGTATACCAAGCTGAGTGAAGTGAATTTGGCTCACTGCA 2160
Db 2101 AGACCGAGTCTTGTCTGTATACCAAGCTGAGTGAAGTGAATTTGGCTCACTGCA 2160
Qy 2161 AGCTTGCCCTCCCGGGGTGGACATTTCTCTGCTCAAGCTCCCAATAGCTTGCC 2220
Db 2161 AGCTTGCCCTCCCGGGGTGGACATTTCTCTGCTCAAGCTCCCAATAGCTTGCC 2220
Qy 2221 TACAGTATCTGCGCACACACCTGCTAATTTTGTACTTTAGTAGAGAGGGTTTC 2280
Db 2221 TACAGTATCTGCGCACACACCTGCTAATTTTGTACTTTAGTAGAGAGGGTTTC 2280
Qy 2281 ACCGTGTAGCCAGGATGCTGATCTTCCTGACCTCGGATCCGCCCTGCTTC 2340
Db 2281 ACCGTGTAGCCAGGATGCTGATCTTCCTGACCTCGGATCCGCCCTGCTTC 2340
Qy 2341 CAAAGTCTGGGATTAACAGGATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTAACAGGATGAGCCACCG 2372

RESULT 8
US-08-390-516C-2
Sequence 2, Application US/08390516C
Patent No. 5708136
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,516C
FILING DATE: 07-APR-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMBB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-516C-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCACCGCGCAGCTTGGCTTCTGGGGCTGTGTGGCCCTGTGTGCGAAGATGGA 60
Db 1 GCACCGCGCAGCTTGGCTTCTGGGGCTGTGTGGCCCTGTGTGCGAAGATGGA 60
Qy 61 GCAGAACCCGAGCCGAGGGGCGGCGCCGACCCCTCTGACCGGATCTCTGCTTTCG 120
Db 61 GCAGAACCCGAGCCGAGGGGCGGCGCCGACCCCTCTGACCGGATCTCTGCTTTCG 120
Qy 121 CAGCGAGGAGCAGCTCCCTCCCGGATTAAGTGGTACGAGGCGCCAGTGCCTTGGCCG 180
Db 121 CAGCGAGGAGCAGCTCCCTCCCGGATTAAGTGGTACGAGGCGCCAGTGCCTTGGCCG 180
Qy 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGTGCTTCCGACGATGATGCTCCGCTG 240
Db 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGTGCTTCCGACGATGATGCTCCGCTG 240
Qy 241 AAGGAACTGGGAGCTCTTGAAGGAGCCCGCACTTCAAGCGCGAAACCCCGATGTGA 300
Db 241 AAGGAACTGGGAGCTCTTGAAGGAGCCCGCACTTCAAGCGCGAAACCCCGATGTGA 300
Qy 301 GGAGCAGGCAATGTCATACCAATCATGTCTGTACTACTGATGCTGTAAACCACT 360
Db 301 GGAGCAGGCAATGTCATACCAATCATGTCTGTACTACTGATGCTGTAAACCACT 360
Qy 361 CACAGATTCGAGCTTGGAGCAAGAGACCTGTTGACCAAGCATTTGTTGAAGT 420
Db 361 CACAGATTCGAGCTTGGAGCAAGAGACCTGTTGACCAAGCATTTGTTGAAGT 420
Qy 421 TATTAAAGTCTGTTGTGTCACAAAAGACACTTAATACATGAAAGAGTCTTTTATTC 480
Db 421 TATTAAAGTCTGTTGTGTCACAAAAGACACTTAATACATGAAAGAGTCTTTTATTC 480
Qy 481 TTGGCAGATATATATGCTAAAGATATATATGATGAGAGCAACAATATTTATAT 540
Db 481 TTGGCAGATATATATGCTAAAGATATATATGATGAGAGCAACAATATTTATAT 540
Qy 541 GTTCAATGATCTTCTAGAGATTTGTTGGGTCGCAAGCTTCTCTGTAAGAGACA 600
Db 541 GTTCAATGATCTTCTAGAGATTTGTTGGGTCGCAAGCTTCTCTGTAAGAGACA 600
Qy 601 GGAATAATATATCATGATCTACAGAACTTGATGTATGATCATGACAGGATCATCGG 660
Db 601 GGAATAATATATCATGATCTACAGAACTTGATGTATGATCATGACAGGATCATCGG 660

ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELE: 197430 HBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-517A-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCGTGTGGGCCCTGTGTGTCGAGAAAGATGA 60
DB 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCGTGTGTGCTGTGTGTGCGAAAGATGA 60
QY 61 GCAGAAACCCGAGCCGAGGGGCGGCGGACCCCTGACCCGAGATCCTGTGCTTTG 120
DB 61 GCAGAAACCCGAGCCGAGGGGCGGCGGACCCCTGACCCGAGATCCTGTGCTTTG 120
QY 121 CAGCCAGAGACCCCTCCCTCCCGGATTAATGTGCTGAGAGGCCGACGCTGCTGACCG 180
DB 121 CAGCCAGAGACCCCTCCCTCCCGGATTAATGTGCTGAGAGGCCGACGCTGCTGACCG 180
QY 181 GAGAGTGAATGATCCCGAGGGCCGAGGGCGTGTGCTTCCGAGTGAATGATCCCGG 240
DB 181 GAGAGTGAATGATCCCGAGGGCCGAGGGCGTGTGCTTCCGAGTGAATGATCCCGG 240
QY 241 AAGAAACCTGGGAGTCTTGAAGGACCCCGACCTCCAGCGGAAACCCCGGATGTGA 300
DB 241 AAGAAACCTGGGAGTCTTGAAGGACCCCGACCTCCAGCGGAAACCCCGGATGTGA 300
QY 301 GGAGAGGCAAAATGTGCAATACCAATGTGTGTACTTACTGATGATGATGCTTGAACCT 360
DB 301 GGAGAGGCAAAATGTGCAATACCAATGTGTGTACTTACTGATGATGATGCTTGAACCT 360
QY 361 CACAGATTCACACTTCGAGCAAGAGACCTGTGTAGACCAAGGACATGCTTTGAAGT 420
DB 361 CACAGATTCACACTTCGAGCAAGAGACCTGTGTAGACCAAGGACATGCTTTGAAGT 420
QY 421 TATTAAGCTGTGGTGCACAAAAGACACTTATCTATGAAGAAGTCTTTTATATC 480
DB 421 TATTAAGCTGTGGTGCACAAAAGACACTTATCTATGAAGAAGTCTTTTATATC 480
QY 481 TTGGCCAGTAATATATGACTAAACGATTATATGATGAGAGCAACAATATTATAT 540
DB 481 TTGGCCAGTAATATATGACTAAACGATTATATGATGAGAGCAACAATATTATAT 540
QY 541 GTTCAATATCTTCTAGAGAGATTTTGGGTGCAAGCTTCTGTGAAGAAGACACA 600
DB 541 GTTCAATATCTTCTAGAGAGATTTTGGGTGCAAGCTTCTGTGAAGAAGACACA 600
QY 601 GGAATAATATACATGATCTACAGAACTTGTGTAAGTCAATCAGCAGAAATCATCG 660
DB 601 GGAATAATATACATGATCTACAGAACTTGTGTAAGTCAATCAGCAGAAATCATCG 660

DB 601 GGAATAATATACATGATCTACAGAACTTGTGTAAGTCAATCAGCAGAAATCATCG 660
QY 661 ACTCAGGATCATCTGTGAGTGAAGACAGTGTCACTTGAAGGTGGAGTATCAAAAG 720
DB 661 ACTCAGGATCATCTGTGAGTGAAGACAGTGTCACTTGAAGGTGGAGTATCAAAAG 720
QY 721 ACCTTGTACAAAGACCTTCAGAGAGAAACCTTCATCTTCAATTTGGTTCAGACCAT 780
DB 721 ACCTTGTACAAAGACCTTCAGAGAGAAACCTTCATCTTCAATTTGGTTCAGACCAT 780
QY 781 CTACCTCATCTAGAGAGAGACATTTAGTGAAGAGAAAGAAATTCAGATCAATATCTG 840
DB 781 CTACCTCATCTAGAGAGAGACATTTAGTGAAGAGAAAGAAATTCAGATCAATATCTG 840
QY 841 GTGAACGCAAAAGAAAAGCCCAATCTGATATTTCCCTTCTCTTGTGATAAGCC 900
DB 841 GTGAACGCAAAAGAAAAGCCCAATCTGATATTTCCCTTCTCTTGTGATAAGCC 900
QY 901 TGGCTGTGTGTATATAGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
DB 901 TGGCTGTGTGTATATAGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
QY 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTGAAGACATTCAGGTGATGCTGG 1020
DB 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTGAAGACATTCAGGTGATGCTGG 1020
QY 1021 ATCAGATTCAGTTAGTATGATCAGTTTATGATGATTTGAAGTGAATCTCTGACTGAG 1080
DB 1021 ATCAGATTCAGTTAGTATGATCAGTTTATGATGATTTGAAGTGAATCTCTGACTGAG 1080
QY 1081 AAGATTATAGCTTATAGTGAAGAGACAAAGACTCTCAGATGAAGATGATGATATATC 1140
DB 1081 AAGATTATAGCTTATAGTGAAGAGACAAAGACTCTCAGATGAAGATGATGATATATC 1140
QY 1141 AAGTACTGTGTATCAGGACAGGAGAGATGATCAAGATTCATTGGAAGAAATCCTGAA 1200
DB 1141 AAGTACTGTGTATCAGGACAGGAGAGATGATCAAGATTCATTGGAAGAAATCCTGAA 1200
QY 1201 TTTCTTACGATGATTTGAAGATGACCTTCATGCAATGAATGAATCCCTCCAT 1260
DB 1201 TTTCTTACGATGATTTGAAGATGACCTTCATGCAATGAATGAATCCCTCCAT 1260
QY 1261 CACATTGCAAGATGTTGGCCCTTCGTGAGAAATGGCTTCTGAAATAAAGGAAAG 1320
DB 1261 CACATTGCAAGATGTTGGCCCTTCGTGAGAAATGGCTTCTGAAATAAAGGAAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACACACTGAAGGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACACACTGAAGGGCT 1380
QY 1381 TTGATGTTCTGATTTGTAAGAACTATATGATGATGATTTCCAGAGAGTCAATGTGTAAG 1440
DB 1381 TTGATGTTCTGATTTGTAAGAACTATATGATGATGATTTCCAGAGAGTCAATGTGTAAG 1440
QY 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAAAGTGAAGCTATTTCTGAC 1500
DB 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAAAGTGAAGCTATTTCTGAC 1500
QY 1501 CATCAACTTCTAGTGAATTTATTTATGACAGCAAGAAAGATGTGAAGGTTTGAAGGG 1560
DB 1501 CATCAACTTCTAGTGAATTTATTTATGACAGCAAGAAAGATGTGAAGGTTTGAAGGG 1560
QY 1561 AAGAAACCAAGAGCAAGAAAGAGATGTGAATCTAGTTGGCCCTTAATGCAATTAAC 1620
DB 1561 AAGAAACCAAGAGCAAGAAAGAGATGTGAATCTAGTTGGCCCTTAATGCAATTAAC 1620
QY 1621 CTTGTGTATTTGTCAAGGTGCACTTAATAATGTTGCAATGTCAGCAAAACAGAC 1680
DB 1621 CTTGTGTATTTGTCAAGGTGCACTTAATAATGTTGCAATGTCAGCAAAACAGAC 1680
QY 1681 ATCTTATGGCTGCTTTATCATGTGCAAGAGCTTAAGAAAGAAATTAAGCCCTCCAG 1740
DB 1681 ATCTTATGGCTGCTTTATCATGTGCAAGAGCTTAAGAAAGAAATTAAGCCCTCCAG 1740

QY 1741 TATGAGACAACTTCAATGATGCTAACTTATTTCCCTAGTGTGCTGCTAT 1800
DB 1741 TATGAGACAACTTCAATGATGCTAACTTATTTCCCTAGTGTGCTGCTAT 1800
QY 1801 AAGAGATATATATTTCTAATATATACCTAGGAATTTAGACAACTGAAATTTAT 1860
DB 1801 AAGAGATATATATTTCTAATATATACCTAGGAATTTAGACAACTGAAATTTAT 1860
QY 1861 CACATATATCAAGGAGAAATGCTCAATTCACATATATTTCTTCTTTAGATAT 1920
DB 1861 CACATATATCAAGGAGAAATGCTCAATTCACATATATTTCTTCTTTAGATAT 1920
QY 1921 TGACCTACTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
DB 1921 TGACCTACTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 CATCTTTACCACTCTTAATTTTAAATTTTCTACTGCTCTTAAATGAGAGTAC 2040
DB 1981 CATCTTTACCACTCTTAATTTTAAATTTTCTACTGCTCTTAAATGAGAGTAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATATGATATGATGATGATGATGATGATGATGAT 2100
DB 2041 TTGGTTTTTTTTTTCTTAATATGATATGATGATGATGATGATGATGATGAT 2100
QY 2101 AGACCGAGTCTGCTGTGTTACCCGAGGCTGAGTGAGTGAGTGAGTGAGTGAG 2160
DB 2101 AGACCGAGTCTGCTGTGTTACCCGAGGCTGAGTGAGTGAGTGAGTGAGTGAG 2160
QY 2161 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
DB 2161 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
QY 2221 TACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
DB 2221 TACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
QY 2281 ACCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
DB 2281 ACCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
QY 2341 CAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2372
DB 2341 CAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2372

RESULT 10
US-08-390-515A-2
Sequence 2, Application US/08390515A
Parent No. 5756455
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDN2 GENE IN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,515A
FILING DATE: 07-APR-1993

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-515A-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTGCTTCTGCGGCGCTGTGTGCTGTGTGCGAAAGATGCA 60
DB 1 GCACCGCGGAGCTTGGCTGCTTCTGCGGCGCTGTGTGCTGTGTGCGAAAGATGCA 60
QY 61 GCAAGAGCGGAGCGCGGAGGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 120
DB 61 GCAAGAGCGGAGCGCGGAGGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 120
QY 121 CAGCCAGAGGACCGTCCCTCCCGGATTAAGCTACGAGCGCCAGTGCCTGCGCCG 180
DB 121 CAGCCAGAGGACCGTCCCTCCCGGATTAAGCTACGAGCGCCAGTGCCTGCGCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGGTGTGCTTCCGACAGTCACTGCTCC 240
DB 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGGTGTGCTTCCGACAGTCACTGCTCC 240
QY 241 AAGGAACTGGGGAGCTTTGAGGGACCCCGGACTCCAGCGGAAACCCCGGATGTGA 300
DB 241 AAGGAACTGGGGAGCTTTGAGGGACCCCGGACTCCAGCGGAAACCCCGGATGTGA 300
QY 301 GGAGCAGGCAATGCAATACCAATGCTGTGTACTGATGAGTGTGCTGTAACCACT 360
DB 301 GGAGCAGGCAATGCAATACCAATGCTGTGTACTGATGAGTGTGCTGTAACCACT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGACCTGCTGTTAGACCAAGGCACTTGTGTAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCTGCTGTTAGACCAAGGCACTTGTGTAAGT 420
QY 421 TATTAAAGTCTGTTGTGCACAAAAAGACCTTATATGATGAAAGGTTCTTTTATATC 480
DB 421 TATTAAAGTCTGTTGTGCACAAAAAGACCTTATATGATGAAAGGTTCTTTTATATC 480
QY 481 TTGGCAGATATATATGACTAAACGATATATGATGAGAGCAACAATATGATATAT 540
DB 481 TTGGCAGATATATATGACTAAACGATATATGATGAGAGCAACAATATGATATAT 540
QY 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGTGCACAACTTCTGTGAAAGAGACA 600
DB 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGTGCACAACTTCTGTGAAAGAGACA 600
QY 601 GGAAATATATACCATGATCTACAGGAACCTTGATGATGATGATGATGATGATGAT 660

Db 601 GGAATAATATATACATGATCTACAGAACTTGATGATGATCATCAGAGAAATCATGG 660
Qy 661 ACTGAGGTACATCTGTGAGTGAAGACAGGTGTCACTTGAAAGTGGAGTATCAAAAG 720
Db 661 ACTGAGGTACATCTGTGAGTGAAGACAGGTGTCACTTGAAAGTGGAGTATCAAAAG 720
Qy 721 ACCGTGATCAAGAGCTTCAGAGAGAAACCTTCATCTTCACATTTGGTTCTGACCAT 780
Db 721 ACCGTGATCAAGAGCTTCAGAGAGAAACCTTCATCTTCACATTTGGTTCTGACCAT 780
Qy 781 CTACCTCATCTAGAGAGAGCAATTTAGTGAACAAGAAATTCAGATGATTTATCTG 840
Db 781 CTACCTCATCTAGAGAGAGCAATTTAGTGAACAAGAAATTCAGATGATTTATCTG 840
Qy 841 GTGAACGCAAAAGAAAGCCCAAAATCTGATGATTTCCCTTCCTTTGATGAAAGC 900
Db 841 GTGAACGCAAAAGAAAGCCCAAAATCTGATGATTTCCCTTCCTTTGATGAAAGC 900
Qy 901 TGGCTCTGTGTATTAAGAGATGATGTAAGAGAGAGTACAGTGAATCTAG 960
Db 901 TGGCTCTGTGTATTAAGAGATGATGTAAGAGAGAGTACAGTGAATCTAG 960
Qy 961 GGAGCCCATCGAATCCGATCTTGATGCTGTGTAGTGAACATTCAGGTGATGGTTGG 1020
Db 961 GGAGCCCATCGAATCCGATCTTGATGCTGTGTAGTGAACATTCAGGTGATGGTTGG 1020
Qy 1021 ATCAGATTCAGTTTCAATCAGTCACTTTAGTGAATTTGAAGTGAATCTCCAGCTAG 1080
Db 1021 ATCAGATTCAGTTTCAATCAGTCACTTTAGTGAATTTGAAGTGAATCTCCAGCTAG 1080
Qy 1081 AAGATTAAGCTTATGTAAGAGAGCAAGAACTTCAGATGAAGATGATGATATC 1140
Db 1081 AAGATTAAGCTTATGTAAGAGAGCAAGAACTTCAGATGAAGATGATGATATC 1140
Qy 1141 AAGTACTGTGTATCAGAGAGAGAGTGAATCAGATTCATTTGAAGAGATCCTGAA 1200
Db 1141 AAGTACTGTGTATCAGAGAGAGAGTGAATCAGATTCATTTGAAGAGATCCTGAA 1200
Qy 1201 TTTCTTACTGATCTATTTGAAGATCACTTCATGCAATGAATGAATCCCTTCAT 1260
Db 1201 TTTCTTACTGATCTATTTGAAGATCACTTCATGCAATGAATGAATCCCTTCAT 1260
Qy 1261 CACATTTGAAGAGATTTGGGCTTCGTAAGATTTGGTCTCTGAAGTAAAGGAAAG 1320
Db 1261 CACATTTGAAGAGATTTGGGCTTCGTAAGATTTGGTCTCTGAAGTAAAGGAAAG 1320
Qy 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATCAACAGCTGAGAGGCT 1380
Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATCAACAGCTGAGAGGCT 1380
Qy 1381 TTGATGTTCTGATTTGTAATAAACTATATGATGATTTCCAGAGATCATGTGTTGAG 1440
Db 1381 TTGATGTTCTGATTTGTAATAAACTATATGATGATTTCCAGAGATCATGTGTTGAG 1440
Qy 1441 AAAATGATGATTAATTTCAAGAGTTCATCAAGAAAGTGAAGCTATTCACG 1500
Db 1441 AAAATGATGATTAATTTCAAGAGTTCATCAAGAAAGTGAAGCTATTCACG 1500
Qy 1501 CATCACTTCTAGTGAATTTATTTATAGCAGCAAGAGATGGAAGGTTGAAAGG 1560
Db 1501 CATCACTTCTAGTGAATTTATTTATAGCAGCAAGAGATGGAAGGTTGAAAGG 1560
Qy 1561 AAGAAACCCAGACAAAGAGAGAGTGTGAATCTAGTTGCTTAAATGCAATTGAAC 1620
Db 1561 AAGAAACCCAGACAAAGAGAGAGTGTGAATCTAGTTGCTTAAATGCAATTGAAC 1620
Qy 1621 CTGTGTATTTGTCAAGGTGCACTTAAATGTTGCTGATTCATGCAAAACAGGAC 1680
Db 1621 CTGTGTATTTGTCAAGGTGCACTTAAATGTTGCTGATTCATGCAAAACAGGAC 1680
Qy 1681 ATCTTATGGCTGCTTTATCATGTGCAAAAGCTAAAGAAAGATAGCCCTGCGCAG 1740

Db 1681 ATCTTATGGCTGCTTTATCATGTGCAAAAGACTTAAAGAAATAGCCCTGCGCAG 1740
Qy 1741 TATGTACACAACCAATCAATGATTTGCTAACTTATTTCCCTAGTGAATGCTAT 1800
Db 1741 TATGTACACAACCAATCAATGATTTGCTAACTTATTTCCCTAGTGAATGCTAT 1800
Qy 1801 AAGAAATTAATATTTCTAATATATGATTAACCTTAGAATTTAGCAACCTGAAATTTAT 1860
Db 1801 AAGAAATTAATATTTCTAATATATGATTAACCTTAGAATTTAGCAACCTGAAATTTAT 1860
Qy 1861 CACATATATCAAGTGAAGAAATGCTCAATTCATGATTTCTCTTATGATTAAT 1920
Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTCATGATTTCTCTTATGATTAAT 1920
Qy 1921 TGACCTACTTGTGATGAGAAATGATGATTTACTTATATTTGATGATGATGAT 1980
Db 1921 TGACCTACTTGTGATGAGAAATGATGATTTACTTATATTTGATGATGATGAT 1980
Qy 1981 CATCTTTACACAACCTCTAATTTTAAATTAATTTTACTCTGTCTTAAATGAGAGTAC 2040
Db 1981 CATCTTTACACAACCTCTAATTTTAAATTAATTTTACTCTGTCTTAAATGAGAGTAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAATATGATGATGATGATTTAAATTTTATTTTATTTT 2100
Db 2041 TTGGTTTTTTTTTTCTTAATATGATGATGATGATTTAAATTTTATTTTATTTT 2100
Qy 2101 AGACGAGCTCTGCTGTTATCCAGGCTGAGAGTGAAGTGGTATCTTGCTCACTGCA 2160
Db 2101 AGACGAGCTCTGCTGTTATCCAGGCTGAGAGTGAAGTGGTATCTTGCTCACTGCA 2160
Qy 2161 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Db 2161 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Qy 2221 TACAGTATCTGCAACACACCTGCTAATTTTGTATCTTTAGTGAAGACAGGTTTC 2280
Db 2221 TACAGTATCTGCAACACACCTGCTAATTTTGTATCTTTAGTGAAGACAGGTTTC 2280
Qy 2281 ACCGTGTAAGCAGAGATGCTGATCTGACCTGCTGATTCGCGCCACCTCGGCTCC 2340
Db 2281 ACCGTGTAAGCAGAGATGCTGATCTGACCTGCTGATTCGCGCCACCTCGGCTCC 2340
Qy 2341 CAAAGTCTGGGATTTACAGCATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTTACAGCATGAGCCACCG 2372

RESULT 11
US-08-801-718-2
; Sequence 2, Application US/08801718
; Patent No. 5858976
; GENERAL INFORMATION:
; APPLICANT: BURELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDN2 GENE IN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,718


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1      FILING DATE: 14-FEB-1997
2      CLASSIFICATION: 514
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: 08/390,515
5      FILING DATE: 07-APR-1993
6      ATTORNEY/AGENT INFORMATION:
7      NAME: KAGAN, SARAH A.
8      REGISTRATION NUMBER: 32,141
9      REFERENCE/DOCKET NUMBER: 01107,42798
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: 202-508-9100
12     TELEFAX: 202-508-9299
13     TELE: 197430 BMBB UT
14     INFORMATION FOR SEQ ID NO: 2:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH: 2372 base pairs
17     TYPE: nucleic acid
18     STRANDEDNESS: double
19     TOPOLOGY: linear
20     MOLECULE TYPE: cDNA
21     HYPOTHEetical: NO
22     ANTI-SENSE: NO
23     ORIGINAL SOURCE:
24     ORGANISM: Homo sapiens
25     CELL LINE: CaCo-2
26     POSITION IN GENOME:
27     MAP POSITION: 12q12-14
28     FEATURE:
29     NAME/KEY: CDS
30     LOCATION: 312..1784
31     OS-08-801-718-2

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QY 721 ACCCTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACATTTGGTTCTAGACCAT 780
DB 721 ACCCTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACATTTGGTTCTAGACCAT 780
QY 781 CTACCTCATCTTAAAGAGAGCAATTAAGTGAAGAGAAATTCAGATGAATTAATCTG 840
DB 781 CTACCTCATCTTAAAGAGAGCAATTAAGTGAAGAGAAATTCAGATGAATTAATCTG 840
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DB 841 GTGAAGAGCAAAAGAAACCCCAATCTGATAGTATTTCCCTTCTTGTGAAGAAAGCC 900
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DB 961 GGAAGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATGGTTGG 1020
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DB 1141 AAGTTATCTGTATCAAGAGAGGAGAGTATCAGATTCATTTGAAGAAATCTCTGAAA 1200
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QY 1261 CACATTGCAACAGATGTGGGCTTCGAGAAATTTGGTCTCTGAGATTAAGAAAGAAAG 1320
DB 1261 CACATTGCAACAGATGTGGGCTTCGAGAAATTTGGTCTCTGAGATTAAGAAAGAAAG 1320
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DB 1441 AAAATGATATTAATTAACAAGCTTCACATCAACAAGAGTGAAGCTATTTCCAGC 1500
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QY 1741 TATGTAGACCAACCAATTCAAATGATTTGCTAACTTAATTTCCCTGATTTGACCTGTCTAT 1800
DB 1741 TATGTAGACCAACCAATTCAAATGATTTGCTAACTTAATTTCCCTGATTTGACCTGTCTAT 1800

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DB 1801 AAGAGATTAATATATTTCTAATATTAACCTTAGAAATTTAGACAACTGAATTAAT 1860
QY 1861 CACATATATCAAGTGAAGAAATGCTCAATTCATATGATTTCTTCTTTAGTAAAT 1920
DB 1861 CACATATATCAAGTGAAGAAATGCTCAATTCATATGATTTCTTCTTTAGTAAAT 1920
QY 1921 TGACCTACTTTGGTATGGAATATGTAATTAATTAATTTGACTGATATATGAGCT 1980
DB 1921 TGACCTACTTTGGTATGGAATATGTAATTAATTAATTTGACTGATATATGAGCT 1980
QY 1981 CATCTTTACCAACCACTCCAAATTTAAATTAATTTACTGCTCTTAATGAGAGTAC 2040
DB 1981 CATCTTTACCAACCACTCCAAATTTAAATTAATTTACTGCTCTTAATGAGAGTAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATAATATATATATGATTAATTAATTAATTTTGG 2100
DB 2041 TTGGTTTTTTTTTTCTTAATAATATATATATGATTAATTAATTAATTTTGG 2100
QY 2101 AGACGAGCTTGTCTGTTTACCAGGCTGAGAGTGAAGTGAATCTTGGCTCACTGCA 2160
DB 2101 AGACGAGCTTGTCTGTTTACCAGGCTGAGAGTGAAGTGAATCTTGGCTCACTGCA 2160
QY 2161 AGCTGAGCTTCCCGGGTTGCGACCATCTCTGCTCAGCCTCCCAATTAAGTTGGCC 2220
DB 2161 AGCTGAGCTTCCCGGGTTGCGACCATCTCTGCTCAGCCTCCCAATTAAGTTGGCC 2220
QY 2221 TACAGTATCTGCAACCAACCACTGCTAATTTTGTATCTTTAGTAGAGACAGGTTTC 2280
DB 2221 TACAGTATCTGCAACCAACCACTGCTAATTTTGTATCTTTAGTAGAGACAGGTTTC 2280
QY 2281 ACCGTGTAGCCAGATGCTGATCTGATCTCTGACCTGATCCGATCCGCTCC 2340
DB 2281 ACCGTGTAGCCAGATGCTGATCTGATCTCTGACCTGATCCGATCCGCTCC 2340
QY 2341 CAAAGTGTGGATTAACAGGCAATGAGCCAGC 2372
DB 2341 CAAAGTGTGGATTAACAGGCAATGAGCCAGC 2372

RESULT 13
US-09-280-805-1
Sequence 1, Application US/09280805
Patent No. 6184212
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDN2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,805
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/048,810
FILING DATE: March 26, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
ANTI-SENSE: No
PUBLICATION INFORMATION:
AUTHORS: Oliner, J.D.
AUTHORS: Kinzler, K.W.
AUTHORS: Melzer, P.S.
AUTHORS: George, D.L.
AUTHORS: Vogelstein, B.
TITLE: Amplification of a gene encoding a
p53-associated protein in human sarcomas
JOURNAL: Nature
VOLUME: 358
ISSUE: 6381
PAGES: 80-83
DATE: 02-JUL-1992
US-09-280-805-1

Query Match 100.0%; Score 2372; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2372; Conservative 0;

QY 1 GCACCCGCGAGCTTGGCTTCTGGGCGCTGTGTGCGCTGTGTGCGAAAGATGGA 60
DB 1 GCACCCGCGAGCTTGGCTTCTGGGCGCTGTGTGCGCTGTGTGCGAAAGATGGA 60
QY 61 GCAAGAACCCGAGCCCGAGGCGCGCGGACCCCTCTGACCGAGATCTCTGCTTGG 120
DB 61 GCAAGAACCCGAGCCCGAGGCGCGCGGACCCCTCTGACCGAGATCTCTGCTTGG 120
QY 121 CAGCAGAGAGCAGCGTCCCTCCCGGATTAAGTGGTGAAGAGGCGCAGTGGCCCTG 180
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DB 241 AAGGAACTGGGAGTCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGTGTGA 300
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DB 361 CACAGATTCAGCTTCGAAACAAGAGACCTGTGTTGACCAAGACCATTTGTAAGT 420
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DB 601 GGAATAATATATACATGATCTACAGAACCTGTGTAGTCAATCAAGAGAAATCATCG 660

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DB 841 GTGAACGACAAAGAAAGCCCAAACTCTGATTAATTTCCCTTCTTGAAGAACCC 900
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DB 1201 TTTCTTGTAGCTATTTGAAGATGCACTTCAATGCAATGAAGATGATCCCTCTCAT 1260
QY 1261 CACATTGCAACAGATGTTGGGCTTCTGTGAATTTGGCTTCTGTAAGATTAAGGAAA 1320
DB 1261 CACATTGCAACAGATGTTGGGCTTCTGTGAATTTGGCTTCTGTAAGATTAAGGAAA 1320
QY 1321 AATAAGGAGAAATCTCTGAGAAAGCAACGAAACCTCAACACAACTGAAGAGGCT 1380
DB 1321 AATAAGGAGAAATCTCTGAGAAAGCAACGAAACCTCAACACAACTGAAGAGGCT 1380
QY 1381 TTGATGTTCTGTGATTTGAAGAACTATAGTGAATGATTCAGAGAGTCAATGTGTAAG 1440
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DB 1501 CATCACTTCTAAGTGAATTTATTAATTAACAGCAAGAAAGATGTAAGGTTGAAAGG 1560
QY 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTTGCCTTAATGCAATTTGAAAC 1620
DB 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTTGCCTTAATGCAATTTGAAAC 1620
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QY 1681 ATCTTATGCTCTGCTTATCATGTGCAAGAAAGCTTAAGAAAGAAATTAAGCCCTGACAG 1740
DB 1681 ATCTTATGCTCTGCTTATCATGTGCAAGAAAGCTTAAGAAAGAAATTAAGCCCTGACAG 1740

1741 TATGTAGACCAACCAATTCAAATGATGTGTCTAACTTATTTCCCTAGTGCCTGTCTAT 1800
1741 TATGTAGACCAACCAATTAATGATGTGTCTAACTTATTTCCCTAGTGCCTGTCTAT 1800
1801 AAGAGATTATATTTCTTACTATATATACCTTAGGAATTTAGCAACCTGAAATTTATT 1860
1801 AAGAGATTATATTTCTTACTATATATACCTTAGGAATTTAGCAACCTGAAATTTATT 1860
1861 CACATATATCAAGTGAAGGAAATGCCCAATTCACATAGATTTCTTCTTTAGTAAAT 1920
1861 CACATATATCAAGTGAAGGAAATGCCCAATTCACATAGATTTCTTCTTTAGTAAAT 1920
1921 TGACCTACTTTGGTAGTGAATAGTGAATCTTAACTTAACTTGAATTTAGTACT 1980
1921 TGACCTACTTTGGTAGTGAATAGTGAATCTTAACTTAACTTGAATTTAGTACT 1980
1981 CATCTTTTACCACTCTCTAATTTTAAATTAATTTTCTCTGTCTTAAATGAGAGTAC 2040
1981 CATCTTTTACCACTCTCTAATTTTAAATTAATTTTCTCTGTCTTAAATGAGAGTAC 2040
2041 TTGGTTTTTTTTTTCTTAAATATGATATATGACATTTTAAATGATATTTATTTTGG 2100
2041 TTGGTTTTTTTTTTCTTAAATATGATATATGACATTTTAAATGATATTTATTTTGG 2100
2101 AGACGAGCTTCTCTCTTAACTTAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160
2101 AGACGAGCTTCTCTCTTAACTTAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160
2161 AGCTGTGCT 2220
2161 AGCTGTGCT 2220
2221 TACAGTATCTGACACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280
2221 TACAGTATCTGACACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280
2281 ACCGTGTAGCCAGATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
2281 ACCGTGTAGCCAGATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
2341 CAAAGTCTGGGATTAACAGGCAATGAGCCAGC 2372
2341 CAAAGTCTGGGATTAACAGGCAATGAGCCAGC 2372

RESULT 14
US-09-048-810-1
Sequence 1, Application US/09048810
Patent No. 6238921
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: MODULATION OF HUMAN MDM2 EXPRESSION
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marleton
STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,810
FILING DATE: herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey

REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0302
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-779-2400
TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Oliner, J.D.
AUTHORS: Kinzler, K.W.
AUTHORS: Meltzer, P.S.
AUTHORS: George, D.L.
AUTHORS: Vogelstein, B.
TITLE: Amplification of a gene encoding a
TITLE: p53-associated protein in human sarcomas
JOURNAL: Nature
VOLUME: 358
ISSUE: 6381
PAGES: 80-83
DATE: 02-JUL-1992
US-09-048-810-1

Query Match 100.0%; Score 2372; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCACCCGCGGAGCTTGGCTGCTTCTGCGGCTGTGTGCTGTGTGTGGAAGATGA 60
1 GCACCCGCGGAGCTTGGCTGCTTCTGCGGCTGTGTGCTGTGTGTGGAAGATGA 60
61 GCAAGAGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGG 120
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121 CAGCCAGAGCACCCT 180
121 CAGCCAGAGCACCCT 180
121 CAGCCAGAGCACCCT 180
181 GAGAGTGAATGATCCCGAGGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGG 240
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241 AAGGAACTGGGAGGATCTTGAAGGACCCCGACTCCAGCGGCAAAACCCCGATGTGA 300
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301 GGAGCAGGCAAAATGTGCAATTAACCAATGTCTGTACTTGTATGATGCTGTAAACCT 360
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421 TATTAAGCTGTGTGTGTCACAAAAGACACTTAATCTATGAAGAGGTTCTTTTATC 480
421 TATTAAGCTGTGTGTGTCACAAAAGACACTTAATCTATGAAGAGGTTCTTTTATC 480
481 TTGGCCAGATATTTATGACTAAACGATATATGATGATGAGCAACATATTTGATAT 540
481 TTGGCCAGATATTTATGACTAAACGATATATGATGATGAGCAACATATTTGATAT 540
541 GTTCAAAATGATCTTGAAGGATTTGTTGGCTGCAAGCTTCTGTGAAGAGCACA 600
541 GTTCAAAATGATCTTGAAGGATTTGTTGGCTGCAAGCTTCTGTGAAGAGCACA 600
601 GGAATATATATCATGATCTACAGGACTTGTGTATGATGATGAGCAAGATATCGG 660

Db	601	GGAAAAATATATACATGATCTTACAGAAACTTGGTAGTGTCAATCAGAGAAATCATCGG	660
Qy	661	ACTCAGGTCATCTGTGATGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGCATCAAAAG	720
Db	661	ACTCAGGTCATCTGTGATGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGCATCAAAAG	720
Qy	721	ACCTGTGTCAAGAGCTTCAGGAAGGAAACCTTCATCTTCACATTTGGTTCCTGACCAT	780
Db	721	ACCTGTGTCAAGAGCTTCAGGAAGGAAACCTTCATCTTCACATTTGGTTCCTGACCAT	780
Qy	781	CTACCTCATCTAGAAGAGAGCAATTAGTGAAGACAGAAAGAAATTCAGATGATTTATCTG	840
Db	781	CTACCTCATCTAGAAGAGAGCAATTAGTGAAGACAGAAAGAAATTCAGATGATTTATCTG	840
Qy	841	GTGAACGACAAAGAAACGCCACAATCTGTATGATTTCCCTTCTTTATGAAGACC	900
Db	841	GTGAACGACAAAGAAACGCCACAATCTGTATGATTTCCCTTCTTTATGAAGACC	900
Qy	901	TGGCTCTGTGTGTATATAGGAGATATGTGTGAAGAAGAGATGACGTGAATCTACAG	960
Db	901	TGGCTCTGTGTGTATATAGGAGATATGTGTGAAGAAGAGATGACGTGAATCTACAG	960
Qy	961	GGAGCCCATCGAATCCGAGTCTTGATGCTGGGTGAAGTGAACATTCAGGTATGTTGG	1020
Db	961	GGAGCCCATCGAATCCGAGTCTTGATGCTGGGTGAAGTGAACATTCAGGTATGTTGG	1020
Qy	1021	ATCAGGATTCAGTTTCAGATCAGTTTAACTGTGAATTTGAAGTGAATCTCTCGACTCAG	1080
Db	1021	ATCAGGATTCAGTTTCAGATCAGTTTAACTGTGAATTTGAAGTGAATCTCTCGACTCAG	1080
Qy	1081	AAGATTTAAGCCTTAAGTGAAGAGACAAAGAACTCTCAGATGAAGATGATAGATATTC	1140
Db	1081	AAGATTTAAGCCTTAAGTGAAGAGACAAAGAACTCTCAGATGAAGATGATAGATATTC	1140
Qy	1141	AAGTTACTGTGTATCAGGACAGGGAGAGTGTATCAGATTCATTTGAAAGAAATCCTGAA	1200
Db	1141	AAGTTACTGTGTATCAGGACAGGGAGAGTGTATCAGATTCATTTGAAAGAAATCCTGAA	1200
Qy	1201	TTTCTCTTAAGCTGACTATTGGAAATGACACTTCATGACATGAATGAATCCCCCTTCAT	1260
Db	1201	TTTCTCTTAAGCTGACTATTGGAAATGACACTTCATGACATGAATGAATCCCCCTTCAT	1260
Qy	1261	CACATTTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCGTGAAGATGAAGGAAAG	1320
Db	1261	CACATTTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCGTGAAGATGAAGGAAAG	1320
Qy	1321	ATTAAGGGGAAATCTCTGAGAAAGCCCAATCTGAAACCTCAACAAGACTGAAGAGGCT	1380
Db	1321	ATTAAGGGGAAATCTCTGAGAAAGCCCAATCTGAAACCTCAACAAGACTGAAGAGGCT	1380
Qy	1381	TTGATGTTCTGATTGTAAAAAAACTATATGATGATGATTCAGAGAGTCATGTGTTGAGG	1440
Db	1381	TTGATGTTCTGATTGTAAAAAAACTATATGATGATGATTCAGAGAGTCATGTGTTGAGG	1440
Qy	1441	AAATATGATGATTAATTCACAAGCTTCAATCAACAAGAAATGAAGCTATTTCTCAGC	1500
Db	1441	AAATATGATGATTAATTCACAAGCTTCAATCAACAAGAAATGAAGCTATTTCTCAGC	1500
Qy	1501	CATCAACTTCTAGTGTGCAATTTATTTATAGAGCAGAAGATGTGAAGAAGTTGAAGAAG	1560
Db	1501	CATCAACTTCTAGTGTGCAATTTATTTATAGAGCAGAAGATGTGAAGAAGTTGAAGAAG	1560
Qy	1561	AAGAAACCCACAGACAAAGAGAGATGTGCAATCTAGTTTGGCCCTTAATGCAATTGAAC	1620
Db	1561	AAGAAACCCACAGACAAAGAGAGATGTGCAATCTAGTTTGGCCCTTAATGCAATTGAAC	1620
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Db	1621	CTTGTGTGATTTGTCAAGGTGCACCTAAAAATGTTGTCATGTGTCATGCGCAAAACAGAC	1680
Qy	1681	ATCTTATGGCCGTCTTACATGTGCAAAAGAACTTAAGAAAAAGAAATTAAGCCCTTGCAG	1740
Db	1681	ATCTTATGGCCGTCTTACATGTGCAAAAGAACTTAAGAAAAAGAAATTAAGCCCTTGCAG	1740

QY	1741	TATGTAGACAAACCAATTCGAATAATGATTTGTGCTAACTTATTTTCCCTAGTTACACCTGCTAT	1800
Db	1741	TATGTAGACAAACCAATTCGAATAATGATTTGTGCTAACTTATTTTCCCTAGTTACACCTGCTAT	1800
QY	1801	AAGAGAAATTAATATTTCTTAACCTTATATACCTTAGAATTTAGACAACCTGAATTTAT	1860
Db	1801	AAGAGAAATTAATATTTCTTAACCTTATATACCTTAGAATTTAGACAACCTGAATTTAT	1860
QY	1861	CACATATATCAAGATGAGAAAATGCTCAATTCAATAGATTTCTTCTTTAGTATAT	1920
Db	1861	CACATATATCAAGATGAGAAAATGCTCAATTCAATAGATTTCTTCTTTAGTATAT	1920
QY	1921	TGACCTTACTTTGGTAGAGGAATAGTAGAATCTTACATTAATTTGACTTGAATAGTAGCT	1980
Db	1921	TGACCTTACTTTGGTAGAGGAATAGTAGAATCTTACATTAATTTGACTTGAATAGTAGCT	1980
QY	1981	CATCCTTTACACCAACTCTTAATTTTAAATATTTCTACTCTGTCTTAAATGAGAAATAC	2040
Db	1981	CATCCTTTACACCAACTCTTAATTTTAAATATTTCTACTCTGTCTTAAATGAGAAATAC	2040
QY	2041	TTGGTTTTTTTTTTCTTAATATGATATATGACATTTTAAATGTAATTTATTTT	2100
Db	2041	TTGGTTTTTTTTTTCTTAATATGATATATGACATTTTAAATGTAATTTATTTT	2100
QY	2101	AGACCGAGTCTTGCTCTGTTATACCAAGGCTGAGTGCAGTGGGTATCTTGGCTCACTGCA	2160
Db	2101	AGACCGAGTCTTGCTCTGTTATACCAAGGCTGAGTGCAGTGGGTATCTTGGCTCACTGCA	2160
QY	2161	AGCTCTGCGCCTCCCGGGTTGCAACCATTTCTGCTGACCTCCGCAATTAAGCTTGACC	2220
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QY	2221	TACAGTCAATCTGACCAACCACTTGGCTAATTTTGTACTTTAGTGAAGACAGGTTTC	2280
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QY	2281	ACCGTGTAGCGCAAGATAGTCTCGATCTCCGACCTGATCCGCCCACTCCGGCTCC	2340
Db	2281	ACCGTGTAGCGCAAGATAGTCTCGATCTCCGACCTGATCCGCCCACTCCGGCTCC	2340
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Db	2341	CAAAAGTCTGGGATTAACAGCGATAGCCACCG	2372
RESULT 15			
US-09-170-159A-2			
; Sequence 2, Application US/09170159A			
; Patent No. 639775			
; GENERAL INFORMATION:			
; APPLICANT: BURELL, MARILEE			
; HILL, DAVID E.			
; KINZLER, KENNETH W.			
; VOGELSTEIN, BERT			
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN			
; HUMAN TUMORS			
NUMBER OF SEQUENCES: 5			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT			
STREET: 1001 G STREET, N.W.			
CITY: WASHINGTON			
STATE: D.C.			
COUNTRY: USA			
ZIP: 20001			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/170,159A			
FILING DATE: 13-Oct-1998			

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-170-159A-2

Query Match 100.0%; Score 2372; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GCAAGAGCGGAGCGCCGAGGCGCGCGGACCCCTCTGACCGAGATCTCTGCTCTTGG 120
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DB 61 GCAAGAGCGGAGCGCCGAGGCGCGCGGACCCCTCTGACCGAGATCTCTGCTCTTGG 120
QY 121 CAGCCAGAGGACCGGCTCCCTCCCGGATTAGTGCCTGACGAGGCGCCGAGTCCCTGCGCG 180
DB 121 CAGCCAGAGGACCGGCTCCCTCCCGGATTAGTGCCTGACGAGGCGCCGAGTCCCTGCGCG 180
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DB 121 CAGCCAGAGGACCGGCTCCCTCCCGGATTAGTGCCTGACGAGGCGCCGAGTCCCTGCGCG 180
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DB 241 AAGGAACTGGGAGAGCTTGAAGGAGACCCCGACTCCAGCGGAGAAACCCCGAGTGTGA 300
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DB 301 GGAGGAGGAGAAATGTCGAACTACCAATGTCTGACTGATGATGCTGTGAACCACT 360
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DB 361 CACAGATTCAGCTTCGAAACAAGAGACCTGTGTTGACCAAGCCATTGCTTTGAAGT 420
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DB 421 TATTTAAGTCTGTGTGTGACAAAAGACACTTATATCTATGAAGAAGTCTTTTATATC 480
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DB 1021 ATCAGGATTCAGTTTCAGATTCAGTTTGTGTAAGTTTGAAGTGAATCTCTCGACTCAG 1080
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DB 1081 AAGATTATAGCTTGTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGATATATC 1140
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DB 1201 TTTCTTGGCTGACTATTTGGAATGCACTTGTGCAATGAAATGAAATCCCTTCCAT 1260
QY 1261 CACATTGCAACAGATGTGGGCTTGTGTGAGAAATGGCTTCTCTGAAGATGAAGGGAAG 1320
DB 1261 CACATTGCAACAGATGTGGGCTTGTGTGAGAAATGGCTTCTCTGAAGATGAAGGGAAG 1320
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DB 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAGCTGAAGGGCT 1380
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Db 1741 TATGTAGCAACCAATTCGAAATGATGCTTAACTTATTTCCCTAGTTGACTGTCTAT 1800
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Db 1861 CACATATATCAAAAGTAGAAAAATGCTCAATTCACATAGATTTCTCTTTAGTAAAT 1920
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Qy 1981 CATCTTTTACACCAACTCTTAATTTTAAATATTTTCTACTCTGTCTTAATGAGAATAC 2040
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Qy 2341 CAAAGTGCTGGGATTACAGGCAATGAGCCACCG 2372
Db 2341 CAAAGTGCTGGGATTACAGGCAATGAGCCACCG 2372

Search completed: August 4, 2006, 19:57:17
Job time : 621 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 11:23:53 ; Search time 146 Seconds
(without alignments)
11129.323 Million cell updates/sec

Title: US-09-966-724B-2

Sequence: 1 GCACCGCGGAGCTTGGCTG.....ATTACAGGCATGAGCCACCG 2372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Database :

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1:  N_Geneseq_8.*
2:  geneseq1960s.*
3:  geneseq1990s.*
4:  geneseq2000s.*
5:  geneseq2001as.*
6:  geneseq2001bs.*
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9:  geneseq2003as.*
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14: geneseq2005s.*
15: geneseq2006s.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
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	2	2372	100.0	2372	2	AAQ94589	AAQ94589	Human MDM
	3	2372	100.0	2372	2	AAT45151	AAT45151	Human MDM
	4	2372	100.0	2372	2	AAT66410	AAT66410	Human MDM
	5	2372	100.0	2372	2	AAT62065	AAT62065	Human MDM
	6	2372	100.0	2372	2	AAV05049	AAV05049	Human MDM
	7	2372	100.0	2372	2	AAV28876	AAV28876	Human MDM
	8	2372	100.0	2372	2	AAV04836	AAV04836	Human MDM
	9	2372	100.0	2372	2	AAV03607	AAV03607	CDNA sequ
	10	2372	100.0	2372	2	AAK03947	AAK03947	Human MDM
	11	2372	100.0	2372	2	AAZ37471	AAZ37471	Human sar
	12	2372	100.0	2372	2	AAK55093	AAK55093	Nucleoid
	13	2372	100.0	2372	3	AAA29389	AAA29389	MDM2 onco
	14	2372	100.0	2372	4	AAAF0625	AAAF0625	Human mdm
	15	2372	100.0	2372	4	AAAD07530	AAAD07530	Human p-5
	16	2372	100.0	2372	5	AAAS29240	AAAS29240	Human mdm4
	17	2372	100.0	2372	6	ABL62113	ABL62113	Colo aden
	18	2372	100.0	2372	6	AAAD42713	AAAD42713	Human dou

ALIGNMENTS

[illegible]

XX Claim 19; Fig 1; 75pp; English.

CC This sequence represents the MDM2 gene. Amplification of this gene is
CC diagnostic of neoplasia or the potential for neoplasia. The protein
CC encoded by this gene interacts with the product of the p53 gene. p53 is a
CC tumour suppressor gene and encodes a protein which appears to be a member
CC of a group of proteins which regulate normal cellular proliferation and
CC suppression of cellular transformation. Inactivation of the p53 gene has
CC been implicated in the formation, or progression of a wide variety of
CC carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or
CC the DNA encoding these, may be used to inhibit the growth of tumour cells
CC containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX Sequence 2372 Bp; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 2; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCACCGCCGAGCTTGCTGCTTCTGCGGCGCTGTGTGCGCTGTGTGTGCGAAAGATGGA 60
QY 61 GCAAGAACCCGAGCCGAGGGGCGCGGACCCCTGACCGAGATCCTGCTGCTTGG 120
DB 61 GCAAGAACCCGAGCCGAGGGGCGCGGACCCCTGACCGAGATCCTGCTGCTTGG 120
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DB 61 GCAAGAACCCGAGCCGAGGGGCGCGGACCCCTGACCGAGATCCTGCTGCTTGG 120
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DB 121 CAGCCAGAGACGCGTCCCTCCCGAATTAGTGCCTAGAGGCGCCAGTGCCCTGGCCG 180
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DB 781 CTACCTCATCTAGAGAGAGACCAATTAGTGAAGAGAAATTCAGATGATATATCTG 840
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DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGAAATCTCAACAACAGCTGAAGGCT 1380
QY 1381 TTGATGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 TTGATGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
DB 1441 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 CATCAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 CATCAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 AAGAAACCCAAAGCAAAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 AAGAAACCCAAAGCAAAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 ATCTTATGAGCTGCTTATCATGTGCAAGAGCTAAAGAAAGAAATGATGATGATGAT 1740
DB 1681 ATCTTATGAGCTGCTTATCATGTGCAAGAGCTAAAGAAAGAAATGATGATGATGAT 1740
QY 1741 TATGTAGCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
DB 1741 TATGTAGCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 AAGAGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
DB 1801 AAGAGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCATGATGATGATGATGATGATGAT 1920
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Db      1861 CACATATATCAAGTAGAAGAAATGCTCAATTCACATAGATTCTCTCTTAGATATAT 1920
Qy      1921 TCACCTACTTGTGTAGTGTGATATGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Db      1921 TCACCTACTTGTGTAGTGTGATATGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Qy      1981 CATCTCTTACCACTCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
Db      1981 CATCTCTTACCACTCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
Qy      2041 TTGGTTTTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 2100
Db      2041 TTGGTTTTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 2100
Qy      2101 AACACGAGCTTGTCTGTGTATCCAGGCTGTGAGTGAGTGAGTGAGTGAGTGAGTG 2160
Db      2101 AACACGAGCTTGTCTGTGTATCCAGGCTGTGAGTGAGTGAGTGAGTGAGTGAGTG 2160
Qy      2161 AGCTGTGACCTCCCGGGTTCGACCATCTCTGTCTGAGCTCCCAATTAAGCTTGGCC 2220
Db      2161 AGCTGTGACCTCCCGGGTTCGACCATCTCTGTCTGAGCTCCCAATTAAGCTTGGCC 2220
Qy      2221 TACAGTCACTGTGCAACACACCTGTGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
Db      2221 TACAGTCACTGTGCAACACACCTGTGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
Qy      2281 ACCGTGTTAGCCAGATGTCTGTGATCTCTGACCTGTGATCCGCCACCTTGGGCTTC 2340
Db      2281 ACCGTGTTAGCCAGATGTCTGTGATCTCTGACCTGTGATCCGCCACCTTGGGCTTC 2340
Qy      2341 CAAGTGTGGGATTAACAGGCAATGAGCCACCG 2372
Db      2341 CAAGTGTGGGATTAACAGGCAATGAGCCACCG 2372

RESULT 2
AA094589
ID      AA094589 standard, cDNA, 2372 BP.
AC      AA094589;
XX      16-OCT-2003 (revised)
DT      01-NOV-1995 (first entry)
XX      Human MDM2 gene.
DE      MDM2; sarcoma; diagnostic; DNA probe; ds.
XX      Homo sapiens; (cell line CaCo-2).
OS      Key      Location/Qualifiers
FH      CDS      312..1784
FT      /*tag= a
XX      US5420263-A.
PN      30-MAY-1995.
PD      07-APR-1993; 93US-00044619.
PF      07-APR-1992; 92US-00867840.
PR      23-0UN-1992; 92US-00903103.
XX      (UUYO ) UNITV JOHNS HOPKINS.
PA      Vogelstein B, Kinzler KW;
XX      MPI. 1995-206312/27.
DR      P-PSDB; AAF76696.
XX      New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
PT      treatment of tumours.

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XX      Claim 1: Col 19-24; 34pp; English.
PS      The human MDM2 gene is genetically altered (i.e. amplified) in human
XX      tumour cells. Detecting that the gene has become amplified or detecting
CC      increased gene product expression (using probes, proteins, antibodies and
CC      inhibitors) allow diagnosis and therapy of cancers such as colorectal
CC      carcinoma, lung cancer and chronic myelogenous leukaemia. The human MDM2
CC      protein binds to human p53 and allows the cell to escape from p53-
CC      regulated growth. (Updated on 16-OCT-2003 to standardise OS field)
XX      SQ      Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Query Match      100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCACGCGGAGCTTGAGCTGCTTCTGAGGCTGTGTGAGGCTGTGTGTGGAAGATGA 60
Db      1 GCACGCGGAGCTTGAGCTGCTTCTGAGGCTGTGTGAGGCTGTGTGTGGAAGATGA 60
Qy      61 GCAAGAGCCGAGCCCGAGGCGGCGGACCTCTTGACCGAATCTGTGCTTTCG 120
Db      61 GCAAGAGCCGAGCCCGAGGCGGCGGACCTCTTGACCGAATCTGTGCTTTCG 120
Qy      121 CAGCCAGAGACACCGTCTCTCCCGGATTAAGTGTGAGAGAGGCGCCAGTCCGCTG 180
Db      121 CAGCCAGAGACACCGTCTCTCCCGGATTAAGTGTGAGAGAGGCGCCAGTCCGCTG 180
Qy      181 GAGAGTGAATATATCCCGAGGCGGAGGCGTGTGCTTCCGAGATGACATGCCCCG 240
Db      181 GAGAGTGAATATATCCCGAGGCGGAGGCGTGTGCTTCCGAGATGACATGCCCCG 240
Qy      241 AAGAAACTGGGAGTCTTGAAGGACCCCGACCTCCAGCGGAAACCCTGGATGTGA 300
Db      241 AAGAAACTGGGAGTCTTGAAGGACCCCGACCTCCAGCGGAAACCCTGGATGTGA 300
Qy      301 GGAGCAGGCAATATGTGCAATACCAATATGTCTGTACTGTATGTGTGTATACCACT 360
Db      301 GGAGCAGGCAATATGTGCAATACCAATATGTCTGTACTGTATGTGTGTATACCACT 360
Qy      361 CACAGATTCAGCTTCGGAACAAGAGACCTCGGTAGACCAAGCATGCTTTGAAGT 420
Db      361 CACAGATTCAGCTTCGGAACAAGAGACCTCGGTAGACCAAGCATGCTTTGAAGT 420
Qy      421 TATTAAGTCTGTGTGACAAAAAGACACTTATATCTATGAAGAGTCTTTTATC 480
Db      421 TATTAAGTCTGTGTGACAAAAAGACACTTATATCTATGAAGAGTCTTTTATC 480
Qy      481 TTGGCCAGTATTTATGACTAAACGATATATGATGAGAGCAACAATTTATATT 540
Db      481 TTGGCCAGTATTTATGACTAAACGATATATGATGAGAGCAACAATTTATATT 540
Qy      541 GTTCAAAATGATCTTGAAGATTTGTTGGGTGCCAAGCTTCTGTGAAGAGCACA 600
Db      541 GTTCAAAATGATCTTGAAGATTTGTTGGGTGCCAAGCTTCTGTGAAGAGCACA 600
Qy      601 GGAATAATATATACATGATCTACAGAACTTGTGTATGATCAATGACAGATCATCG 660
Db      601 GGAATAATATATACATGATCTACAGAACTTGTGTATGATCAATGACAGATCATCG 660
Qy      661 ACTCAGTACATCTGTGAGTGAGAAACAGGTGCACCTTGAAAGTGTATCAAAAG 720
Db      661 ACTCAGTACATCTGTGAGTGAGAAACAGGTGCACCTTGAAAGTGTATCAAAAG 720
Qy      721 ACCTGTACAGAGCTTCAGAAAGAAACCTTCATCTTCAATTTGGTTCTAGACAT 780
Db      721 ACCTGTACAGAGCTTCAGAAAGAAACCTTCATCTTCAATTTGGTTCTAGACAT 780
Qy      781 CTACCTCATTTAAGAGAGAGCAATTAAGTGTGAGAGAGAAATTCAGATGAATATCTG 840
Db      781 CTACCTCATTTAAGAGAGAGCAATTAAGTGTGAGAGAGAAATTCAGATGAATATCTG 840

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XX AAT45151 is a cDNA clone of the human MDM-2 gene derived from a human
CC colon carcinoma cell line CaCo-2. The MDM-2 protein produced by this
CC clone is used in a method for identifying compounds that interfere with
CC the binding of p53 and MDM-2. In binding the p53 protein, the MDM-2
CC protein releases a cell from p53-regulated growth, allowing cancers to
CC develop. Therefore compounds identified as interfering with the binding
CC of MDM-2 to p53 are potentially useful in the treatment of human
CC neoplastic cells. In the method pref. one or both of the proteins is a
CC fusion protein and esp. with an antibody or antibody fragment which aids
CC separation and identification. (Updated on 25-MAR-2003 to correct PF
CC field.)

Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 2; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCACCGCGGAGTGGCTGCTTCTGCGGCGTGTGCGCCGTGTGTGCGAAAGATGGA 60
DB 1 GCACCGCGGAGTGGCTGCTTCTGCGGCGTGTGCGCCGTGTGTGCGAAAGATGGA 60
QY 61 GCAGAGCGGAGCGCCGAGGCGGCGCGGACCCCTGTGACGAGATCCTGCTGCTTGG 120
DB 61 GCAGAGCGGAGCGCCGAGGCGGCGCGGACCCCTGTGACGAGATCCTGCTGCTTGG 120
QY 121 CAGCCAGAGACACCGCTCCCGGATTAAGTCGAGAGCGCCGAGTCCCTGCGCCG 180
DB 121 CAGCCAGAGACACCGCTCCCGGATTAAGTCGAGAGCGCCGAGTCCCTGCGCCG 180
QY 181 GAGAGTGAATATCCCGAGGCGCGGCGGCTGCTTCCGAGTATGATGCTCCCGTGG 240
DB 181 GAGAGTGAATATCCCGAGGCGCGGCGGCTGCTTCCGAGTATGATGCTCCCGTGG 240
QY 241 AAGGAACTGSGGAGTCTTGAAGGACCCCGGACTCCGACGCGGAAACCCCGGATGTA 300
DB 241 AAGGAACTGSGGAGTCTTGAAGGACCCCGGACTCCGACGCGGAAACCCCGGATGTA 300
QY 301 GGAGAGCGCAATGTGCAATACCAATGTGTACTGATGATGATGATGATGATGATGAT 360
DB 301 GGAGAGCGCAATGTGCAATACCAATGTGTACTGATGATGATGATGATGATGATGAT 360
QY 361 CACAGATTCGAGCTTCGGAACAAGAGACCCGTGTAAGCAAAAGCATTTGCTTGAAGT 420
DB 361 CACAGATTCGAGCTTCGGAACAAGAGACCCGTGTAAGCAAAAGCATTTGCTTGAAGT 420
QY 421 TATTAAGTCTGTGTGCAAAAAGACACTTATCTATGAAAGGTTCTTTTATATC 480
DB 421 TATTAAGTCTGTGTGCAAAAAGACACTTATCTATGAAAGGTTCTTTTATATC 480
QY 481 TTGGCCAGTATATATGACTTAAACGATTAATGATGAGAGCAACAATATTGATAT 540
DB 481 TTGGCCAGTATATATGACTTAAACGATTAATGATGAGAGCAACAATATTGATAT 540
QY 541 GTTCAAAATGATCTTGAAGAGTTTGTGGCGTGCAGGCTTCTCTGGAAGAAGCACA 600
DB 541 GTTCAAAATGATCTTGAAGAGTTTGTGGCGTGCAGGCTTCTCTGGAAGAAGCACA 600
QY 601 GGAATAATATATACATCTACAGAACTTGTGTAGTCAATGACAGCAATATATGAG 660
DB 601 GGAATAATATATACATCTACAGAACTTGTGTAGTCAATGACAGCAATATATGAG 660
QY 661 ACTGAGTATCTGTGAGTGAAGCAGGTGTCACTTGAAGTGGAGTGAATCAAAAG 720
DB 661 ACTGAGTATCTGTGAGTGAAGCAGGTGTCACTTGAAGTGGAGTGAATCAAAAG 720
QY 721 ACCTGTACAGAGCTTCAGAGAGAAACCTTCACTTCAATTTGGTTTCAAGCAT 780
DB 721 ACCTGTACAGAGCTTCAGAGAGAAACCTTCACTTCAATTTGGTTTCAAGCAT 780
QY 781 CTACCTCATCTGAGAGAGCAATTAAGTGAAGAGAAATTCAGATGAATATATC 840
DB 781 CTACCTCATCTGAGAGAGCAATTAAGTGAAGAGAAATTCAGATGAATATATC 840
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DB 781 CTACCTCATCTGAGAGAGCAATTAAGTGAAGAGAAATTCAGATGAATATATC 840
QY 841 GTGAAGCAAAAGAAACCCCAATCTGATATGATTTCCCTTCTTGTGTAAGCC 900
DB 841 GTGAAGCAAAAGAAACCCCAATCTGATATGATTTCCCTTCTTGTGTAAGCC 900
QY 901 TGGCTCTGTGTGAATTAAGAGATATGTTGTAAGAAAGCAGTACAGTATCTACAG 960
DB 901 TGGCTCTGTGTGAATTAAGAGATATGTTGTAAGAAAGCAGTACAGTATCTACAG 960
QY 961 GAGCGCATCGAATCCGATCTTGAATGCTGTGTGAAGTGAATTCAGGATGATGGTTGG 1020
DB 961 GAGCGCATCGAATCCGATCTTGAATGCTGTGTGAAGTGAATTCAGGATGATGGTTGG 1020
QY 1021 ATCAGAGTTCAGTTTCAATCACTTATGATGATTTGAAGTGAATCTTCTGACTCAG 1080
DB 1021 ATCAGAGTTCAGTTTCAATCACTTATGATGATTTGAAGTGAATCTTCTGACTCAG 1080
QY 1081 AAGATTATAGCCTTGTGTAAGAGCAAGAACTCTCAGATGAAGTGAAGTATATC 1140
DB 1081 AAGATTATAGCCTTGTGTAAGAGCAAGAACTCTCAGATGAAGTGAAGTATATC 1140
QY 1141 AAGTTACTGTATCAGAGGAGAGATGATACAGATTCATTTGAAGAAATCTCGAAA 1200
DB 1141 AAGTTACTGTATCAGAGGAGAGATGATACAGATTCATTTGAAGAAATCTCGAAA 1200
QY 1201 TTTCTTACCTGATTAATGGAATGCACTTCATGCAATGAATGCCCTTCCAT 1260
DB 1201 TTTCTTACCTGATTAATGGAATGCACTTCATGCAATGAATGCCCTTCCAT 1260
QY 1261 CACATTGCAAGATGTTGGGCGCTTGTGTAAGTATGGCTTCTGTAAGTAAAGGAAAG 1320
DB 1261 CACATTGCAAGATGTTGGGCGCTTGTGTAAGTATGGCTTCTGTAAGTAAAGGAAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGGAAGCAAACTGGAAGAACTCAACAAGCTGAAGAGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGGAAGCAAACTGGAAGAACTCAACAAGCTGAAGAGGCT 1380
QY 1381 TTGATGTTCTGATTTGTAAGAACTATATGTAATGATTCAGAGAGTCAATGTTGAG 1440
DB 1381 TTGATGTTCTGATTTGTAAGAACTATATGTAATGATTCAGAGAGTCAATGTTGAG 1440
QY 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAGTGAAGCTATTTGAC 1500
DB 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAGTGAAGCTATTTGAC 1500
QY 1501 CATCACTTCTAGTGAATTTATTAAGAGCAAGAGATGTAAGAGTGAAGG 1560
DB 1501 CATCACTTCTAGTGAATTTATTAAGAGCAAGAGATGTAAGAGTGAAGG 1560
QY 1561 AAGAAACCCAGACAAAGAGAGAGTGAATCTAATTTGCCCTTAATGCAATGAAC 1620
DB 1561 AAGAAACCCAGACAAAGAGAGAGTGAATCTAATTTGCCCTTAATGCAATGAAC 1620
QY 1621 CTGTGTGATTTGTCAAGGTGACCTAAATATGTTGACATTTGCAATGCAACAGAC 1680
DB 1621 CTGTGTGATTTGTCAAGGTGACCTAAATATGTTGACATTTGCAATGCAACAGAC 1680
QY 1681 ATCTAATGCGCTTTCATGTGCAAGAGCTAAAGAAAGAAAGAAAGCCCTCCAG 1740
DB 1681 ATCTAATGCGCTTTCATGTGCAAGAGCTAAAGAAAGAAAGAAAGCCCTCCAG 1740
QY 1741 TATGTAGCAACCAATTCATTAATTTGCTAATTTCCCTTATGTAAGCTGTAT 1800
DB 1741 TATGTAGCAACCAATTCATTAATTTGCTAATTTCCCTTATGTAAGCTGTAT 1800
QY 1801 AAGAGAAATTAATTTTAACTAATTAACCTAGAAATTAAGAAACCTGAAATTTAT 1860
DB 1801 AAGAGAAATTAATTTTAACTAATTAACCTAGAAATTAAGAAACCTGAAATTTAT 1860
QY 1861 CACATATATCAAGAGGAAAGTGCCTCAATTCATGATTTCTTCTTATGATAT 1920
DB 1861 CACATATATCAAGAGGAAAGTGCCTCAATTCATGATTTCTTCTTATGATAT 1920
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OY 1921 TGACCTACTTGTGTAAGTGAATGATTAATTAATTTGACTGAATATAGTACT 1980
DB 1921 TGACCTACTTGTGTAAGTGAATGATTAATTAATTTGACTGAATATAGTACT 1980
OY 1981 CATCTTACCAACAACCTCTAATTTTAAATAATTTCTACTCTGTCTTAAATGAGAATAC 2040
DB 1981 CATCTTACCAACAACCTCTAATTTTAAATAATTTCTACTCTGTCTTAAATGAGAATAC 2040
OY 2041 TTTGTTTTTTTTTTCTTAATATGATATGACATTAAATGAACTTTATTTTTTTT 2100
DB 2041 TTTGTTTTTTTTTTCTTAATATGATATGACATTAAATGAACTTTATTTTTTTT 2100
OY 2101 AGACGAGCTTGTCTGTGTAACCCAGGCTGAGTSCAGTGGGTGATCTTGCTCACTGCA 2160
DB 2101 AGACGAGCTTGTCTGTGTAACCCAGGCTGAGTSCAGTGGGTGATCTTGCTCACTGCA 2160
OY 2161 AGCTCTGCTCTCCCGGGTTCGACCAATCTCTGCTCAAGCTCCCAATTAGCTTGCC 2220
DB 2161 AGCTCTGCTCTCCCGGGTTCGACCAATCTCTGCTCAAGCTCCCAATTAGCTTGCC 2220
OY 2221 TACAGTCACTGCGCACCACTGCTAATTTTTTTTACTTTTACTAGACAGAGTTTC 2280
DB 2221 TACAGTCACTGCGCACCACTGCTAATTTTTTTTACTTTTACTAGACAGAGTTTC 2280
OY 2281 ACCGTTAGGCGAGATGATCTGATCTCTGACCTCGGATCCGCCACCTCGGCTCC 2340
DB 2281 ACCGTTAGGCGAGATGATCTGATCTCTGACCTCGGATCCGCCACCTCGGCTCC 2340
OY 2341 CAAAGTGTGGGATTACAGGCATGAGCCACCG 2372
DB 2341 CAAAGTGTGGGATTACAGGCATGAGCCACCG 2372
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RESULT 4

AAT66410
ID AAT66410 standard; cDNA; 2372 BP.

AC AAT66410;

DT 25-MAR-2003 (revised)
DT 14-SEP-2000 (revised)
DT 18-JUN-1997 (first entry)

XX Human MDM2 coding sequence.

XX Human; MDM2 protein; antibody; detection; cancer; diagnosis;
KW p53-regulated growth; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 312..1787
FT FT /*tag= a
FT FT /product= "MDM2"

XX US5618921-A.

XX 08-APR-1997.

XX 17-FEB-1995; 95US-00390479.

XX 07-APR-1992; 92US-00867840.

XX 23-JUN-1992; 92US-00903103.

XX 07-APR-1993; 93US-00044619.

XX (UNYD) UNIV JOHNS HOPKINS.

XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;
DR WPI; 1997-225474/20.
XX P-PSDB; AAM15463.

PT Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
PS Claim 1; Col 19-24; 35pp; English.
XX This sequence encodes the human MDM2 protein. Antibodies that
CC specifically bind to human MDM2 protein may be used for detecting
CC elevated expression of the MDM2 gene in a human tissue or body fluid
CC sample, esp. for cancer diagnosis. The antibodies may be used to
CC interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC to sequester p53 and allow the cell to escape from p53-regulated growth.
CC (N.B. Revised record issued to correct the sequence analysis field.)
XX (Updated on 25-MAR-2003 to correct PF field.)
XX

SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GCACCGCGCGAGCTTGCTGCTCTGCGGCGCTGATGAGCCCTGTGTGTGCGAAGATGGA 60
DB 1 GCACCGCGCGAGCTTGCTGCTCTGCGGCGCTGATGAGCCCTGTGTGTGCGAAGATGGA 60
OY 61 GCAAGAAAGCCGAGCCCGAGGCGCGCGGCAACCCCTTACCGAGATCTGCTTTCG 120
DB 61 GCAAGAAAGCCGAGCCCGAGGCGCGCGGCAACCCCTTACCGAGATCTGCTTTCG 120
OY 121 CAGCGAGGAGGACCGTCCCTCCCGGATTAAGTGTGCGTACGAGCGCCAGTGCCTGCGCCG 180
DB 121 CAGCGAGGAGGACCGTCCCTCCCGGATTAAGTGTGCGTACGAGCGCCAGTGCCTGCGCCG 180
OY 181 GAGAGTGATATGATCCCGAGGCGCCAGGCGCTGCTGCTTCGCGAGTACGTCCCGCTG 240
DB 181 GAGAGTGATATGATCCCGAGGCGCCAGGCGCTGCTGCTTCGCGAGTACGTCCCGCTG 240
OY 241 AAGGAACTGGGAGTCTTGAGGGAACCCCGCATCTCCAAAGCCGAAACCCCGAGTGTGA 300
DB 241 AAGGAACTGGGAGTCTTGAGGGAACCCCGCATCTCCAAAGCCGAAACCCCGAGTGTGA 300
OY 301 GGAGCGGCAAAATGTCAAATCCAAAGTCTGTAACCTAGATGATGATGATGATGATGATGAT 360
DB 301 GGAGCGGCAAAATGTCAAATCCAAAGTCTGTAACCTAGATGATGATGATGATGATGATGAT 360
OY 361 CACAGATTCAGCTTCGGAACAAGAGACCTGCTTGAACCAAGCATTCCTTTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCTGCTTGAACCAAGCATTCCTTTTGAAGT 420
OY 421 TATTAAAGTCTGTGTGTGCAAAAAGACACTTATATATGAAAGAGTCTTTTATTC 480
DB 421 TATTAAAGTCTGTGTGTGCAAAAAGACACTTATATATGAAAGAGTCTTTTATTC 480
OY 481 TTGGCAGATATATATATGCTAAAGATATATATATATATATATATATATATATATATAT 540
DB 481 TTGGCAGATATATATATGCTAAAGATATATATATATATATATATATATATATATATAT 540
OY 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGTGCCAAAGCTTCTCTGTGAAGAGCA 600
DB 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGTGCCAAAGCTTCTCTGTGAAGAGCA 600
OY 601 GGAATAATATATATATATATATATATATATATATATATATATATATATATATATATAT 660
DB 601 GGAATAATATATATATATATATATATATATATATATATATATATATATATATATATAT 660
OY 661 ACTGAGTATATCTGTGTGTGAGAAACAGGTGACCTTGAAGTGGAGTGTCAAAAGG 720
DB 661 ACTGAGTATATCTGTGTGTGAGAAACAGGTGACCTTGAAGTGGAGTGTCAAAAGG 720
OY 721 ACCTGTACAAGAGCTTACAGAAAGAAACCTTCACTTCACTTCACTTCACTTCACTTCACT 780
DB 721 ACCTGTACAAGAGCTTACAGAAAGAAACCTTCACTTCACTTCACTTCACTTCACTTCACT 780
OY 781 CTACCTCATCTAAGAGAGAGCAATTAAGTACAGAAAGAAATTCAGATGATATATCTG 840
DB 781 CTACCTCATCTAAGAGAGAGCAATTAAGTACAGAAAGAAATTCAGATGATATATCTG 840
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Db      781 CTACCTCATCTAGAGAGAGCAATTAGTGAAGAGAGAAATTCAGATGAATTATCTG 840
Qy      841 GTGACGACAAAGAAAACGCCACAATCTGATGTAATTCCTTCTTCTTGATGAAGCC 900
Db      841 GTGACGACAAAGAAAACGCCACAATCTGATGTAATTCCTTCTTCTTGATGAAGCC 900
Qy      901 TGGCTCTGTGTATATAGGAGATATGTTGTAAAAGACAGTAGCAGTAATCTACAG 960
Db      901 TGGCTCTGTGTATATAGGAGATATGTTGTAAAAGACAGTAGCAGTAATCTACAG 960
Qy      961 GGAAGCCATGCAATCCGGATCTTGATGCTGTGTAAAGTGAACATTCAGGTGATGG 1020
Db      961 GGAAGCCATGCAATCCGGATCTTGATGCTGTGTAAAGTGAACATTCAGGTGATGG 1020
Qy      1021 ATCAGGATTCAGTTTTCAGATGATGTAATTTGAAATTTGAAATCTCTGACTCAG 1080
Db      1021 ATCAGGATTCAGTTTTCAGATGATGTAATTTGAAATTTGAAATCTCTGACTCAG 1080
Qy      1081 AAGATTATAGCCTTAGTGAAGAGACAAAGACTCTCAGATGAAGATGATGATATTC 1140
Db      1081 AAGATTATAGCCTTAGTGAAGAGACAAAGACTCTCAGATGAAGATGATGATATTC 1140
Qy      1141 AAGTACTGTGTATCAGGACAGGGAGATGATACAGATTCATTTGAAGAGATCTGAAA 1200
Db      1141 AAGTACTGTGTATCAGGACAGGGAGATGATACAGATTCATTTGAAGAGATCTGAAA 1200
Qy      1201 TTTCCTTACTGATCTTATTTGAAAATGCACTTCATGCAATGAATGAATCCCTCCCTCAT 1260
Db      1201 TTTCCTTACTGATCTTATTTGAAAATGCACTTCATGCAATGAATGAATCCCTCCCTCAT 1260
Qy      1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATGGCTCTGTAAGATTAAGGGAAG 1320
Db      1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATGGCTCTGTAAGATTAAGGGAAG 1320
Qy      1321 ATPAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGAGGCT 1380
Db      1321 ATPAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGAGGCT 1380
Qy      1381 TTGATGTTCTGATTTGTAATAAACTATGTAATGTCAGAGAGTCATGTTGAGG 1440
Db      1381 TTGATGTTCTGATTTGTAATAAACTATGTAATGTCAGAGAGTCATGTTGAGG 1440
Qy      1441 AAAATGATATAAATTTACACAAGCTTCAATCAACAAGAGTGAAGCTATTCACAG 1500
Db      1441 AAAATGATATAAATTTACACAAGCTTCAATCAACAAGAGTGAAGCTATTCACAG 1500
Qy      1501 CATCAACTTCTAGTAGCATTATTTATAGAGCCAAAGAGATGGAAGAGTTGAAAGG 1560
Db      1501 CATCAACTTCTAGTAGCATTATTTATAGAGCCAAAGAGATGGAAGAGTTGAAAGG 1560
Qy      1561 AAGAAACCCAGACAAAGAGAGTGTGAATCTAGTTGCCCTTAAATGCCATTGAAC 1620
Db      1561 AAGAAACCCAGACAAAGAGAGTGTGAATCTAGTTGCCCTTAAATGCCATTGAAC 1620
Qy      1621 CTGTGTGATTTGTCAAGGTGCACTTAAATGTTGCAATGGCAAAACAGGAC 1680
Db      1621 CTGTGTGATTTGTCAAGGTGCACTTAAATGTTGCAATGGCAAAACAGGAC 1680
Qy      1681 ATCTTATGAGCTGCTTTATCATGTGCAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
Db      1681 ATCTTATGAGCTGCTTTATCATGTGCAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
Qy      1741 TATGTAGACACAAATTCAAATGATGTTGCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
Db      1741 TATGTAGACACAAATTCAAATGATGTTGCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
Qy      1801 AAGAGATATATATTTCTAATCTATTAACCTTAAAGATTTTGAACAACCTGAATTTAT 1860
Db      1801 AAGAGATATATATTTCTAATCTATTAACCTTAAAGATTTTGAACAACCTGAATTTAT 1860
Qy      1861 CACATATATCAAGTGAAGAAAATGCCCTCAATTCACATAGATTTCTCTTTAGTATAT 1920
Db      1861 CACATATATCAAGTGAAGAAAATGCCCTCAATTCACATAGATTTCTCTTTAGTATAT 1920

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Qy      1921 TGACCTACTTTGGTAGTGAATAGTGAATACTACTATATAATTTGACTGAATATGAGCT 1980
Db      1921 TGACCTACTTTGGTAGTGAATAGTGAATACTACTATATAATTTGACTGAATATGAGCT 1980
Qy      1981 CATCTTTACACCACTCTCTAATTTTAAATTAATTTTACTCTGTCTTAAATGAGATAC 2040
Db      1981 CATCTTTACACCACTCTCTAATTTTAAATTAATTTTACTCTGTCTTAAATGAGATAC 2040
Qy      2041 TTGGTTTTTTTTTTCTTAAATATGTAATGACATTTAAATGTAATTAATTTTATTTT 2100
Db      2041 TTGGTTTTTTTTTTCTTAAATATGTAATGACATTTAAATGTAATTAATTTTATTTT 2100
Qy      2101 AAGACGAGTCTGCTCTGTATACCAAGCTGAGATGAGAGGATCTTGACTCAGTCA 2160
Db      2101 AAGACGAGTCTGCTCTGTATACCAAGCTGAGATGAGAGGATCTTGACTCAGTCA 2160
Qy      2161 AGCTGACCTCCCGGGTTGCAACATCTCTGCTCAGCTCCCAATTAAGCTTGAGCC 2220
Db      2161 AGCTGACCTCCCGGGTTGCAACATCTCTGCTCAGCTCCCAATTAAGCTTGAGCC 2220
Qy      2221 TACAGTCACTGCGCACACACCTGCTAATTTTGTACTTTTATGAGACAGAGGTTTC 2280
Db      2221 TACAGTCACTGCGCACACACCTGCTAATTTTGTACTTTTATGAGACAGAGGTTTC 2280
Qy      2281 ACCGTGTAGCCAGATGATCTCTGATCTCTGACCTGATGATCCGCCACTTGCCCTCC 2340
Db      2281 ACCGTGTGTAGCCAGATGATGATCTCTGATCTCTGACCTGATGATCCGCCACTTGCCCTCC 2340
Qy      2341 CAAAGTCTGGGATTTACAGGATGAGCCAGC 2372
Db      2341 CAAAGTCTGGGATTTACAGGATGAGCCAGC 2372

RESULT 5
AAT62065
ID AAT62065 strand: cDNA; 2372 BP.
XX
AC AAT62065;
XX
DT 25-MAR-2003 (revised)
DT 05-JUN-1997 (first entry)
XX
DE Human MDM2 cDNA.
XX
KW Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
KW elevation; expression; diagnosis; neoplasia; neoplastic transformation;
KW sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 312..1787
FT /tag="a
FT /product="MDM2"
XX
PN US5606044-A.
XX
PD 25-FEB-1997.
XX
PF 17-FEB-1995; 95US-00390546.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (U930 ) UNIV JOHNS HOPKINS.
XX
PI Kinzler KW, Vogelstein B, Hill DE, Burrell M;
XX
DR WPI; 1997-153623/14.
XX
DR P-PSDB; AAW13380.
XX

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PT Detection of amplification of human MDM2 gene - useful for diagnosis of
PT neoplasia or potential neoplastic transformation.

PS Claim 1; Col 21-24; 35pp; English.

XX The present sequence is the human MDM2 cDNA, which was isolated from a
CC human CaCo-2 colonic carcinoma cell cDNA library using a murine MDM2 cDNA
CC probe. The MDM2 cDNA can be used as a probe to detect the amplification
CC or elevated expression of a human MDM2 gene, which is diagnostic of
CC neoplasia or the potential for neoplastic transformation, useful for the
CC detection of, e.g. sarcomas, colorectal carcinoma, lung cancer and
CC chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to correct FP
CC field.)

CC Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

SO Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCACCGCCGAGCTTGGCTGCTTCTGGGGCCCTGTGAGCCCTGTGTGCGAAAGATGGA 60
DB 1 GCACCGCCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGAGCCCTGTGTGCGAAAGATGGA 60
QY 61 GCAGAGACCCGAGCCCGAGGGGCGCGGACCCCTGTGACCGAGATCCTGCTGCTTTCG 120
DB 61 GCAGAGACCCGAGCCCGAGGGGCGCGGACCCCTGTGACCGAGATCCTGCTGCTTTCG 120
QY 121 CAGCCAGAGACCGCTGCTTCTCCCGATTAATGCGTAGAGGCGCCAGTCCCTTGCCCG 180
DB 121 CAGCCAGAGACCGCTGCTTCTCCCGATTAATGCGTAGAGGCGCCAGTCCCTTGCCCG 180
QY 181 GAGAGTGAATATATCCCCGAGGCGCGAGGCGTGTGCTTCCGAGATGACATGCCCGTG 240
DB 181 GAGAGTGAATATATCCCCGAGGCGCGAGGCGTGTGCTTCCGAGATGACATGCCCGTG 240
QY 241 AAGGAACTGGGGAGTCTTGAAGGACCCCGACCTCCAGCGGAGAAACCCCGAGTGTGA 300
DB 241 AAGGAACTGGGGAGTCTTGAAGGACCCCGACCTCCAGCGGAGAAACCCCGAGTGTGA 300
QY 301 GGAGGAGGCAATATGTCATATACCAATATCTGTACTTACTGATGTGTGTAAACCACT 360
DB 301 GGAGGAGGCAATATGTCATATACCAATATCTGTACTTACTGATGTGTGTAAACCACT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTCCTTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTCCTTTGAAGT 420
QY 421 TATTAAGTCTGTGGTGTGCAAAAAAGACACTTATATCTATGAAGAAGTCTTTTATTC 480
DB 421 TATTAAGTCTGTGGTGTGCAAAAAAGACACTTATATCTATGAAGAAGTCTTTTATTC 480
QY 481 TTGGCCAGTATATATGATTAACGATTTATGATGAGAGAACCAACATATTTGATAT 540
DB 481 TTGGCCAGTATATATGATTAACGATTTATGATGAGAGAACCAACATATTTGATAT 540
QY 541 GTTCAATGATCTTCTAGAGAGATTTGTTGGCGTGCAGCTTCTCTGTGAAGAAGACA 600
DB 541 GTTCAATGATCTTCTAGAGAGATTTGTTGGCGTGCAGCTTCTCTGTGAAGAAGACA 600
QY 601 GGAATAATATATCAATGATCTACAGGAACCTTGATAGTCAATCAGCAGATCATCGG 660
DB 601 GGAATAATATATCAATGATCTACAGGAACCTTGATAGTCAATCAGCAGATCATCGG 660
QY 661 ACTCAGTATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGAATCAAGG 720
DB 661 ACTCAGTATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGAATCAAGG 720
QY 721 ACCCTGTAAGAAGCTTGAAGAGAAACCTTCACTTCACTTGTGTTCTAGACAT 780
DB 721 ACCCTGTAAGAAGCTTGAAGAGAAACCTTCACTTCACTTGTGTTCTAGACAT 780
QY 781 CTAACCTCATTAAGAAGAGCAATTAATGAGACAGAGAAATTCAGATGAATATCTG 840
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DB 781 CTAACCTCATTAAGAAGAGCAATTAATGAGACAGAGAAATTCAGATGAATATCTG 840
QY 841 GTGAACGACAAAGAAAACGACCAATCTGATGATATTCCTTCTTTGATGAAGCC 900
DB 841 GTGAACGACAAAGAAAACGACCAATCTGATGATATTCCTTCTTTGATGAAGCC 900
QY 901 TGGCTGTGTGTATTAAGGAGATATGTTGTGAAGAAGAGTAGACAGTGAATCTACG 960
DB 901 TGGCTGTGTGTATTAAGGAGATATGTTGTGAAGAAGAGTAGACAGTGAATCTACG 960
QY 961 GGAGGCCATCGAATCCGATTTTGATGTGTGTATGATGAGACATTCAGGTGATGTTGG 1020
DB 961 GGAGGCCATCGAATCCGATTTTGATGTGTGTATGATGAGACATTCAGGTGATGTTGG 1020
QY 1021 ATCAGATTCAGTTTCAATGATCAGTTTATGATGAGATTTGAAGTGAATCTCTGAC 1080
DB 1021 ATCAGATTCAGTTTCAATGATCAGTTTATGATGAGATTTGAAGTGAATCTCTGAC 1080
QY 1081 AAGATTAATAGCTTATGTAAGAAGACAAAGACTCTCAGATGAAGATGATGATATTC 1140
DB 1081 AAGATTAATAGCTTATGTAAGAAGACAAAGACTCTCAGATGAAGATGATGATATTC 1140
QY 1141 AAGTACTGTGTATCAGGACAGGAGAGTGTATCAGATTTCAATTTGAAGAAGATCTG 1200
DB 1141 AAGTACTGTGTATCAGGACAGGAGAGTGTATCAGATTTCAATTTGAAGAAGATCTG 1200
QY 1201 TTTCCCTAGTGAATATGAGAAATGACATTCATGCAATGAATGAATCCCCCTTCAT 1260
DB 1201 TTTCCCTAGTGAATATGAGAAATGACATTCATGCAATGAATGAATCCCCCTTCAT 1260
QY 1261 CACATTTGACAGATGTTGGCCCTTGTGAGAAATGGCTTCTGAAGATTAAGGAAAG 1320
DB 1261 CACATTTGACAGATGTTGGCCCTTGTGAGAAATGGCTTCTGAAGATTAAGGAAAG 1320
QY 1321 ATTAAGGGGAAATCTCTGAAGAAAGCCAAATCTGAAATCTCAACACAGCTGAAGGCT 1380
DB 1321 ATTAAGGGGAAATCTCTGAAGAAAGCCAAATCTGAAATCTCAACACAGCTGAAGGCT 1380
QY 1381 TTGATGTTCTGATTTGTAAATAAATATATGATGATTTCCAGAGAGTCAATGTGTTG 1440
DB 1381 TTGATGTTCTGATTTGTAAATAAATATATGATGATTTCCAGAGAGTCAATGTGTTG 1440
QY 1441 AAAATGATGATTAATAATTAACAAGGTTTCAATCAACAAGAAAGTGAAGATATTC 1500
DB 1441 AAAATGATGATTAATAATTAACAAGGTTTCAATCAACAAGAAAGTGAAGATATTC 1500
QY 1501 CATCAACTTCTATGATGATTTTATTTATGACAGCCAAAGAGATGTGAAGATTTGA 1560
DB 1501 CATCAACTTCTATGATGATTTTATTTATTTATGACAGCCAAAGAGATGTGAAGATTTGA 1560
QY 1561 AAGAAACCCAAAGACAAAGAGAGTGTGATCTAGTTGGCCCTTAATGCAATTTGA 1620
DB 1561 AAGAAACCCAAAGACAAAGAGAGTGTGATCTAGTTGGCCCTTAATGCAATTTGA 1620
QY 1621 CTTGTGATTTGTCAAGTGTGACCTTAATAAATGTTGATTCATGCGCAAAACAG 1680
DB 1621 CTTGTGATTTGTCAAGTGTGACCTTAATAAATGTTGATTCATGCGCAAAACAG 1680
QY 1681 ATCTATGAGCTGTCTTAATGTCAGAAAGCTTAAGAAAGAAATTAAGCCCTGCG 1740
DB 1681 ATCTATGAGCTGTCTTAATGTCAGAAAGCTTAAGAAAGAAATTAAGCCCTGCG 1740
QY 1741 TATGTAGCAACCAATTAAGATGATGCTAATTTTCCCTAGTTGACCTGTAT 1800
DB 1741 TATGTAGCAACCAATTAAGATGATGCTAATTTTCCCTAGTTGACCTGTAT 1800
QY 1801 AAGAAATTAATATTTCTAATATATTAACCTTAGAATTTAGACAACCTGAATTTAT 1860
DB 1801 AAGAAATTAATATTTCTAATATATTAACCTTAGAATTTAGACAACCTGAATTTAT 1860
QY 1861 CACATTAATCAAGTGAAGAAATGCTCAATTCATAGATTTCTTCTTTAGATAT 1920
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Db 1861 CACATATATCAAGTAGAAGAAATGCTCATATTCATAGATTTCTCTTAGTATTAAT 1920
QY 1921 TGACCTACTTTGGTAGAGATAGTAATCTTACTATATATTGACTTGAATATGAGCT 1980
Db 1921 TGACCTACTTTGGTAGAGATAGTAATCTTACTATATATTGACTTGAATATGAGCT 1980
QY 1981 CATCTCTTACACCAACTCTCTTAATTTTAAATATTTTCTACTCTGCTTAAATGAGAATAC 2040
Db 1981 CATCTCTTACACCAACTCTCTTAATTTTAAATATTTTCTACTCTGCTTAAATGAGAATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAATGTAATTTATTTTCTT 2100
Db 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAATATGTAATTTATTTTCTT 2100
QY 2101 AGACGAGTCTGCTGTTTACCCAGCTGAGTGAAGTGGTGTGATGGCTCACTGCA 2160
Db 2101 AGACGAGTCTGCTGTTTACCCAGCTGAGTGAAGTGGTGTGATGGCTCACTGCA 2160
QY 2161 AGCTCGACCTCCCGGGTTGCGACCATTTCTCTGCTCAGCTCCCAATTAGCTTGGCC 2220
Db 2161 AGCTCGACCTCCCGGGTTGCGACCATTTCTCTGCTCAGCTCCCAATTAGCTTGGCC 2220
QY 2221 TACAGTCATCTGCGACACACCTGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
Db 2221 TACAGTCATCTGCGACACACCTGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
QY 2281 ACCGTGTTAGCCAGGATGCTGCTGATCTCTGACCTGCTGATCCGCCACCTTGGCTTC 2340
Db 2281 ACCGTGTTAGCCAGGATGCTGCTGATCTCTGACCTGCTGATCCGCCACCTTGGCTTC 2340
QY 2341 CAAAGTGTGGGATTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTACAGGATGAGCCACCG 2372

RESULT 6
AAV20549
ID AAV20549 standard; cDNA; 2372 BP.
XX
AC AAV20549;
XX
DT 18-JUN-1998 (first entry)
XX
DE Human MDM2 encoding cDNA.
XX
KW Human; MDM2; tumour; cancer; diagnosis; neoplastic disease;
KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 312..1787
FT /tag= a
FT /product= "MDM2"
XX
PN US5736338-A.
XX
PD 07-APR-1998.
XX
PF 17-FEB-1995; 95US-00390517.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYGO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;
DR WPI, 1998-239206/21.
DR P-PSDB; AAW48241.
XX
PT Cancer diagnosis - by determination of MDM2 protein.

XX
PS Claim 1: Col 21-24; 35pp; English.
XX
CC The present sequence encodes human MDM2 (hMDM2) which is used in the
CC method of the present invention. The present invention describes a method
CC for diagnosing a neoplastic disease caused by overexpression of MDM2
CC protein. The method comprises detecting an elevated cellular amount of
CC this protein. The method is useful for the diagnosis of sarcoma,
CC especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma
XX
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGGAGAGCTTGGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGCGAAAGATGA 60
Db 1 GCACCGCGGAGAGCTTGGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGCGAAAGATGA 60
QY 61 GCAAGAGCCGAGCCGAGGGGCGCCGAGACCCCTCTGACCGAGATCTGCTGCTTTCG 120
Db 61 GCAAGAGCCGAGCCGAGGGGCGCCGAGACCCCTCTGACCGAGATCTGCTGCTTTCG 120
QY 121 CAGCCAGAGCA CCGTCCCTCCCGGATTAGGCGGTACAGAGCGCCAGTGGCCCTGGCCCG 180
Db 121 CAGCCAGAGCACCGTCCCTCCCGGATTAGGCGGTACAGAGCGCCAGTGGCCCTGGCCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCGAGGCGTGTCTTCCGAGTATCATGCCCCGTTG 240
Db 181 GAGAGTGAATGATCCCGAGGCGCGAGGCGTGTCTTCCGAGTATCATGCCCCGTTG 240
QY 241 AAGGAAACTGGGAGTCTTGAAGGACCCCGACTCCAGCCGAGAAACCCCGAGTGTGA 300
Db 241 AAGGAAACTGGGAGTCTTGAAGGACCCCGACTCCAGCCGAGAAACCCCGAGTGTGA 300
QY 301 GGAGCAGGCAAAATGTGCAATACCAATGTCTGACTCTGATGCTGTATACCACT 360
Db 301 GGAGCAGGCAAAATGTGCAATACCAATGTCTGACTCTGATGCTGTATACCACT 360
QY 361 CACAGATTCACCTTCGAAACAAGAGACCTGTGTAGACCAAGCCATTTGTTGAAGT 420
Db 361 CACAGATTCACCTTCGAAACAAGAGACCTGTGTAGACCAAGCCATTTGTTGAAGT 420
QY 421 TATTAAGTCTGTGGTGCACAAAAGACCTTATCTATGAAAGGTTCTTTTATTC 480
Db 421 TATTAAGTCTGTGGTGCACAAAAGACCTTATCTATGAAAGGTTCTTTTATTC 480
QY 481 TTGGCCAGTATTTATGACTTAAACGATTATGATGAGAAAGCAACATTTGTATTT 540
Db 481 TTGGCCAGTATTTATGACTTAAACGATTATGATGAGAAAGCAACATTTGTATTT 540
QY 541 GTTCAAAATGATCTTTCAGAGATTGTTGGGCTGCAAGCTTCTCTGAAAGAGACACA 600
Db 541 GTTCAAAATGATCTTTCAGAGATTGTTGGGCTGCAAGCTTCTCTGAAAGAGACACA 600
QY 601 GGAAATATATATACATGATCTACAGGAATTGTGTAGTCAATCAGCAGATCATCG 660
Db 601 GGAAATATATATACATGATCTACAGGAATTGTGTAGTCAATCAGCAGATCATCG 660
QY 661 ACTCAGTATCATCTGTGAGTGAACAGGTGTCACTTAAAGTGGAGTGAATCAAAAG 720
Db 661 ACTCAGTATCATCTGTGAGTGAACAGGTGTCACTTAAAGTGGAGTGAATCAAAAG 720
QY 721 ACCTGTACAAAGCTTCAGAAAGAAACCTTCACTTCACTTGGTTTCTAGACAT 780
Db 721 ACCTGTACAAAGCTTCAGAAAGAAACCTTCACTTCACTTGGTTTCTAGACAT 780
QY 781 CTACCTCATCTTGAAGAGAGCAATTAAGTGAACAGAAATTCAGATGAATATCTG 840
Db 781 CTACCTCATCTTGAAGAGAGCAATTAAGTGAACAGAAATTCAGATGAATATCTG 840
QY 841 GTGAACGACAAAGAAAGCCCAAAATCTGATGATTTCTTCTTCTTGTGATGAAGCC 900

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Db      841  GTGAACGCAAAAGAAAAGCCAAATCTGATAGATTCCCTTCCCTTGTATGAAAAGCC 900
Qy      901  TGGCTCTGTGTGTAATAAGGAGATATGTGTGAAAAGACGATGCGATGAATCTTAAG 960
Db      901  TGGCTCTGTGTGTAATAAGGAGATATGTGTGAAAAGACGATGCGATGAATCTTAAG 960
Qy      961  GGAGGCCATCGAATCCGATCTTGATGTGTGTAGTGAACAATTCAAGTGATGGTTGG 1020
Db      961  GGAGGCCATCGAATCCGATCTTGATGTGTGTAGTGAACAATTCAAGTGATGGTTGG 1020
Qy      1021  ATCAGAGATTCAAGTTGAGATCAATTAAGTGAATTTGAAGTGAATCTCTCGACTGAG 1080
Db      1021  ATCAGAGATTCAAGTTGAGATCAATTAAGTGAATTTGAAGTGAATCTCTCGACTGAG 1080
Qy      1081  AAGATTATAGCCTTAGTAAGAAGACAAGAACTCTCAGATGAAATATATAGATATATC 1140
Db      1081  AAGATTATAGCCTTAGTAAGAAGACAAGAACTCTCAGATGAAATATATAGATATATC 1140
Qy      1141  AAGTTACTGTGTATCAGGACGAGGAGATGATACAGATTCAATTTGAAGAATCCCTGAAA 1200
Db      1141  AAGTTACTGTGTATAGGACGAGGAGATGATACAGATTCAATTTGAAGAATCCCTGAAA 1200
Qy      1201  TTTCTTAGCTGACTATTGGAATGCACTTCATGCAATGAAATGAAATCCCTCCCTTCAT 1260
Db      1201  TTTCTTAGCTGACTATTGGAATGCACTTCATGCAATGAAATGAAATCCCTCCCTTCAT 1260
Qy      1261  CACATTGCAACAGATGTTGGCCCTTCGTGAGAAATTTGGCTTCCCTTAAGTAAAGGAAAG 1320
Db      1261  CACATTGCAACAGATGTTGGCCCTTCGTGAGAAATTTGGCTTCCCTTAAGTAAAGGAAAG 1320
Qy      1321  ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACACAGCTGAGAGGGCT 1380
Db      1321  ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACACAGCTGAGAGGGCT 1380
Qy      1381  TTGATGTTCTGTATGTAAAAAACTATATGTAATGATTTCCAGAGAGTCATGTGTTGAG 1440
Db      1381  TTGATGTTCTGTATGTAAAAAACTATATGTAATGATTTCCAGAGAGTCATGTGTTGAG 1440
Qy      1441  AAAATGATGATTAATTAACAAGAGTTCACATCAACAAGAAAGTAAAGCTATTTCTCAGC 1500
Db      1441  AAAATGATGATTAATTAACAAGAGTTCACATCAACAAGAAAGTAAAGCTATTTCTCAGC 1500
Qy      1501  CATCAACTTCTAGTGAATTAATTTATAGAGCCCAAGAGATGTAAGAGTTTGAAGGG 1560
Db      1501  CATCAACTTCTAGTGAATTAATTTATAGAGCCCAAGAGATGTAAGAGTTTGAAGGG 1560
Qy      1561  AAGAAACCCCAAGACAAGAAAGAGTGTGAATCTAGTTTGCCTTAATGCCATTGAAC 1620
Db      1561  AAGAAACCCCAAGACAAGAAAGAGTGTGAATCTAGTTTGCCTTAATGCCATTGAAC 1620
Qy      1621  CTTGTGTGATTTGTCAAGGTGCACTAAAAATGTGTGCAATGTCCCAATGCAAAACAGGAC 1680
Db      1621  CTTGTGTGATTTGTCAAGGTGCACTAAAAATGTGTGCAATGTCCCAATGCAAAACAGGAC 1680
Qy      1681  ATCTTATGSCCTGCTTTTACATGTCAGAAAGCTAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1740
Db      1681  ATCTTATGSCCTGCTTTTACATGTCAGAAAGCTAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1740
Qy      1741  TATGTAGCAACCAATTCATATGATGTGCTTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
Db      1741  TATGTAGCAACCAATTCATATGATGTGCTTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
Qy      1801  AAGAGATTATATATTTCTTAACTATATACCTTAGAATTTTGAACAACCTGAAATTTAT 1860
Db      1801  AAGAGATTATATATTTCTTAACTATATACCTTAGAATTTTGAACAACCTGAAATTTAT 1860
Qy      1861  CACATATATCAAAAGTGAAGAAATGCTCAATTCACTAATGATTTCTTCTTTAGTATAT 1920
Db      1861  CACATATATCAAAAGTGAAGAAATGCTCAATTCACTAATGATTTCTTCTTTAGTATAT 1920
Qy      1921  TGACCTACTTGTGTAGTGAATAGTAATCTTACTATATTTGACTTGAATATGTAGCT 1980

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Db      1921  TGACCTACTTGTGTAGTGAATAGTAATCTTACTATATTTGACTTGAATATGTAGCT 1980
Qy      1981  CATCCTTTACCAACAACCTCTAATTTTAAATATTTCTACTGTCTTAAATGAGAAGTAC 2040
Db      1981  CATCCTTTACCAACAACCTCTAATTTTAAATATTTCTACTGTCTTAAATGAGAAGTAC 2040
Qy      2041  TTGGTTTTTTTTTTCTTAATATATATATGACATTTTAAATGTAATTTTATTTTGTG 2100
Db      2041  TTGGTTTTTTTTTTCTTAATATATATATGACATTTTAAATGTAATTTTATTTTGTG 2100
Qy      2101  AGACCGAGTCTTGTCTGTATCCCAAGCTGAGAGGAGTGGGTATCTTGCTCACTGCA 2160
Db      2101  AGACCGAGTCTTGTCTGTATCCCAAGCTGAGAGGAGTGGGTATCTTGCTCACTGCA 2160
Qy      2161  AGCTTGCCCTCCCGGGGTTGCAACATTTCTCTGCTCAAGCTCCCAATTAAGCTTGGCC 2220
Db      2161  AGCTTGCCCTCCCGGGGTTGCAACATTTCTCTGCTCAAGCTCCCAATTAAGCTTGGCC 2220
Qy      2221  TACAGTCACTGCGACCAACACCTGAGCTAATTTTTTGTATCTTTTATAGTAGACAGGGTTTC 2280
Db      2221  TACAGTCACTGCGACCAACACCTGAGCTAATTTTTTGTATCTTTTATAGTAGACAGGGTTTC 2280
Qy      2281  ACCGTGTTAGCCAGATAGTCTCGATCTCTGACTCGTGTATCCGCCCACTCGGCTCC 2340
Db      2281  ACCGTGTTAGCCAGATAGTCTCGATCTCTGACTCGTGTATCCGCCCACTCGGCTCC 2340
Qy      2341  CAAAGTGTGGGATTTACAGCATGAGCCACCG 2372
Db      2341  CAAAGTGTGGGATTTACAGCATGAGCCACCG 2372

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RESULT 7
AAV28876
ID AAV28876 standard; cDNA; 2372 BP.
XX
XX AAV28876;
AC 10-AUG-1998 (first entry)
XX
XX DE Human MDM2 gene.
XX
XX KW Human; p53; MDM2; tumour; growth inhibition; amplification;
XX malignant fibrous histiocytoma; liposarcoma; ds.
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 312..1787
XX FT /*tag= a
XX FT /product= "MDM2 protein"
XX
XX PN US5756455-A.
XX
XX PD 26-MAY-1998.
XX
XX PF 17-FEB-1995; 95US-00390515.
XX
XX PR 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PR 07-APR-1993; 93US-00044619.
XX
XX PA (U9DO ) UNIV JOHNS HOPKINS.
XX
XX PI Vogelstein B, Kinzler KW;
XX
XX DR WPI; 1998-321574/28.
XX DR P-PSDB; AAW57241.
XX
XX PT Inhibiting growth of tumour cells having MDM2 gene amplification - with
XX p53 protein fragment.
XX
XX Example 1; Col 19-24; 40bp; English.
XX

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CC A method has been developed for inhibiting the growth of tumour cells
CC containing a human MDM2 gene amplification. The method comprises creating
CC the tumour cells with a DNA molecule that expresses a polypeptide capable
CC of binding to human MDM2 protein. The present sequence represents the
CC human MDM2 gene. The present invention describes three preferred
CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino
CC acids 1-50 of p53 (see AAM57240); (2) the polypeptide comprises amino
CC acids 13-41 of p53 (see AAM57240) and at least one additional p53
CC residues on the N- or C-terminal side, provided that the polypeptide
CC lacks the homoligomerisation domain of p53; (3) the polypeptide
CC comprises amino acids 13-41 of p53 (see AAM57241) and at least nine
CC additional p53 residues on the N- or C-terminal side, provided that the
CC polypeptide lacks amino acids 138-193 of p53. Some malignant fibrous
CC histiocytomas and liposarcomas have an MDM2 gene amplification, so
CC detection of increased expression of MDM2 gene products indicates
CC tumourigenesis

XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCGCGAGCTTGCTGCTTCTGCGGCTGTGTGCGCTGTGTGCGAAAGATGA 60
DB 1 GCAACCGCGAGCTTGCTGCTTCTGCGGCTGTGTGCGCTGTGTGCGAAAGATGA 60
QY 61 GCAAGAACCGGAGCCGAGGCGCGCGGAGCCCTCTGACCGAGATCCTGCTGCTTTCG 120
DB 61 GCAAGAACCGGAGCCGAGGCGCGCGGAGCCCTCTGACCGAGATCCTGCTGCTTTCG 120
QY 121 CAGCCGAGAGCAGCCGCTCCCGGATTAAGTCCGTAAGAGCGCCAGTGCCTTGCCCG 180
DB 121 CAGCCGAGAGCAGCCGCTCCCGGATTAAGTCCGTAAGAGCGCCAGTGCCTTGCCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCGAGGCTGTGCTTCCGAGTATGACAGTCCCGTG 240
DB 181 GAGAGTGAATGATCCCGAGGCGCGAGGCTGTGCTTCCGAGTATGACAGTCCCGTG 240
QY 241 AAGAAAATGGGAGAGTCTTGAAGGAGCCCGACTCCAGCGCGAAACCCCGAGTGTGA 300
DB 241 AAGAAAATGGGAGAGTCTTGAAGGAGCCCGACTCCAGCGCGAAACCCCGAGTGTGA 300
QY 301 GAGAGCGGCAATGTGCAATACCAATGTCTGTACTTACTGATGTGCTGTACCACT 360
DB 301 GAGAGCGGCAATGTGCAATACCAATGTCTGTACTTACTGATGTGCTGTACCACT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGACCTGTGTTAGACCAAGCCATTGCTTTGAAAT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCTGTGTTAGACCAAGCCATTGCTTTGAAAT 420
QY 421 TATTAAAGTCTGTGTGTCACAAAAGACATTAATCTATGAAGAAGTCTTTTATTC 480
DB 421 TATTAAAGTCTGTGTGTCACAAAAGACATTAATCTATGAAGAAGTCTTTTATTC 480
QY 481 TTGGCCAGTATATATGACTTAAACGATTATATGATGAGAAAGCAACAATATTGATAT 540
DB 481 TTGGCCAGTATATATGACTTAAACGATTATATGATGAGAAAGCAACAATATTGATAT 540
QY 541 GTTCAAATGATCTCTAGAGAGATTGTTGGGTGCGCAAGCTTCTCTGGAAGAAGCA 600
DB 541 GTTCAAATGATCTCTAGAGAGATTGTTGGGTGCGCAAGCTTCTCTGGAAGAAGCA 600
QY 601 GGAATAATATATACATGATCTACAGAACTTGTATAGTCAATCAGAGATCATCGG 660
DB 601 GGAATAATATATACATGATCTACAGAACTTGTATAGTCAATCAGAGATCATCGG 660
QY 661 ACTCAGTATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGTCAAAAG 720
DB 661 ACTCAGTATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGTCAAAAG 720
QY 721 ACCTGTACAAGGCTTCAAGAAAGAACTTCACTTCACTTGGTTTCTAGACAT 780
DB 721 ACCTGTACAAGGCTTCAAGAAAGAACTTCACTTCACTTGGTTTCTAGACAT 780

DB 721 ACCTGTACAAGGCTTCAAGAAAGAACTTCACTTCACTTGGTTTCTAGACAT 780
QY 781 CTACCTCATCTAGAGAGAGCAATTAGTACAGAGAAAGAAATTCAGATGATATTCG 840
DB 781 CTACCTCATCTAGAGAGAGCAATTAGTACAGAGAAAGAAATTCAGATGATATTCG 840
QY 841 GTGAACGACAAAGAAAACGCCCAATCTGATAGTATTCCTTCTCTTGTGAAGGCC 900
DB 841 GTGAACGACAAAGAAAACGCCCAATCTGATAGTATTCCTTCTCTTGTGAAGGCC 900
QY 901 TGGCTCTGTGTATATAGGAGATATGTTGAAAAGACAGTACAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTATATAGGAGATATGTTGAAAAGACAGTACAGTGAATCTACAG 960
QY 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTATAGTAACTTCAAGTGTGTTGG 1020
DB 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTATAGTAACTTCAAGTGTGTTGG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTATGTAAGTGAATTTGAAGTGAATCTCGACTCAG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTATGTAAGTGAATTTGAAGTGAATCTCGACTCAG 1080
QY 1081 AAGATTATAGCCTTATAGTGAAGAGCAAGAACTCTCAGATGAAGTATGATATATC 1140
DB 1081 AAGATTATAGCCTTATAGTGAAGAGCAAGAACTCTCAGATGAAGTATGATATATC 1140
QY 1141 AAGTTATCTGTATACAGGAGGAGAGTGTATCAGATTCATTGGAAGAAATCCTGAAA 1200
DB 1141 AAGTTATCTGTATACAGGAGGAGAGTGTATCAGATTCATTGGAAGAAATCCTGAAA 1200
QY 1201 TTTCTGTAGCTATTTGGAATGCACTTCAATGCAATGAATGAAATCCCCCTTCAT 1260
DB 1201 TTTCTGTAGCTATTTGGAATGCACTTCAATGCAATGAATGAAATCCCCCTTCAT 1260
QY 1261 CACATTGCAACAGATGTTGGGCTTCTGGAATTTGGCTTCTGTAAGATTAAGGGAAG 1320
DB 1261 CACATTGCAACAGATGTTGGGCTTCTGGAATTTGGCTTCTGTAAGATTAAGGGAAG 1320
QY 1321 ATAAAAGGGAATCTCTGAGAAAGCCAACTGAAAACCTCAACAGCTGAAGAGGCT 1380
DB 1321 ATAAAAGGGAATCTCTGAGAAAGCCAACTGAAAACCTCAACAGCTGAAGAGGCT 1380
QY 1381 TTGATGTTCTGATTTGTAAGAAATCTATATGTAATGATTCGAGAGTATGTTGAG 1440
DB 1381 TTGATGTTCTGATTTGTAAGAAATCTATATGTAATGATTCGAGAGTATGTTGAG 1440
QY 1441 AAAATGATGATTAATTAACAAGCTTCAATCAACAAGAGTGAATTCCTCAGC 1500
DB 1441 AAAATGATGATTAATTAACAAGCTTCAATCAACAAGAGTGAATTCCTCAGC 1500
QY 1501 CATCAACTCTAGTACATTTATTTATAGCAGCCAAAGATGTGAAGAGTTGAAAGG 1560
DB 1501 CATCAACTCTAGTACATTTATTTATAGCAGCCAAAGATGTGAAGAGTTGAAAGG 1560
QY 1561 AAGAAACCCAGACAAAGAGAGTGTGAATCTAGTTCGCCCTTAATGCCATTGAAC 1620
DB 1561 AAGAAACCCAGACAAAGAGAGTGTGAATCTAGTTCGCCCTTAATGCCATTGAAC 1620
QY 1621 CTGTGTGATTTGTGAAGTGCACCTTAAGAAAGTGTGCAATGTCATGCAAGCAAGGAC 1680
DB 1621 CTGTGTGATTTGTGAAGTGCACCTTAAGAAAGTGTGCAATGTCATGCAAGCAAGGAC 1680
QY 1681 ATCTTAGGCTCTGCTTATCATGTGCAAGAGCTTAAGAAAGATAGCCCTGCCAG 1740
DB 1681 ATCTTAGGCTCTGCTTATCATGTGCAAGAGCTTAAGAAAGATAGCCCTGCCAG 1740
QY 1741 TATGTAGCAACCAATTCAAATGATGTGCTAACTTATTTCCCTTAAGTGAACCTGTAT 1800
DB 1741 TATGTAGCAACCAATTCAAATGATGTGCTAACTTATTTCCCTTAAGTGAACCTGTAT 1800
QY 1801 AAGAAATTAATATTTCTAATATATAACCTTAGAATTTGACAACTGAAATTTAT 1860
DB 1801 AAGAAATTAATATTTCTAATATATAACCTTAGAATTTGACAACTGAAATTTAT 1860

QY 1861 CACATATATCAAAAGTGAAGAAAATGCGTCAATTCATAGATTTCTTCTTTAGTATAT 1920
Db 1861 CACATATATCAAAAGTGAAGAAAATGCGTCAATTCATAGATTTCTTCTTTAGTATAT 1920
QY 1921 TGACCTACTTTGGTATGTAATGTAATCTTACTATTAATTTGACTGAATATGACT 1980
Db 1921 TGACCTACTTTGGTATGTAATGTAATCTTACTATTAATTTGACTGAATATGACT 1980
QY 1981 CATCTTTACACCAACCTCTAATTTTAATATCTTCTGCTGCTTAAATGAGAATGAC 2040
Db 1981 CATCTTTACACCAACCTCTAATTTTAATATCTTCTGCTGCTTAAATGAGAATGAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATAATGATATGACATTTAATGATCTAATTTTCTTGG 2100
Db 2041 TTGGTTTTTTTTTTCTTAATAATGATATGACATTTAATGATCTAATTTTCTTGG 2100
QY 2101 AGACCGAGTCTTCTCTGTTATCCAGGCTGAGTCAAGTGGTATCTTGGCTCACTGCA 2160
Db 2101 AGACCGAGTCTTCTCTGTTATCCAGGCTGAGTCAAGTGGTATCTTGGCTCACTGCA 2160
QY 2161 AGCTCTGCGCTCCCGGGTGGGACATTCCTGCTGAGCTGCCAATTAAGCTTGGCC 2220
Db 2161 AGCTCTGCGCTCCCGGGTGGGACATTCCTGCTGAGCTGCCAATTAAGCTTGGCC 2220
QY 2221 TACAGTCACTGCGACACACACCTGGCTAATTTTGTACTTTAGTAGACAGGGTTTC 2280
Db 2221 TACAGTCACTGCGACACACACCTGGCTAATTTTGTACTTTAGTAGACAGGGTTTC 2280
QY 2281 ACCGTGTTAGCCAGGATGCTGATCTTCTGACCTGATCGGCCACCTCGGCTTCC 2340
Db 2281 ACCGTGTTAGCCAGGATGCTGATCTTCTGACCTGATCGGCCACCTCGGCTTCC 2340
QY 2341 CAAAGTCTGGGATTAACAGGCACTGAGCCGCG 2372
Db 2341 CAAAGTCTGGGATTAACAGGCACTGAGCCGCG 2372

RESULT 8

AAV04836 standard; cDNA; 2372 BP.

AAV04836; 30-APR-1998 (first entry)
cDNA sequence of human MDM2.
MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
binding; tumour cell; p53-regulated growth; inhibition;
anti-cancer agent; db.
Homo sapiens.
Key Location/Qualifiers
FT CDS 312..1787
FT /tag= a
FN US5708136-A.
PD 13-JAN-1998.
PF 17-FEB-1995; 95US-00390516.
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX (UNJO) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;
XX WPI; 1998-100408/09.

XX Human MDM2 binding polypeptide - comprises fragments of p53, useful in re-
PT establisning p53-regulated growth control in cells over-expressing MDM2.
PT
XX
XX
BS Disclosure; Col 19-24; 41pp; English.
CC The present sequence encodes human MDM2. The MDM2 gene is amplified in
CC some human tumours. The amplification of this gene is diagnostic of
CC neoplasia or its potential. It is speculated that the MDM2 protein is a
CC potential DNA binding protein that functions in the modulation of
CC expression of other genes and, when present in excess, interferes with
CC normal constraints on cell growth. A cell containing three recombinant
CC DNA constructs was produced. These constructs encode an MDM2 protein
CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
CC to a transcriptional activation domain, and a reporter gene downstream
CC from a DNA element which is recognised by the sequence-specific DNA-
CC binding domain. The cell is used to identify a compound which interferes
CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
CC cells and since binding of MDM2 to p53 appears to allow tumour cells to
CC escape from p53-regulated growth, compounds that inhibit such binding
CC would be useful as anti-cancer agents
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGTGGAAGATGA 60
Db 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGTGGAAGATGA 60
QY 61 GCAAGAACCGAGCCGAGCGGAGCGGCGGACCCCTGACCGAGATCTCTGCTTTCG 120
Db 61 GCAAGAACCGAGCCGAGCGGAGCGGCGGACCCCTGACCGAGATCTCTGCTTTCG 120
QY 121 CAGCCAGAGGACCGTCCCTCCCGGATTAAGTGTGCGTACGAGCGCCAGTCCCTGGCCG 180
Db 121 CAGCCAGAGGACCGTCCCTCCCGGATTAAGTGTGCGTACGAGCGCCAGTCCCTGGCCG 180
QY 181 GAGAGTGAATGATCCCGGAGGCCCGAGGCGTCCGCTTCCGCAATTCAGTCCCGCTG 240
Db 181 GAGAGTGAATGATCCCGGAGGCCCGAGGCGTCCGCTTCCGCAATTCAGTCCCGCTG 240
QY 241 AAGGAACTGGGAGATCTTGAAGGACCCCGACCTCAACCGCGAAGAACCCCGAGATGGA 300
Db 241 AAGGAACTGGGAGATCTTGAAGGACCCCGACCTCAACCGCGAAGAACCCCGAGATGGA 300
QY 301 GGAGCAGGCAAAATGTGCAATACCAATGCTGTACTAGATGCTGTACACACT 360
Db 301 GGAGCAGGCAAAATGTGCAATACCAATGCTGTACTAGATGCTGTACACACT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGACCTGTGTATGACCAAGCATTTGCTTTGAAGT 420
Db 361 CACAGATTCAGCTTCGGAACAAGAGACCTGTGTATGACCAAGCATTTGCTTTGAAGT 420
QY 421 TATTAAAGCTGTGGTGCACAAAAGACACTTATACATGAAAGAGGTTCTTTTATC 480
Db 421 TATTAAAGCTGTGGTGCACAAAAGACACTTATACATGAAAGAGGTTCTTTTATC 480
QY 481 TTGGCCAGTATATATGACTAAACGATTAATGATGAGAGGCAACAATATTTATATT 540
Db 481 TTGGCCAGTATATATGACTAAACGATTAATGATGAGAGGCAACAATATTTATATT 540
QY 541 GTTCAAATGATCTTGAAGAGATTTGTTGGCTGCCAAGCTTCTCTGTGAAGAGACA 600
Db 541 GTTCAAATGATCTTGAAGAGATTTGTTGGCTGCCAAGCTTCTCTGTGAAGAGACA 600
QY 601 GGAATAATATATACCATGATCTTACAGAACTGGTATGATCAATCAGAGGAATCATCG 660
Db 601 GGAATAATATATACCATGATCTTACAGAACTGGTATGATCAATCAGAGGAATCATCG 660
QY 661 ACTCAGTACATCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGATCAAAAGG 720

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Db      661  |||...|||
      ACTCAGGTACATCTGTGAGTGAGAAACAGGTCACCTTGAGGTGGAGATCAAAAG 720
Qy      721  |||...|||
      ACCTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780
Db      721  |||...|||
      ACCGTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCAT 780
Qy      781  |||...|||
      CTACCTCATCTAGAAAGAGAGCAATTAGTAGACAGAGAGAAATTGAGATTAATTCAG 840
Db      781  |||...|||
      CTACCTCATCTAGAAAGAGAGCAATTAGTAGACAGAGAGAAATTGAGATTAATTCAG 840
Qy      841  |||...|||
      GTGAAGCAGAAAGAAACCCCAAAATCTGATAGTATTTCCCTTTCCTTGTGATGAAGCC 900
Db      841  |||...|||
      GTGAAGCAGAAAGAAACCCCAAAATCTGATAGTATTTCCCTTTCCTTGTGATGAAGCC 900
Qy      901  |||...|||
      TGGCTCTGTGTATATAGGGAGATATGTGTGAAAAGACAGTACAGTGAATCTACAG 960
Db      901  |||...|||
      TGGCTCTGTGTATATAGGGAGATATGTGTGAAAAGACAGTACAGTGAATCTACAG 960
Qy      961  |||...|||
      GGAAGCATCGAATCCGATCTTGATGCTGCTGTAAGTGAACATTCAGGTGATGGTTGG 1020
Db      961  |||...|||
      GGAAGCATCGAATCCGATCTTGATGCTGCTGTAAGTGAACATTCAGGTGATGGTTGG 1020
Qy      1021  |||...|||
      ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAAATTTGAAGTTGAATCTTCGACTCAG 1080
Db      1021  |||...|||
      ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAAATTTGAAGTTGAATCTTCGACTCAG 1080
Qy      1081  |||...|||
      AAGATTATAGCTTGTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGATATATC 1140
Db      1081  |||...|||
      AAGATTATAGCTTGTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGATATATC 1140
Qy      1141  |||...|||
      AAGTTACTGTGTATCAGGAGGGGAGAGTATACAGATTCATTTGAAGAAATCCTGAAA 1200
Db      1141  |||...|||
      AAGTTACTGTGTATCAGGAGGGGAGAGTATACAGATTCATTTGAAGAAATCCTGAAA 1200
Qy      1201  |||...|||
      TTTCTTCTAGCTGACTATTGGAATGCACTTCATGCAATGAATGAATGCCCTTCAT 1260
Db      1201  |||...|||
      TTTCTTCTAGCTGACTATTGGAATGCACTTCATGCAATGAATGAATGCCCTTCAT 1260
Qy      1261  |||...|||
      CACATTGCAACAGATGTTGGGCTTCGTGAGAAATGGCTTCCTGAAGATGAAGGGAAAG 1320
Db      1261  |||...|||
      CACATTGCAACAGATGTTGGGCTTCGTGAGAAATGGCTTCCTGAAGATGAAGGGAAAG 1320
Qy      1321  |||...|||
      ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATCTCAACACAGCTGAAGGGCT 1380
Db      1321  |||...|||
      ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATCTCAACACAGCTGAAGGGCT 1380
Qy      1381  |||...|||
      TTGATGTTCTGATTTGTAAAAAACTATAGTGAATGATTCAGAGAGTCATGTTGAGG 1440
Db      1381  |||...|||
      TTGATGTTCTGATTTGTAAAAAACTATAGTGAATGATTCAGAGAGTCATGTTGAGG 1440
Qy      1441  |||...|||
      AAAATGATGATTAATTAACAAAGCTTCACAAATCAACAAAGAAAGTAAATTCACAGC 1500
Db      1441  |||...|||
      AAAATGATGATTAATTAACAAAGCTTCACAAATCAACAAAGAAAGTAAATTCACAGC 1500
Qy      1501  |||...|||
      CATCAACTTCTAGTGAATTTATTAAGACGCCAAGAGATGTGAAGAGTTGAAAAGG 1560
Db      1501  |||...|||
      CATCAACTTCTAGTGAATTTATTAAGACGCCAAGAGATGTGAAGAGTTGAAAAGG 1560
Qy      1561  |||...|||
      AAGAAACCCAAAGAAAGAGAGTGAATCTAGTTTGGCCCTTAATGCAATTTGAAC 1620
Db      1561  |||...|||
      AAGAAACCCAAAGAAAGAGAGTGAATCTAGTTTGGCCCTTAATGCAATTTGAAC 1620
Qy      1621  |||...|||
      CTGTGTGTATTTGTCAAGGTTCGACCTAAATATGTTGCAATGTCATTTGAAC 1680
Db      1621  |||...|||
      CTGTGTGTATTTGTCAAGGTTCGACCTAAATATGTTGCAATGTCATTTGAAC 1680
Qy      1681  |||...|||
      ATCTTAGGCTGCTTTATAGTGAAGAAAGCTAAAGAAAGAAAGAAAGAAAGAAAG 1740
Db      1681  |||...|||
      ATCTTAGGCTGCTTTATAGTGAAGAAAGCTAAAGAAAGAAAGAAAGAAAGAAAG 1740
Qy      1741  |||...|||
      TATGTAGAACCAATTCAAATGATGTGCTAATTAATTTCCCTAGTGAACCTGCTAT 1800

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Db      1741  TATGTAGAACCAATTCAAATGATGTGCTAATTAATTTCCCTAGTGAACCTGCTAT 1800
Qy      1801  AAGAGAAATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Db      1801  AAGAGAAATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Qy      1861  CACATTAATCAAGAGAAAGAAAGTGCCTCAATCACAATAGATTTCTCTTGTAGTAAT 1920
Db      1861  CACATTAATCAAGAGAAAGAAAGTGCCTCAATCACAATAGATTTCTCTTGTAGTAAT 1920
Qy      1921  TGACCTACTTGTGTAGTGAATAGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Db      1921  TGACCTACTTGTGTAGTGAATAGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Qy      1981  CATCTTTACCAACTCTTAATTTTAATTAATTTCTACTCTGTCTTAATGAGAAATAC 2040
Db      1981  CATCTTTACCAACTCTTAATTTTAATTAATTTCTACTCTGTCTTAATGAGAAATAC 2040
Qy      2041  TTGGTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 2100
Db      2041  TTGGTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 2100
Qy      2101  AGACCGAGTCTGTCTGTATACCAAGCTGAGAGTGAAGTGAATCTTGCTCACTGCA 2160
Db      2101  AGACCGAGTCTGTCTGTATACCAAGCTGAGAGTGAAGTGAATCTTGCTCACTGCA 2160
Qy      2161  AGCTTGCCCTCCCGGGGTTGACACATTCCTGCTCAGGCTGCCAATTAAGCTTGGCC 2220
Db      2161  AGCTTGCCCTCCCGGGGTTGACACATTCCTGCTCAGGCTGCCAATTAAGCTTGGCC 2220
Qy      2221  TACAGTCAATTCGACACACACCTGCTAATTTTGTACTTTTGTAGTAGACAGGGTTTC 2280
Db      2221  TACAGTCAATTCGACACACACCTGCTAATTTTGTACTTTTGTAGTAGACAGGGTTTC 2280
Qy      2281  ACCGTGTAGCAGAGATGCTCGATCTCTGACCTCGATCCGATCCGACCTCGGCTCC 2340
Db      2281  ACCGTGTAGCAGAGATGCTCGATCTCTGACCTCGATCCGATCCGACCTCGGCTCC 2340
Qy      2341  CAAAGTGTGGGATTAACAGGCAATGAGCCACCG 2372
Db      2341  CAAAGTGTGGGATTAACAGGCAATGAGCCACCG 2372

RESULT 9
AAV03607
ID      AAV03607 standard; cDNA; 2372 BP.
XX
AC      AAV03607;
XX
DT      29-APR-1998 (first entry)
XX
DE      cDNA sequence of human MDM2.
XX
KW      MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
      binding; tumour cell; p53-regulated growth; inhibition;
      anti-cancer agent; ds.
XX
OS      Homo sapiens.
XX
FH      Key
FT      CDS
FT      312..1787
FT      /tag= a
PN      US5702903-A.
PD      30-DEC-1997.
XX
PE      13-NOV-1995; 95US-00557393.
XX
PR      07-APR-1992; 92US-00867840.
PR      23-JUN-1992; 92US-00903103.
PR      07-APR-1993; 93US-00044619.
PR      18-MAY-1994; 94US-00245500.

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XX (UJVO) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW;
XX WPI; 1998-076411/07.
XX P-PSDB; AAM42971.
XX
XX Cell containing reporter construct containing human MDM2 and p53 genes -
XX for identifying compounds that interfere with binding of human MDM2 to
XX human p53, useful as anti-cancer agents.
XX
XX Disclosure: Columns 21-26; 37pp; English.
XX
XX The present sequence encodes human MDM2. The MDM2 gene is amplified in
XX some human tumours. The amplification of this gene is diagnostic of
XX neoplasia or its potential. It is speculated that the MDM2 protein is a
XX potential DNA binding protein that functions in the modulation of
XX expression of other genes and, when present in excess, interferes with
XX normal constraints on cell growth. A cell containing three recombinant
XX DNA constructs was produced. These constructs encode an MDM2 protein
XX fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
XX to a transcriptional activation domain, and a reporter gene downstream
XX from a DNA element which is recognised by the sequence-specific DNA-
XX binding domain. The cell is used to identify a compound which interferes
XX with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
XX cells and since binding of MDM2 to p53 appears to allow tumour cells to
XX escape from p53-regulated growth, compounds that inhibit such binding
XX would be useful as anti-cancer agents
XX
XX
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 541 GTTCAATGATCTCTAGAGATTGTTGGCCGCGCAAGCTTCTGTGAAGACACA 600
Qy GGAATATATATACCATGATCTACAGAACTTGTAGTATGCAATCAGACAGAAATCATCG 660
Qy 601 GGAATATATATACCATGATCTACAGAACTTGTAGTATGCAATCAGACAGAAATCATCG 660
Db 601 GGAATATATATACCATGATCTACAGAACTTGTAGTATGCAATCAGACAGAAATCATCG 660
Qy 661 ACTCAGGTACATCTGTGAGTGAAGACAGTGTCACTTGAAGGTGGAGTATCAAAAG 720
Db 661 ACTCAGGTACATCTGTGAGTGAAGACAGTGTCACTTGAAGGTGGAGTATCAAAAG 720
Qy 721 ACCTTGTAACAAGACTTCAGAGAGAACTTATATCTTCAATTTGGTTCTAGACAT 780
Db 721 ACCTTGTAACAAGACTTCAGAGAGAACTTATATCTTCAATTTGGTTCTAGACAT 780
Qy 781 CTACCTCATCTAGAAAGGAGCAATTTGTGAGACAGAAAGAAATTCAGATGAATATCTG 840
Db 781 CTACCTCATCTAGAAAGGAGCAATTTGTGAGACAGAAAGAAATTCAGATGAATATCTG 840
Qy 841 GTGAACGACAAAGAAACGCCCAAAATCTGATATATTTCCCTTCTTGTATGAAGCC 900
Db 841 GTGAACGACAAAGAAACGCCCAAAATCTGATATATTTCCCTTCTTGTATGAAGCC 900
Qy 901 TGGCTGTGTGTATATAGGAGATATGTTGTGAAGAGAGTACAGTGAATCTACAG 960
Db 901 TGGCTGTGTGTATATAGGAGATATGTTGTGAAGAGAGTACAGTGAATCTACAG 960
Qy 961 GGAAGCCATGGAATCCGGATCTTGATGCTGTGTATGAAACATTCAGATGATTTGGT 1020
Db 961 GGAAGCCATGGAATCCGGATCTTGATGCTGTGTATGAAACATTCAGATGATTTGGT 1020
Qy 1021 ATCAGATTCAGTTCAGATCAGTTAGTATGATTAATTTGAAGTTGAATCTTCGACTAG 1080
Db 1021 ATCAGATTCAGTTCAGATCAGTTAGTATGATTAATTTGAAGTTGAATCTTCGACTAG 1080
Qy 1081 AAGATTATAGCTTATAGTGAAGAGACAAAGACTTCAGATGAAGATATGATATATC 1140
Db 1081 AAGATTATAGCTTATAGTGAAGAGACAAAGACTTCAGATGAAGATATGATATATC 1140
Qy 1141 AAGTTACTGTGTATCAGGAGAGAGATGATATGATTAATTTGAAGAAATCTTGAA 1200
Db 1141 AAGTTACTGTGTATCAGGAGAGAGATGATATGATTAATTTGAAGAAATCTTGAA 1200
Qy 1201 TTTCTTATGATCATTATGAAATGACCTTCATGCAATGAATGATATCCCTTCAT 1260
Db 1201 TTTCTTATGATCATTATGAAATGACCTTCATGCAATGAATGATATCCCTTCAT 1260
Qy 1261 CACATTGCAACAGATGTTGGCCCTTCGTGAAATTTGCTTCGAAATTAAGGAAAG 1320
Db 1261 CACATTGCAACAGATGTTGGCCCTTCGTGAAATTTGCTTCGAAATTAAGGAAAG 1320
Qy 1321 AATAAGGGGAAATCTCTAGAAAGCAACCTGAAATCTCAACCAAGCTGAAGGGCT 1380
Db 1321 AATAAGGGGAAATCTCTAGAAAGCAACCTGAAATCTCAACCAAGCTGAAGGGCT 1380
Qy 1381 TTGATGTTCTGATTTGTAATAAATACTATAGTATGATTTCAAGAGATCATGTGTAAG 1440
Db 1381 TTGATGTTCTGATTTGTAATAAATACTATAGTATGATTTCAAGAGATCATGTGTAAG 1440
Qy 1441 AAAATGATATTAATTAACAAGCTTCAATCAAGAAAGTGAAGCTATTTTCAGC 1500
Db 1441 AAAATGATATTAATTAACAAGCTTCAATCAAGAAAGTGAAGCTATTTTCAGC 1500
Qy 1501 CATCAACTTCTAGTACATTTATTTATACAGCAAGAAAGTGAAGGTTTGAAGGG 1560
Db 1501 CATCAACTTCTAGTACATTTATTTATACAGCAAGAAAGTGAAGGTTTGAAGGG 1560
Qy 1561 AAGAAACCAAGACAAAGAGAGATGAGATCTAGTTTGCCTTATATGCAATTGAC 1620
Db 1561 AAGAAACCAAGACAAAGAGAGATGAGATCTAGTTTGCCTTATATGCAATTGAC 1620
Qy 1621 CTTGTGTATTTGTCAAGTGCACCTAAATATGTTGATTTCCATGGCAAAACAGAC 1680
Db 1621 CTTGTGTATTTGTCAAGTGCACCTAAATATGTTGATTTCCATGGCAAAACAGAC 1680

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Db      1621 CTGTGTGATTTGTCAAGGTGCACTTAAATGGTTGCAATTCATGCGCAAAACAGAGC 1680
Qy      1681 ATCTTATGGCTGCTTTACATGNCAGAGAGCTAAAGAAAGATAGCCCTGCCAG 1740
Db      1681 ATCTTATGGCTGCTTTACATGNCAGAGAGCTAAAGAAAGATAGCCCTGCCAG 1740
Qy      1741 TATGTAGACCAACCAATTCATGATGCTACTATTTCCCTAGTGAACCTGTCTAT 1800
Db      1741 TATGTAGACCAACCAATTCATGATGCTACTATTTCCCTAGTGAACCTGTCTAT 1800
Qy      1801 AAGAGATATATATTTCTTACTATATTAACCTAGGAATTTAGACAACCTGAATTTAT 1860
Db      1801 AAGAGATATATATTTCTTACTATATTAACCTAGGAATTTAGACAACCTGAATTTAT 1860
Qy      1861 CACATATATCAAGAGAAATGCTCAATTCACATATTTCTTCTTTAGTATAT 1920
Db      1861 CACATATATCAAGAGAAATGCTCAATTCACATATTTCTTCTTTAGTATAT 1920
Qy      1921 TGACCTACTTTGTGTGATAGTAAATGTAATTAATTAATTTGACTTGAATATAGCT 1980
Db      1921 TGACCTACTTTGTGTGATAGTAAATGTAATTAATTAATTTGACTTGAATATAGCT 1980
Qy      1981 CATCTTTACACCAACTCTTAATTTAAATTAATTTCTGCTCTTAAATGAGAGTAC 2040
Db      1981 CATCTTTACACCAACTCTTAATTTAAATTAATTTCTGCTCTTAAATGAGAGTAC 2040
Qy      2041 TTGCTTTTCTTTCTTAAATATGTAATGATTAATTAATTAATTTTCTTAAATTTT 2100
Db      2041 TTGCTTTTCTTTCTTAAATATGTAATGATTAATTAATTAATTTTCTTAAATTTT 2100
Qy      2101 AGACGAGCTTGTCTGTATACCCAGAGCTGAGAGTGAAGGAGTCTTGCTGCTAC 2160
Db      2101 AGACGAGCTTGTCTGTATACCCAGAGCTGAGAGTGAAGGAGTCTTGCTGCTAC 2160
Qy      2161 AGCTTGCCCTTCCCGGGTTGCAACCTTCTCTGCTGAGCTCCCAATTAAGTGGCC 2220
Db      2161 AGCTTGCCCTTCCCGGGTTGCAACCTTCTCTGCTGAGCTCCCAATTAAGTGGCC 2220
Qy      2221 TACAGTCACTGTCACACCACTGGGTAATTTTGTACTTTAGTGAAGACAGGTTTC 2280
Db      2221 TACAGTCACTGTCACACCACTGGGTAATTTTGTACTTTAGTGAAGACAGGTTTC 2280
Qy      2281 ACCGTTAGCCAGAGTGTCTGATCTCTGACCTGATCCGCGCACTCGGCTCC 2340
Db      2281 ACCGTTAGCCAGAGTGTCTGATCTCTGACCTGATCCGCGCACTCGGCTCC 2340
Qy      2341 CAAAGTGTGGATTACAGGCAATGAGCCAGC 2372
Db      2341 CAAAGTGTGGATTACAGGCAATGAGCCAGC 2372

RESULT 10
AAK03947
ID      AAK03947 standard; cDNA; 2372 BP.
XX
AC      AAK03947;
XX
DT      13-APR-1999 (first entry)
XX
DE      Human MDM2 encoding cDNA.
XX
KW      Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis;
KM      malignant fibrous histiocytoma; MFH; liposarcoma; ds.
OS      Homo sapiens.
XX
FT      Key 312..1787 location/Qualifiers
FT      CDS /+tag= a
PN      US5858976-A.
PD      12-JAN-1999.

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XX      14-FEB-1997; 97US-00801718.
PF      07-APR-1992; 92US-00867840.
PR      23-JUN-1992; 92US-00903103.
PR      07-APR-1993; 93US-00044619.
PR      17-FEB-1995; 95US-00390515.
XX
PA      (UYJO ) UNITV JOHNS HOPKINS.
XX
PI      Kinzler KW, Vogelstein B;
XX
DR      MPI; 1999-152105/13.
DR      P-PSDB; AAW94304.
XX
PT      Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT      MDM2-binding p53 fragment.
XX
PS      Example 1; Col 19-24; 41dp; English.
XX
CC      The present invention describes: (1) a method for inhibiting the growth
CC      of tumour cells which contain a human MDM2 gene amplification, comprising
CC      administering to the cells a DNA molecule that expresses a polypeptide
CC      consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino
CC      acid sequence given in AAW94303, the polypeptide being capable of binding
CC      to human MDM2 (see AAW94304); (2) a method as in (1) where the
CC      polypeptide lacks the homo-oligomerisation domain of p53; and (3) a
CC      method as in (1) where the polypeptide lacks amino acids 138-393 of p53.
CC      The method is useful for treating the following tumour types which have a
CC      MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20
CC      MFH, L-9 liposarcoma, K17 liposarcoma, K128 liposarcoma, K130
CC      liposarcoma, and OSA-CL MFH. The present sequence encodes human MDM2
XX
SQ      Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCACGCGCGAGCTTGGCTGCTTGTGGGCGCTGTGTGCGCTGTGTGGAAGATGGA 60
Db      1 GCACGCGCGAGCTTGGCTGCTTGTGGGCGCTGTGTGCGCTGTGTGGAAGATGGA 60
Qy      61 GCAAGAGCCGAGCCCGAGGGGCGCGGACCCCTCTGACCGAGATCTGCTGCTTTGG 120
Db      61 GCAAGAGCCGAGCCCGAGGGGCGCGGACCCCTCTGACCGAGATCTGCTGCTTTGG 120
Qy      121 CAGCGAGAGGACCGTCCCTCCCGGATTAGTGGCGTGAAGGCGCCAGTCCGCGCG 180
Db      121 CAGCGAGAGGACCGTCCCTCCCGGATTAGTGGCGTGAAGGCGCCAGTCCGCGCG 180
Qy      181 GAGAGTGAATGATCCCGAGGCGCCAGGCGTGTGTCTTCCGAGTACAGTCCCGTG 240
Db      181 GAGAGTGAATGATCCCGAGGCGCCAGGCGTGTGTCTTCCGAGTACAGTCCCGTG 240
Qy      241 AAGGAACTGGGGAATCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGTGTGA 300
Db      241 AAGGAACTGGGGAATCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGTGTGA 300
Qy      301 GGAGGAGGCAATGTCATTAACAATGTCTGTACCTATGATGTGTGTAACCACT 360
Db      301 GGAGGAGGCAATGTCATTAACAATGTCTGTACCTATGATGTGTGTAACCACT 360
Qy      361 CACAGATTCAGCTTCGGAACAAGAGACCTGTGTAGACCAAGCCATGCTTTGGAAGT 420
Db      361 CACAGATTCAGCTTCGGAACAAGAGACCTGTGTAGACCAAGCCATGCTTTGGAAGT 420
Qy      421 TATTAAGTCTGTGTGTGCAAAAAGACCTTAATACATGAAAGAGTTCTTTTATC 480
Db      421 TATTAAGTCTGTGTGTGCAAAAAGACCTTAATACATGAAAGAGTTCTTTTATC 480
Qy      481 TTGGCCAGATATTATGACTAAAGATTATATGATGAGAGCAACAATATTGTATAT 540

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Db 481 TTGGCAGTATATTATGACTAAACGATTATATGATGAGAGCAACAATATTTGATATT 540
Qy 541 GTTCAATGATCTTCTAGAGATTTTGTGGCGTCCAGCTTCTCTGTGAAGAAGCA 600
Db 541 GTTCAATGATCTTCTAGAGATTTTGTGGCGTCCAGCTTCTCTGTGAAGAAGCA 600
Qy 601 GGAATAATATATACCATGATCTACAGAACTTGTGTAGTCAATCAGCAGGATCATCG 660
Db 601 GGAATAATATATACCATGATCTACAGAACTTGTGTAGTCAATCAGCAGGATCATCG 660
Qy 661 ACTCAGGATCATCTGTAGTGAAGCAAGTGTCACTTGAAGGTGGAATCAAAAG 720
Db 661 ACTCAGGATCATCTGTAGTGAAGCAAGTGTCACTTGAAGGTGGAATCAAAAG 720
Qy 721 ACCTTGTACAGAGCTTCAAGAGAGAACTTCACTTCCACATTTGGTTCTAGACCAT 780
Db 721 ACCTTGTACAGAGCTTCAAGAGAGAACTTCACTTCCACATTTGGTTCTAGACCAT 780
Qy 781 CTACCTCATCTAGAGAGAGCAATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 CTACCTCATCTAGAGAGAGCAATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 841 GTGAACGACAAAG 900
Db 841 GTGAACGACAAAG 900
Qy 901 TGGCTCTGTGTATTAAGAGAGATATGTGTGAAGAAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 TGGCTCTGTGTATTAAGAGAGATATGTGTGAAGAAGAGAGAGAGAGAGAGAGAGAG 960
Qy 961 GAGAGCCATCGAATCCGATCTTGAATCTGTGTGAAGAAGAGAGAGAGAGAGAGAGAG 1020
Db 961 GAGAGCCATCGAATCCGATCTTGAATCTGTGTGAAGAAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 ATCAGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1080
Db 1021 ATCAGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1080
Qy 1081 AAGATTATAGCTTGTGTGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 AAGATTATAGCTTGTGTGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 1141 AAGTACTGTGTATCAG 1200
Db 1141 AAGTACTGTGTATCAG 1200
Qy 1201 TTTCTTGTAGTGAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1260
Db 1201 TTTCTTGTAGTGAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1260
Qy 1261 CACATTTGCAAG 1320
Db 1261 CACATTTGCAAG 1320
Qy 1321 ATAAAGGGGAAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 ATAAAGGGGAAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 TTGATGTTCTGTATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 TTGATGTTCTGTATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1441 AAAATGATGATTAATTAACAAGCTTCAATCACAAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 AAAATGATGATTAATTAACAAGCTTCAATCACAAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 CATCAACTCTGTAGATTAATTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 CATCAACTCTGTAGATTAATTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Qy 1561 AAGAAACCCAG 1620
Db 1561 AAGAAACCCAG 1620

Qy 1621 CTTGTGATTTTGTCAAGGTGCACTTAAATATGTTGATTCATGCAAAACAGAGAC 1680
Db 1621 CTTGTGATTTTGTCAAGGTGCACTTAAATATGTTGATTCATGCAAAACAGAGAC 1680
Qy 1681 ATCTTATGAGCTGTCTTATACATGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ATCTTATGAGCTGTCTTATACATGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 TATGTAGCAACCAATTCAAATGATTTGTGCTTATTTTCCCTAGTGAACGTCTAT 1800
Db 1741 TATGTAGCAACCAATTCAAATGATTTGTGCTTATTTTCCCTAGTGAACGTCTAT 1800
Qy 1801 AAGAGATTAATATTTCTAATCTATATACCTTGAAGATTTAGCAACCTGAATTTAT 1860
Db 1801 AAGAGATTAATATTTCTAATCTATATACCTTGAAGATTTAGCAACCTGAATTTAT 1860
Qy 1861 CACATATATCAAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 CACATATATCAAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Qy 1921 TGACCTACTTGTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 TGACCTACTTGTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy 1981 CATCCTTTACACCAACTCTTAAATTTTAAATTTTCTACTGTCTTAAATGAGAGATAC 2040
Db 1981 CATCCTTTACACCAACTCTTAAATTTTAAATTTTCTACTGTCTTAAATGAGAGATAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGATTTTATTTTATTTT 2100
Db 2041 TTGGTTTTTTTTTTCTTAAATATGATATGATTTAAATGATTTTATTTTATTTT 2100
Qy 2101 AGACCGAGTCTTGTCTGTATACCAAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Db 2101 AGACCGAGTCTTGTCTGTATACCAAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Qy 2161 AGCTGTGCTTCCCGGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Db 2161 AGCTGTGCTTCCCGGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Qy 2221 TACAGTCACTGTGCAACCACTGTGCTTAAATTTTGTATTTTGTATGAGAGAGAGAGAG 2280
Db 2221 TACAGTCACTGTGCAACCACTGTGCTTAAATTTTGTATTTTGTATGAGAGAGAGAGAG 2280
Qy 2281 ACCGTGTAG 2340
Db 2281 ACCGTGTAG 2340
Qy 2341 CAAAGTGTGGGATTTACAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2372
Db 2341 CAAAGTGTGGGATTTACAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2372

RESULT 11
AAZ37471
ID AAZ37471 standard; cdna; 2372 BP.
XX AAZ37471;
DT 07-JAN-2000 (first entry)
XX
DE Human sarcoma p53-associated gene.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
XX hyperproliferation; blood cancer; brain cancer; breast cancer;
XX lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
XX restenosis; ss.
XX
XX Homo sapiens.
OS
XX
XX
PN W09949065-A1.

XX 30-SEP-1999.
 PD 26-MAR-1999; 99WO-US006702.
 XX PF 26-MAR-1999; 98US-00048810.
 XX PR 26-MAR-1999; 98US-00048810.
 XX (ISIS-) ISIS PHARM INC.
 XX Mirgila LJ, Nero P, Graham MJ, Moria BP, Cowseert LM;
 XX WPI, 1999-610754/52.
 XX New antisense compounds used to treat eg. hyperproliferative conditions.
 XX Example 2; Page 79-81; 157pp; English.
 PS AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.
 CC AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the
 CC exemplification of the present invention. The present invention describes
 CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
 CC translation termination codon, or 3' untranslated region of a nucleic
 CC acid encoding human mdm2, that modulates expression of human mdm2. The
 CC oligonucleotides mediate their effect by antisense inhibition of
 CC hyperproliferative gene expression. The antisense compound is used to
 CC treat an animal having a disease or condition associated with mdm2,
 CC particularly a hyperproliferative condition, more particularly cancer,
 CC especially of the blood, brain, breast, lung or soft tissue, or
 CC psoriasis, fibrosis, atherosclerosis or restenosis
 CC
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2372; DB 2; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCCGTGTGCGCCGTGTGTGCGAAAGATGGA 60
 DB 1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCCGTGTGCGCCGTGTGTGCGAAAGATGGA 60
 QY 61 GCAGAGCCGAGCCGAGGGGCGGCGGAGCCCTCTGACCGAGATCCCTGCTGCTTGG 120
 DB 61 GCAGAGCCGAGCCGAGGGGCGGCGGAGCCCTCTGACCGAGATCCCTGCTGCTTGG 120
 QY 121 CAGCCAGGAGCAGCCTGCTTCTCCCGGATTAATGCGTGAAGGCCAGTGGCTTGGCCG 180
 DB 121 CAGCCAGGAGCAGCCTGCTTCTCCCGGATTAATGCGTGAAGGCCAGTGGCTTGGCCG 180
 QY 121 CAGCCAGGAGCAGCCTGCTTCTCCCGGATTAATGCGTGAAGGCCAGTGGCTTGGCCG 180
 DB 121 CAGCCAGGAGCAGCCTGCTTCTCCCGGATTAATGCGTGAAGGCCAGTGGCTTGGCCG 180
 QY 181 GAGAGTGAATGATCCCGAGGCGCAGGGCGTGTGCTTCCGAGATGCAATCCCGGTG 240
 DB 181 GAGAGTGAATGATCCCGAGGCGCAGGGCGTGTGCTTCCGAGATGCAATCCCGGTG 240
 QY 181 GAGAGTGAATGATCCCGAGGCGCAGGGCGTGTGCTTCCGAGATGCAATCCCGGTG 240
 DB 181 GAGAGTGAATGATCCCGAGGCGCAGGGCGTGTGCTTCCGAGATGCAATCCCGGTG 240
 QY 241 AAGGAACCTGGGAGATCTTGAAGGAGCCCGGAGCTCCAGCGGAGAAACCCCGATGTA 300
 DB 241 AAGGAACCTGGGAGATCTTGAAGGAGCCCGGAGCTCCAGCGGAGAAACCCCGATGTA 300
 QY 241 AAGGAACCTGGGAGATCTTGAAGGAGCCCGGAGCTCCAGCGGAGAAACCCCGATGTA 300
 DB 241 AAGGAACCTGGGAGATCTTGAAGGAGCCCGGAGCTCCAGCGGAGAAACCCCGATGTA 300
 QY 301 GGAGCAGGAGAAATGTCATTAACCAATGCTGTGTAATTAATGATGATGATGATGATGAT 360
 DB 301 GGAGCAGGAGAAATGTCATTAACCAATGCTGTGTAATTAATGATGATGATGATGATGAT 360
 QY 301 GGAGCAGGAGAAATGTCATTAACCAATGCTGTGTAATTAATGATGATGATGATGATGAT 360
 DB 301 GGAGCAGGAGAAATGTCATTAACCAATGCTGTGTAATTAATGATGATGATGATGATGAT 360
 QY 361 CACAGATTCGAGCTTCCGAGAAAGAGACCTTGTGTAAGCAAGCAATGCTTGTGTAAGT 420
 DB 361 CACAGATTCGAGCTTCCGAGAAAGAGACCTTGTGTAAGCAAGCAATGCTTGTGTAAGT 420
 QY 361 CACAGATTCGAGCTTCCGAGAAAGAGACCTTGTGTAAGCAAGCAATGCTTGTGTAAGT 420
 DB 361 CACAGATTCGAGCTTCCGAGAAAGAGACCTTGTGTAAGCAAGCAATGCTTGTGTAAGT 420
 QY 421 TATTAAGTCTGTGTGTCAGAAAGACACTTATATGTAAGAGGTTCTTTTATATC 480
 DB 421 TATTAAGTCTGTGTGTCAGAAAGACACTTATATGTAAGAGGTTCTTTTATATC 480
 QY 421 TATTAAGTCTGTGTGTCAGAAAGACACTTATATGTAAGAGGTTCTTTTATATC 480
 DB 421 TATTAAGTCTGTGTGTCAGAAAGACACTTATATGTAAGAGGTTCTTTTATATC 480
 QY 481 TTGGCAGATATTTATGACTAAACGATTTATATGATGAGAGCAACATATTTATAT 540
 DB 481 TTGGCAGATATTTATGACTAAACGATTTATATGATGAGAGCAACATATTTATAT 540
 QY 481 TTGGCAGATATTTATGACTAAACGATTTATATGATGAGAGCAACATATTTATAT 540
 DB 481 TTGGCAGATATTTATGACTAAACGATTTATATGATGAGAGCAACATATTTATAT 540
 QY 541 GTTCAATGATCTTGAAGATTTGTTGGGTGCAAGCTTCTGTGAAAGAGCA 600

DB 541 GTTCAATGATCTTGAAGATTTGTTGGGTGCAAGCTTCTGTGAAAGAGCA 600
 QY 601 GGAATAATATATCCATGATCTACAGAACTTGTGTAGTCAATCAAGCAATCATCG 660
 DB 601 GGAATAATATATCCATGATCTACAGAACTTGTGTAGTCAATCAAGCAATCATCG 660
 QY 661 ACTCAGGTATCTGTAGTGAAGCAGGTGACCTTGAAGTGGAGTATCAAAAG 720
 DB 661 ACTCAGGTATCTGTAGTGAAGCAGGTGACCTTGAAGTGGAGTATCAAAAG 720
 QY 661 ACTCAGGTATCTGTAGTGAAGCAGGTGACCTTGAAGTGGAGTATCAAAAG 720
 DB 661 ACTCAGGTATCTGTAGTGAAGCAGGTGACCTTGAAGTGGAGTATCAAAAG 720
 QY 721 ACCCTGTACAAAGCTTACAGAAAGAAACCTTCAATCTTCAATTTGTTTACAGCAT 780
 DB 721 ACCCTGTACAAAGCTTACAGAAAGAAACCTTCAATCTTCAATTTGTTTACAGCAT 780
 QY 721 ACCCTGTACAAAGCTTACAGAAAGAAACCTTCAATCTTCAATTTGTTTACAGCAT 780
 DB 721 ACCCTGTACAAAGCTTACAGAAAGAAACCTTCAATCTTCAATTTGTTTACAGCAT 780
 QY 781 CTACCTCATCTAGAAAGAGAGCAATTAATGAGACAGAAAGAAATTCAGATGATATCTG 840
 DB 781 CTACCTCATCTAGAAAGAGAGCAATTAATGAGACAGAAAGAAATTCAGATGATATCTG 840
 QY 781 CTACCTCATCTAGAAAGAGAGCAATTAATGAGACAGAAAGAAATTCAGATGATATCTG 840
 DB 781 CTACCTCATCTAGAAAGAGAGCAATTAATGAGACAGAAAGAAATTCAGATGATATCTG 840
 QY 841 GTGAACGACAAAGAAAGCCCAAAATCTGATGATATTTCCCTTCTTGTGTAAGGCC 900
 DB 841 GTGAACGACAAAGAAAGCCCAAAATCTGATGATATTTCCCTTCTTGTGTAAGGCC 900
 QY 841 GTGAACGACAAAGAAAGCCCAAAATCTGATGATATTTCCCTTCTTGTGTAAGGCC 900
 DB 841 GTGAACGACAAAGAAAGCCCAAAATCTGATGATATTTCCCTTCTTGTGTAAGGCC 900
 QY 901 TGGCTCTGTGTATTAAGGAGATATGTTGAAAGAGCAAGTACAGTATCTACAG 960
 DB 901 TGGCTCTGTGTATTAAGGAGATATGTTGAAAGAGCAAGTACAGTATCTACAG 960
 QY 901 TGGCTCTGTGTATTAAGGAGATATGTTGAAAGAGCAAGTACAGTATCTACAG 960
 DB 901 TGGCTCTGTGTATTAAGGAGATATGTTGAAAGAGCAAGTACAGTATCTACAG 960
 QY 961 GGAGCCCATCGAATCCGATCTTGAATGCTGTGATGATGATGATGATGATGATGATGAT 1020
 DB 961 GGAGCCCATCGAATCCGATCTTGAATGCTGTGATGATGATGATGATGATGATGATGAT 1020
 QY 961 GGAGCCCATCGAATCCGATCTTGAATGCTGTGATGATGATGATGATGATGATGATGAT 1020
 DB 961 GGAGCCCATCGAATCCGATCTTGAATGCTGTGATGATGATGATGATGATGATGATGAT 1020
 QY 1021 ATCAGATTCAGTTTCAATCAGTTTCAATCAGTTTCAATCAGTTTCAATCAGTTTCAATCAG 1080
 DB 1021 ATCAGATTCAGTTTCAATCAGTTTCAATCAGTTTCAATCAGTTTCAATCAGTTTCAATCAG 1080
 QY 1021 ATCAGATTCAGTTTCAATCAGTTTCAATCAGTTTCAATCAGTTTCAATCAGTTTCAATCAG 1080
 DB 1021 ATCAGATTCAGTTTCAATCAGTTTCAATCAGTTTCAATCAGTTTCAATCAGTTTCAATCAG 1080
 QY 1081 AAGATTATAGCTTATGTAAGAGCAAGAACTCTCAGATGAAGTATGATATATC 1140
 DB 1081 AAGATTATAGCTTATGTAAGAGCAAGAACTCTCAGATGAAGTATGATATATC 1140
 QY 1081 AAGATTATAGCTTATGTAAGAGCAAGAACTCTCAGATGAAGTATGATATATC 1140
 DB 1081 AAGATTATAGCTTATGTAAGAGCAAGAACTCTCAGATGAAGTATGATATATC 1140
 QY 1141 AAGTTACTGTATATCAGGAGGAGAGTATGATGATGATGATGATGATGATGATGATGAT 1200
 DB 1141 AAGTTACTGTATATCAGGAGGAGAGTATGATGATGATGATGATGATGATGATGATGAT 1200
 QY 1141 AAGTTACTGTATATCAGGAGGAGAGTATGATGATGATGATGATGATGATGATGATGAT 1200
 DB 1141 AAGTTACTGTATATCAGGAGGAGAGTATGATGATGATGATGATGATGATGATGATGAT 1200
 QY 1201 TTTCTTACGTAATTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 DB 1201 TTTCTTACGTAATTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 QY 1201 TTTCTTACGTAATTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 DB 1201 TTTCTTACGTAATTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 QY 1261 CACATTTGAAGAGATGTTGGGCTTGTGAGAAATTTGGCTTCTGAAGATTAAGGAGAAAG 1320
 DB 1261 CACATTTGAAGAGATGTTGGGCTTGTGAGAAATTTGGCTTCTGAAGATTAAGGAGAAAG 1320
 QY 1261 CACATTTGAAGAGATGTTGGGCTTGTGAGAAATTTGGCTTCTGAAGATTAAGGAGAAAG 1320
 DB 1261 CACATTTGAAGAGATGTTGGGCTTGTGAGAAATTTGGCTTCTGAAGATTAAGGAGAAAG 1320
 QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAGAGCTGAAGAGGCT 1380
 DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAGAGCTGAAGAGGCT 1380
 QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAGAGCTGAAGAGGCT 1380
 DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAGAGCTGAAGAGGCT 1380
 QY 1381 TTGATGTTCTGTATTTAAAGAACTATATGATGATGATGATGATGATGATGATGATGAT 1440
 DB 1381 TTGATGTTCTGTATTTAAAGAACTATATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1381 TTGATGTTCTGTATTTAAAGAACTATATGATGATGATGATGATGATGATGATGATGAT 1440
 DB 1381 TTGATGTTCTGTATTTAAAGAACTATATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1441 AAAATGATGATTAATTAACAAGCTTCAATCAAGAAAGTGAAGATATTTCTCAGC 1500
 DB 1441 AAAATGATGATTAATTAACAAGCTTCAATCAAGAAAGTGAAGATATTTCTCAGC 1500
 QY 1441 AAAATGATGATTAATTAACAAGCTTCAATCAAGAAAGTGAAGATATTTCTCAGC 1500
 DB 1441 AAAATGATGATTAATTAACAAGCTTCAATCAAGAAAGTGAAGATATTTCTCAGC 1500
 QY 1501 CATCAATCTTATGATGATTAATTTATGAGCAGCAAGAGATGTAAGAGTGAAGAGG 1560
 DB 1501 CATCAATCTTATGATGATTAATTTATGAGCAGCAAGAGATGTAAGAGTGAAGAGG 1560
 QY 1501 CATCAATCTTATGATGATTAATTTATGAGCAGCAAGAGATGTAAGAGTGAAGAGG 1560
 DB 1501 CATCAATCTTATGATGATTAATTTATGAGCAGCAAGAGATGTAAGAGTGAAGAGG 1560
 QY 1561 AAGAAACCAAGACAAAGAGAGAGTGTGAATCTTATGATGATGATGATGATGATGATGAT 1620
 DB 1561 AAGAAACCAAGACAAAGAGAGAGTGTGAATCTTATGATGATGATGATGATGATGATGAT 1620
 QY 1561 AAGAAACCAAGACAAAGAGAGAGTGTGAATCTTATGATGATGATGATGATGATGATGAT 1620
 DB 1561 AAGAAACCAAGACAAAGAGAGAGTGTGAATCTTATGATGATGATGATGATGATGATGAT 1620
 QY 1621 CTGTGATATTTGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1680

Db 1621 CTGTGTGATTTGTCAAGTGCACCTTAAATGTTGCTATGTCCATGCAAAACAGAGAC 1680
Qy 1681 ATCTTATGGCCGTGCTTATCATGTGCAGAAAGCTTAAAGAAATAGAGCCCTGCCAG 1740
Db 1681 ATCTTATGGCCGTGCTTATCATGTGCAGAAAGCTTAAAGAAATAGAGCCCTGCCAG 1740
Qy 1741 TATGTAGCAACCAATTCAAATGATTTGCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
Db 1741 TATGTAGCAACCAATTCAAATGATTTGCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
Qy 1801 AAGGAATATATATTTCTAACTATATACCTTAGAAATTTAGACAACTGAAATTTAT 1860
Db 1801 AAGGAATATATATTTCTAACTATATACCTTAGAAATTTAGACAACTGAAATTTAT 1860
Qy 1861 CACATATATCAAGGAGAAATGCTCAATTCATGATTTCTCTCTTATATAT 1920
Db 1861 CACATATATCAAGGAGAAATGCTCAATTCATGATTTCTCTCTTATATAT 1920
Qy 1921 TGACCTACTTTGTAGTGAATAGTAAATCTTACTATATATTTGAATTGAAATATAGCT 1980
Db 1921 TGACCTACTTTGTAGTGAATAGTAAATCTTACTATATATTTGAAATATAGCT 1980
Qy 1981 CATCTTATACCAACCTCTTAAATTTTAAATATTTCTCTCTTAAATAGAGATAC 2040
Db 1981 CATCTTATACCAACCTCTTAAATTTTAAATATTTCTCTCTTAAATAGAGATAC 2040
Qy 2041 TTGGTTTTTTTTTCTTAAATATATATATATATATATATATATATATATATATAT 2100
Db 2041 TTGGTTTTTTTTTCTTAAATATATATATATATATATATATATATATATATATAT 2100
Qy 2101 AGACCGAGCTTGTCTGTCTTACCCAGGCTGAGTGCAGTGGTGAATCTTGCTCACTGA 2160
Db 2101 AGACCGAGCTTGTCTGTCTTACCCAGGCTGAGTGCAGTGGTGAATCTTGCTCACTGA 2160
Qy 2161 AGCTTGCCTCTCCCGGGTTCGACCAATCTCTGCTCAGCTCCCAATTTAGCTTGGCC 2220
Db 2161 AGCTTGCCTCTCCCGGGTTCGACCAATCTCTGCTCAGCTCCCAATTTAGCTTGGCC 2220
Qy 2221 TACAGTCAATTCGCAACCACTGGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
Db 2221 TACAGTCAATTCGCAACCACTGGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
Qy 2281 ACCGTGTTAGCCAGGATGCTCGATCTCTGACCTCGATCCGCCACTTCGGCTTC 2340
Db 2281 ACCGTGTTAGCCAGGATGCTCGATCTCTGACCTCGATCCGCCACTTCGGCTTC 2340
Qy 2341 CAAAGTGTGGGATTTACAGGCATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTTACAGGCATGAGCCACCG 2372

RESULT 12
AAX35093 standard; cDNA; 2372 BP.
ID AAX35093;
AC AAX35093;
XX 01-JUL-1999 (first entry)
DE Nucleotide sequence of human MDM2 cDNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
XX Homo sapiens.
OS
XX
XX WO910486-A2.
XX
XX 04-MAR-1999.
XX
XX 18-AUG-1998; 98WO-US017147.
XX
XX 22-AUG-1997; 97US-00916384.

PR 06-MAY-1998; 98US-00073567.
XX
XX (HYBR-) HYBRIDON INC.
XX
XX Chen J, Agrawal S, Zhang R;
XX WPI; 1999-254219/21.
XX
XX New MDM2-specific antisense oligonucleotides.
XX
XX Disclosure; Fig 1A; 5pp; English.
XX
XX The present sequence represents the cDNA sequence encoding human MDM2
XX protein. The specification describes antisense oligonucleotides that
XX inhibit MDM2 protein expression. The antisense oligonucleotides can be
XX used to activate a tumour suppressor. The antisense oligonucleotides are
XX used to inhibit tumour growth in a mammal, including a human,
XX particularly in conjunction with a DNA-damaging agent such as
XX camptothecin
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCCGAGCTTGGCTCTCTGAGGCGCTGTGTGCGCTGTGTGCGAAAGATGA 60
Db 1 GCACCGCCGAGCTTGGCTCTCTGAGGCGCTGTGTGCGCTGTGTGCGAAAGATGA 60
Qy 61 GCAGAGCCGAGCCGAGGCGCGCGGAGCCCTCTGACCGAGATCTGCTGCTTTCG 120
Db 61 GCAGAGCCGAGCCGAGGCGCGCGGAGCCCTCTGACCGAGATCTGCTGCTTTCG 120
Qy 121 CAGCGAGAGACCGCTCCCTCCCGGATTAATGTGTAGAGCGCCAGTGCCTGGCCCG 180
Db 121 CAGCGAGAGACCGCTCCCTCCCGGATTAATGTGTAGAGCGCCAGTGCCTGGCCCG 180
Qy 121 CAGCGAGAGACCGCTCCCTCCCGGATTAATGTGTAGAGCGCCAGTGCCTGGCCCG 180
Db 121 CAGCGAGAGACCGCTCCCTCCCGGATTAATGTGTAGAGCGCCAGTGCCTGGCCCG 180
Qy 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGCTGCTTCCGAGTACAGTCCCGCTG 240
Db 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGCTGCTTCCGAGTACAGTCCCGCTG 240
Qy 241 AAGGAATGGGAGTCTTGAAGGACCCCGCATTCGAAAGCGGAAACCCCGAGTGTGA 300
Db 241 AAGGAATGGGAGTCTTGAAGGACCCCGCATTCGAAAGCGGAAACCCCGAGTGTGA 300
Qy 301 GAGAGGCGCAATGTGCAATACCAATGTCTGTACTTACTATGATGTGCTGTAACCACT 360
Db 301 GAGAGGCGCAATGTGCAATACCAATGTCTGTACTTACTATGATGTGCTGTAACCACT 360
Qy 361 CACAGATTCAGCTTCGGAACAGAGACCTGCTTGAACCAAGCCATTGCTTTGAAGT 420
Db 361 CACAGATTCAGCTTCGGAACAGAGACCTGCTTGAACCAAGCCATTGCTTTGAAGT 420
Qy 421 TATTAAGTCTGTGTCGACAAAGACACTTATATATGAGAGAGGTTCTTTTATATC 480
Db 421 TATTAAGTCTGTGTCGACAAAGACACTTATATATGAGAGAGGTTCTTTTATATC 480
Qy 481 TTGGCCAGTATATTAATGACTAAAGCATATATATGATGAGAGCAACATATATATAT 540
Db 481 TTGGCCAGTATATTAATGACTAAAGCATATATATGATGAGAGCAACATATATATAT 540
Qy 541 GTTCAATGATCTTGAAGATTTGTTGGGCTGCCAAGCTTCTGTGAAAGAGACA 600
Db 541 GTTCAATGATCTTGAAGATTTGTTGGGCTGCCAAGCTTCTGTGAAAGAGACA 600
Qy 601 GGAAT 660
Db 601 GGAAT 660
Qy 661 ACTCAGGTACATCTGTGAGTGAAGCAAGGTGTCACCTTGAAGTGGAGATGATCAAAAG 720
Db 661 ACTCAGGTACATCTGTGAGTGAAGCAAGGTGTCACCTTGAAGTGGAGATGATCAAAAG 720

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QY 721 ACCCTGTACAGAGCTTCAAGAGAACTTCATCTTCACTTTGGTTTCTAGACCAT 780
DB 721 ACCCTGTACAGAGCTTCAAGAGAACTTCATCTTCACTTTGGTTTCTAGACCAT 780
QY 781 CTACCTCATCTGAGAGAGACATTTAGTGAACAGAGAAATTCAGATGAATTAATCTG 840
DB 781 CTACCTCATCTGAGAGAGACATTTAGTGAACAGAGAAATTCAGATGAATTAATCTG 840
QY 841 GTGAACGACAAAGAAACCCCAATCTGATGATTTTCCCTTCTTGTGTAAGGCC 900
DB 841 GTGAACGACAAAGAAACCCCAATCTGATGATTTTCCCTTCTTGTGTAAGGCC 900
QY 901 TGGCTCTGTGTAAATTAAGGAGATATGTTGTAAGAAAGACAGTACAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTAAATTAAGGAGATATGTTGTAAGAAAGACAGTACAGTGAATCTACAG 960
QY 961 GGAAGCCATCGAATCCGATCTTGATGCTGTGTAAAGTGAACATTCAGGTGATGGTTGG 1020
DB 961 GGAAGCCATCGAATCCGATCTTGATGCTGTGTAAAGTGAACATTCAGGTGATGGTTGG 1020
QY 1021 ATCAGAGATTCAGTTCAATCACTTATGCTGATGATTTGAAGTTGAATCTTCGACTCAG 1080
DB 1021 ATCAGAGATTCAGTTCAATCACTTATGCTGATGATTTGAAGTTGAATCTTCGACTCAG 1080
QY 1081 AAGATTATAGCTTATGTAAGAGACAAAGCTCTCAGATGAAGTGAATGATATC 1140
DB 1081 AAGATTATAGCTTATGTAAGAGACAAAGCTCTCAGATGAAGTGAATGATATC 1140
QY 1141 AAGTTACTGTGTATCAGGAGGAGAGATGATACAGATTCATTTGAAAGAAATCCCTGAA 1200
DB 1141 AAGTTACTGTGTATCAGGAGGAGAGATGATACAGATTCATTTGAAAGAAATCCCTGAA 1200
QY 1201 TTTCTTGTAGCTACATTTGGAATGATCACTTCATGCAATGAATGAATCCCTTCCAT 1260
DB 1201 TTTCTTGTAGCTACATTTGGAATGATCACTTCATGCAATGAATGAATCCCTTCCAT 1260
QY 1261 CACATTGCAACAGATGTTGGGCCCTTCGTAAGAAATGGCTTCTGTAAGTAAGGAAG 1320
DB 1261 CACATTGCAACAGATGTTGGGCCCTTCGTAAGAAATGGCTTCTGTAAGTAAGGAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGAAATCTCAACACAGCTGAAGAGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGAAATCTCAACACAGCTGAAGAGGCT 1380
QY 1381 TTGATGTTCTGTATGTAAGAACTATAGTAATGATTCAGAGAGTCAATGTTGAAG 1440
DB 1381 TTGATGTTCTGTATGTAAGAACTATAGTAATGATTCAGAGAGTCAATGTTGAAG 1440
QY 1441 AAAATGATGATTAATTAACAGAGCTTCACATTCACAGAAAGTGAAGCTATTTCTCAGC 1500
DB 1441 AAAATGATGATTAATTAACAGAGCTTCACATTCACAGAAAGTGAAGCTATTTCTCAGC 1500
QY 1501 CATCACTTCTAGTACATTTATTTATGACAGCAAGAGATGTAAGAGTTGAAGGG 1560
DB 1501 CATCACTTCTAGTACATTTATTTATGACAGCAAGAGATGTAAGAGTTGAAGGG 1560
QY 1561 AAGAAACCAAGACAAAGAGAGAGTGTGAATCTAGTTGGCCCTTAATGCAATGAAC 1620
DB 1561 AAGAAACCAAGACAAAGAGAGAGTGTGAATCTAGTTGGCCCTTAATGCAATGAAC 1620
QY 1621 CTGTGTATTTTGTCAAGTGCACCTAAATAATGTTGCAATTCGACAAACAGAGC 1680
DB 1621 CTGTGTATTTTGTCAAGTGCACCTAAATAATGTTGCAATTCGACAAACAGAGC 1680
QY 1681 ATCTTATGAGCTGCTTTATCATGTGCAAGAAAGCTAAAGAAAGAAAGAAAGCTGCTCAG 1740
DB 1681 ATCTTATGAGCTGCTTTATCATGTGCAAGAAAGCTAAAGAAAGAAAGAAAGCTGCTCAG 1740
QY 1741 TATGTAGCAACCAATTCAAATGATTTGCTACTTAATTTCCCTAGTTGACCTGTCTAT 1800
DB 1741 TATGTAGCAACCAATTCAAATGATTTGCTACTTAATTTCCCTAGTTGACCTGTCTAT 1800

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QY 1801 AAGAGATTAATATTTCTAATCATATTAACCTTAGAATTTAGACAACTGAAATTAAT 1860
DB 1801 AAGAGATTAATATTTCTAATCATATTAACCTTAGAATTTAGACAACTGAAATTAAT 1860
QY 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTTTAGATTAAT 1920
DB 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGATTAAT 1920
QY 1921 TGACCTACTTGGTATGATGATATGATATCTTACTATTAATTTGACTTGAATATGAGCT 1980
DB 1921 TGACCTACTTGGTATGATGATATGATATCTTACTATTAATTTGACTTGAATATGAGCT 1980
QY 1981 CATCTTTACCAACTCTCTAATTTTAATTAATTTTACTCTGTCTTAATAGAAATAC 2040
DB 1981 CATCTTTACCAACTCTCTAATTTTAATTAATTTTACTCTGTCTTAATAGAAATAC 2040
QY 2041 TTGGTTTTTTTTTCTTAATATGATATGATATTAATTAATTAATTTTATTTTGG 2100
DB 2041 TTGGTTTTTTTTTCTTAATATGATATGATATTAATTAATTAATTTTATTTTGG 2100
QY 2101 AAGCCGAGCTTGTCTGTATACCCAGGCTGAGAGTGAAGTGGTATCTTGCTCACTGCA 2160
DB 2101 AAGCCGAGCTTGTCTGTATACCCAGGCTGAGAGTGAAGTGGTATCTTGCTCACTGCA 2160
QY 2161 AGCTGCGCCCTCCCGGGTTGACACATTCCTGCTCAGGCTCCCATTTAGCTGGCC 2220
DB 2161 AGCTGCGCCCTCCCGGGTTGACACATTCCTGCTCAGGCTCCCATTTAGCTGGCC 2220
QY 2221 TACAGTCACTGCTGACACACACACCTGGCTAATTTTGTACTTTTATGAGAGACAGGGTTTC 2280
DB 2221 TACAGTCACTGCTGACACACACACCTGGCTAATTTTGTACTTTTATGAGAGACAGGGTTTC 2280
QY 2281 ACCGTGTAGCCAGATGGTCTGATCTCTGACCTCGATCGGCCACCTCGGCTCC 2340
DB 2281 ACCGTGTAGCCAGATGGTCTGATCTCTGACCTCGATCGGCCACCTCGGCTCC 2340
QY 2341 CAAGTGTGGGATTAACAGGCAATGAGCCACCG 2372
DB 2341 CAAGTGTGGGATTAACAGGCAATGAGCCACCG 2372

RESULT 13
AAA29389
ID AAA29389 standard; cDNA; 2372 BP.
XX
XX AAA29389;
AC
XX
XX 12-SEP-2000 (first entry)
DT
XX
DE MDM2 oncoprotein coding sequence.
XX
XX hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
XX retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
XX proliferation; immortal; tumour therapy; macular degeneration; activator;
XX INK4; s8.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX FT 312..1787
XX CDS /*tag= a
XX FT /product= "MDM2_oncoprotein"
XX
XX WO200031238-A2.
XX
XX 02-JUN-2000.
XX
XX 24-NOV-1999; 99WO-US027907.
XX
XX 25-NOV-1998; 98US-0109891P.
XX 17-FEB-1999; 99US-0120549P.
XX
XX (GENE-) GENETICA INC.
PA

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QY 1501 CATCACTTCTAGTAGCATTATTATAGACGCCAAGAGATGTGAAGATTGAAAGG 1560
DB 1501 CATCACTTCTAGTAGCATTATTATAGACGCCAAGAGATGTGAAGATTGAAAGG 1560
QY 1561 AAGAAACCCAAAGCAAAAGAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
DB 1561 AAGAAACCCAAAGCAAAAGAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
QY 1621 CTGTGTGATTTGTCAAGGTCGACCTAAAGATGTGGCAATGGCCATGGCAAAACGAGAC 1680
DB 1621 CTGTGTGATTTGTCAAGGTCGACCTAAAGATGTGGCAATGGCCATGGCAAAACGAGAC 1680
QY 1681 ATCTTAGGCTGCTTTACATGTGCAAGAGAGCTAAAGAAAGAAAGATTAAGCCCTGCCAG 1740
DB 1681 ATCTTAGGCTGCTTTACATGTGCAAGAGAGCTAAAGAAAGAAAGATTAAGCCCTGCCAG 1740
QY 1741 TATGTAGACCAACCAATTCAATGATGTGTCTAATTTATTTCCCTAGTTGACCTGTCTAT 1800
DB 1741 TATGTAGACCAACCAATTCAATGATGTGTCTAATTTATTTCCCTAGTTGACCTGTCTAT 1800
QY 1801 AAGAGATTAATATTTCTTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
DB 1801 AAGAGATTAATATTTCTTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
QY 1861 CACATATATCAAGTAGAGAAATGCTCAATTCAATAGATTCTTCTAGTAGTAAT 1920
DB 1861 CACATATATCAAGTAGAGAAATGCTCAATTCAATAGATTCTTCTAGTAGTAAT 1920
QY 1921 TGACCTACTTTGGTAGTGAATAGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
DB 1921 TGACCTACTTTGGTAGTGAATAGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
QY 1981 CATCTTTACACCACTCTTAATTTAAATTAATTTACTCTGTCTTAATGAAGATAC 2040
DB 1981 CATCTTTACACCACTCTTAATTTAAATTAATTTACTCTGTCTTAATGAAGATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATATATATATATATATATATATATATATATATATATATAT 2100
DB 2041 TTGGTTTTTTTTTTCTTAATATATATATATATATATATATATATATATATATATATAT 2100
QY 2101 AGACCGAGTCTGTCTGTATACCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160
DB 2101 AGACCGAGTCTGTCTGTATACCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160
QY 2161 AGCTTGTGCTCTCCCGGGTTCGACCACTTCTCTGCTCAGCTCCCAATTAAGCTTGCC 2220
DB 2161 AGCTTGTGCTCTCCCGGGTTCGACCACTTCTCTGCTCAGCTCCCAATTAAGCTTGCC 2220
QY 2221 TACAGTCACTGSCACCACTGGCTAATTTTGTACTTTTATAGAGACAGGCTTTC 2280
DB 2221 TACAGTCACTGSCACCACTGGCTAATTTTGTACTTTTATAGAGACAGGCTTTC 2280
QY 2281 ACCGTGTAGCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCACTCGGCTCC 2340
DB 2281 ACCGTGTAGCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCACTCGGCTCC 2340
QY 2341 CAAAGTGTGGGATTAACAGGCATGAGCCACCG 2372
DB 2341 CAAAGTGTGGGATTAACAGGCATGAGCCACCG 2372

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RESULT 14

AAE80625 standard; cDNA; 2372 BP.

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XX AA80625;
XX
XX 02-MAY-2001 (first entry)
XX
XX Human mdm2 cDNA.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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OS Homo sapiens.
XX
XX US6184212-B1.
XX
XX 06-FEB-2001.
XX
XX 26-MAR-1999; 99US-00280805.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
XX WPI; 2001-190948/19.
XX
XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
XX acid molecule encoding human mdm-2 useful for modulating the expression
XX of human mdm-2 and reducing hyperproliferation of human cells.
XX
XX Example 2; Col 43-46; 77bp; English.
XX
XX The present invention relates to an antisense compound 8-30 nucleobases
XX in length targeted to nucleobases 1-308 of the 5' untranslated region,
XX 1776-1806 of the translation termination codon region or 1818-2370 of the
XX 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
XX The invention is useful for reducing hyperproliferation of human cells,
XX modulating the expression of mdm2 in human cells or tissues or in vitro.
XX The hyperproliferative disorder includes cancer or psoriasis
XX
XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other.

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Query Match 100.0%; Score 2372; DB 4; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0; Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCACCGCGGAGCTTGGCTCTTCTGGGCGCTGTGTGCGCCCTGTGTGCGAAATGGA 60
DB 1 GCACCGCGGAGCTTGGCTCTTCTGGGCGCTGTGTGCGCCCTGTGTGCGAAATGGA 60
QY 61 GCAGAGCGGAGCGGCGGAGGCGGCGGAGCCCTCTGACCGAGATCTCTGCTGCTTGC 120
DB 61 GCAGAGCGGAGCGGCGGAGGCGGCGGAGCCCTCTGACCGAGATCTCTGCTGCTTGC 120
QY 121 CAGCAGAGACGACGCTCCCTCCCGGATTAAGTGCCTGACGAGCGCCAGTCCCTGCGCG 180
DB 121 CAGCAGAGAGACGCTCCCTCCCGGATTAAGTGCCTGACGAGCGCCAGTCCCTGCGCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGGAGGCGGCGGAGCGGCGGAGCGGAGCGGAGCGGAG 240
DB 181 GAGAGTGAATGATCCCGAGGCGGAGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 240
QY 241 AAGGAACTGGGGAATCTTTGAGGGAACCCCGGACTCCAGCGGAGAAACCCCGGATGAGTA 300
DB 241 AAGGAACTGGGGAATCTTTGAGGGAACCCCGGACTCCAGCGGAGAAACCCCGGATGAGTA 300
QY 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACTTACTGATGAGTGTCTGTAACCACT 360
DB 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACTTACTGATGAGTGTCTGTAACCACT 360
QY 361 CACAGATTCAGCTTGGGAAACAGAGACCTGTGTAGACCAAAAGCATTTGCTTTGAAGT 420
DB 361 CACAGATTCAGCTTGGGAAACAGAGACCTGTGTAGACCAAAAGCATTTGCTTTGAAGT 420
QY 421 TATTAAGTCTGTGTGCACAAAAGACATTTACTATGAAAGAGGTTCTTTTATATC 480
DB 421 TATTAAGTCTGTGTGCACAAAAGACATTTACTATGAAAGAGGTTCTTTTATATC 480
QY 481 TTGGCCAGTATATATATGCTAAACGATTAATATGATGAGAGCAACATATTTGATAT 540
DB 481 TTGGCCAGTATATATATGCTAAACGATTAATATGATGAGAGCAACATATTTGATAT 540
QY 541 GTTCAAATGATCTTAGAGATTTGTTGGCGTGCACAGCTTCTGTGAAAGAGCACA 600

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Db 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGCCAACTCTCTGTGAAGAGACA 600
Qy 601 GGAATAATATACCATGATCTACAGAACTTGTAATGTCAATCAGAGAAATCATCGG 660
Db 601 GGAATAATATACCATGATCTACAGAACTTGTAATGTCAATCAGAGAAATCATCGG 660
Qy 661 ACTCAGGATCATCTGTAGTGAAGACAGGTGTCACTTGAAGTGGAGATCAAAAG 720
Db 661 ACTCAGGATCATCTGTAGTGAAGACAGGTGTCACTTGAAGTGGAGATCAAAAG 720
Qy 721 ACCTTGTAACAAGACCTTCAAGAGAAACCTTCATCTTCAATTTGGTTTCTAGACCAT 780
Db 721 ACCTTGTAACAAGACCTTCAAGAGAAACCTTCATCTTCAATTTGGTTTCTAGACCAT 780
Qy 781 CTACCTCATCTGAAGAGAGACCAATTAAGTGAACAGAGAAATTCAGATTAATCTG 840
Db 781 CTACCTCATCTGAAGAGAGACCAATTAAGTGAACAGAGAAATTCAGATTAATCTG 840
Qy 841 GTGAACGACAAAGAAACGCCACAATCTGATGATTTCCCTTCTTTGATGAAGCC 900
Db 841 GTGAACGACAAAGAAACGCCACAATCTGATGATTTCCCTTCTTTGATGAAGCC 900
Qy 901 TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAAAGCAGTGAATCTACAG 960
Db 901 TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAAAGCAGTGAATCTACAG 960
Qy 961 GGAGCCCATGCAATCCGATCTTGATGCTGGTGAAGCAATTCAGATGATTTGG 1020
Db 961 GGAGCCCATGCAATCCGATCTTGATGCTGGTGAAGCAATTCAGATGATTTGG 1020
Qy 1021 ATCAGGATTCAGTTTCAATCAGTTTGTAGTGAATTTGAAGTTGAATCTCTGAC 1080
Db 1021 ATCAGGATTCAGTTTCAATCAGTTTGTAGTGAATTTGAAGTTGAATCTCTGAC 1080
Qy 1081 AAGATTATAGCTTATAGTGAAGAGACAAGAACTCTCAGATGAAGATGATGATATC 1140
Db 1081 AAGATTATAGCTTATAGTGAAGAGACAAGAACTCTCAGATGAAGATGATGATATC 1140
Qy 1141 AAGTTACTGTGTATCAGGAGGAGAGATGATACAGATTTCTTGAAGAAATCTTGAA 1200
Db 1141 AAGTTACTGTGTATCAGGAGGAGAGATGATACAGATTTCTTGAAGAAATCTTGAA 1200
Qy 1201 TTTCTTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 TTTCTTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Qy 1261 CACATTCGACAGATGTTGGGCTTCTGTAGAAATTTGGCTTCTGAAGTAAAGGAAAG 1320
Db 1261 CACATTCGACAGATGTTGGGCTTCTGTAGAAATTTGGCTTCTGAAGTAAAGGAAAG 1320
Qy 1321 ATTAAGGGGAAATCTCTGAGAAAGCAAACTGAGAAATCTCAACAAGGTGAAGGGCT 1380
Db 1321 ATTAAGGGGAAATCTCTGAGAAAGCAAACTGAGAAATCTCAACAAGGTGAAGGGCT 1380
Qy 1381 TTGATGTTCTGATTTGTAATAAACTATAGTGAATGATTCAGAGAGTCAATGTTGAGG 1440
Db 1381 TTGATGTTCTGATTTGTAATAAACTATAGTGAATGATTCAGAGAGTCAATGTTGAGG 1440
Qy 1441 AAAATGATGATTAATAATACAAAGCTTCAATCAAGAAAGTGAAGCTATTTCTCAGC 1500
Db 1441 AAAATGATGATTAATAATACAAAGCTTCAATCAAGAAAGTGAAGCTATTTCTCAGC 1500
Qy 1501 CATCACTTTCTAGTGAATTAATTAAGAGCCAAAGAGATGTAAGAGTTGAAAGGG 1560
Db 1501 CATCACTTTCTAGTGAATTAATTAAGAGCCAAAGAGATGTAAGAGTTGAAAGGG 1560
Qy 1561 AAGAAACCAAGACAAAGAGAGAGTGAAGTGAATTTGACCTTAATGCAATTTGAAAC 1620
Db 1561 AAGAAACCAAGACAAAGAGAGAGTGAAGTGAATTTGACCTTAATGCAATTTGAAAC 1620
Qy 1621 CTGTGTGATTTGTCAAGGTGCACTTAATAATGTTGCAATTTGCAAGCAAGAC 1680
Db 1621 CTGTGTGATTTGTCAAGGTGCACTTAATAATGTTGCAATTTGCAAGCAAGAC 1680

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Db 1621 CTGTGTGATTTGTCAAGGTGCACTTAATAATGTTGCAATTTGCAAGCAAGAC 1680
Qy 1681 ATCTTATGGCCCTGCTTACATGTGCAAGAAAGCTTAAGAAAGAAATTAAGCCCTGACAG 1740
Db 1681 ATCTTATGGCCCTGCTTACATGTGCAAGAAAGCTTAAGAAAGAAATTAAGCCCTGACAG 1740
Qy 1741 TATGTAGCAACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1741 TATGTAGCAACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Qy 1801 AAGGAAATTAATTAATTTCTAATATTAACCTTAAGAAATTTAGCAACCTGAATTAAT 1860
Db 1801 AAGGAAATTAATTAATTTCTAATATTAACCTTAAGAAATTTAGCAACCTGAATTAAT 1860
Qy 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCATAGATTTCTCTTTAGTATAT 1920
Db 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCATAGATTTCTCTTTAGTATAT 1920
Qy 1921 TGACCTTACTTGTAGTGAATTAAGTAACTTAATTAATTTGATTAATGATGATGAT 1980
Db 1921 TGACCTTACTTGTAGTGAATTAAGTAACTTAATTAATTTGATTAATGATGATGAT 1980
Qy 1981 CATCTTTACCAACCAATCTTAATTTTAATTAATTTCTAATCTGCTTAATTAAGAGATAC 2040
Db 1981 CATCTTTACCAACCAATCTTAATTTTAATTAATTTCTAATCTGCTTAATTAAGAGATAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAATATATATGATGATGATGATGATGATGATGATGATGAT 2100
Db 2041 TTGGTTTTTTTTTTCTTAATATATATGATGATGATGATGATGATGATGATGATGAT 2100
Qy 2101 AGACGAGTCTTGCTCTGTTAACCAGGCTGAGAGTGCAGTGGTGAATCTTGCTCACTGCA 2160
Db 2101 AGACGAGTCTTGCTCTGTTAACCAGGCTGAGAGTGCAGTGGTGAATCTTGCTCACTGCA 2160
Qy 2161 AGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220
Db 2161 AGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220
Qy 2221 TACAGTCACTGCGACCAACCACTGAGCTTAATTTTGTAGTGAAGAGAGAGGTTTC 2280
Db 2221 TACAGTCACTGCGACCAACCACTGAGCTTAATTTTGTAGTGAAGAGAGAGGTTTC 2280
Qy 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCTGACCTGCTGATCCGCCACCTCGGCTCC 2340
Db 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCTGACCTGCTGATCCGCCACCTCGGCTCC 2340
Qy 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372

RESULT 15
AAD07530 standard; DNA; 2372 BP.
AAD07530;
AAD07530; (first entry)
10-AUG-2001
Human p-53 associated mdm2 gene.
Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
tumour; prophylaxis; ds.
Homo sapiens.
US6238921-B1.
29-MAY-2001.
26-MAR-1998; 98US-00048810.
26-MAR-1998; 98US-00048810.
PR

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XX (ISIS-) ISIS PHARM INC.
 PA
 XX Miraglia LJ, Nero P, Graham MJ, Monia BP;
 PI WPI; 2001-366477/38.
 XX
 XX New oligonucleotides 16506, 16507, 16518, 16520, 16521, 16522 and 16524,
 PT which inhibit human mdm2 expression, useful for inhibiting, diagnosing
 PT or treating abnormal proliferative conditions associated with mdm2.
 XX
 XX Example 2; Col 19-24; 19p; English.
 XX
 XX The present invention relates to compositions and methods for modulating
 CC the expression of human mdm2 gene, a naturally present cellular gene
 CC implicated in abnormal cell proliferation and tumour formation. The
 CC invention also provides antisense oligonucleotides which are targeted to
 CC the mdm2 gene and are capable of inhibiting the expression of mdm2 gene.
 CC The oligonucleotides are useful in diagnostics, therapeutics, prophylaxis
 CC and as research reagents. They are especially useful for inhibiting
 CC diagnosing and treating abnormal proliferative conditions associated with
 CC mdm2. The method is useful for detecting and determining the role of mdm2
 CC expression in various cell functions and physiological processes and
 CC conditions, and for diagnosing conditions associated with mdm2
 CC expression. The present sequence is p-53 associated mdm2 gene from human
 XX
 XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 2372; DB 4; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 1495 secs

Whiteman, B.
09/19/2006 Page 1
Seq. ID 2GenCore version 5.1.9
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15: gb_da:*Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	2372	100.0	2372	2	AR028963 Sequence
4	2372	100.0	2372	2	AR154584 Sequence
5	2372	100.0	2372	2	BD073962 Sequence
6	2372	100.0	2372	2	BD138075 Antisense
7	2372	100.0	2372	2	BD233925 Method an
8	2372	100.0	2372	2	111727 Sequence 1
9	2372	100.0	2372	2	112226 Sequence 1
10	2372	100.0	2372	2	125341 Sequence 1
11	2372	100.0	2372	2	125472 Sequence 2
12	2372	100.0	2372	2	136472 Sequence 2
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23	2372	100.0	2372	5	HUMSP53A
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ALIGNMENTS

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LOCUS AR000256 2372 bp DNA linear PAT 04-DBC-1998
DEFINITION Sequence 2 from patent US 5736338.
ACCESSION AR000256
VERSION AR000256.1 GI:3962787
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2372)
Burrell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.
TITLE Method of diagnosing Neoplastic disease by detecting increased
expression of human MDM2 protein
JOURNAL Patent: US 5736338-A 2 07-Apr-1998;
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ORIGIN

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

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DEFINITION AR009781 Sequence 2 from patent US 5756455.
ACCESSION AR009781
VERSION AR009781.1 GI:3968586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Kinzler, K.W. and Vogelstein, B.
TITLE Amplification of human MDM2 gene in human tumors
JOURNAL Patent: US 5756455-A 2 26-MAY-1998;
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ORIGIN

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AR028963
VERSION AR028963.1 GI:5940936
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.
TITLE Methods for inhibiting interaction of human MDM2 and p53
JOURNAL Patent: US 5858976-A 2 12-JUN-1999;
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LOCUS AR154584
DEFINITION Sequence 1 from patent US 6238921.
ACCESSION AR154584
VERSION AR154584.1 GI:15122637
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
Mitsugaki, L.J., Nero, P., Graham, M.J. and Montia, B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 1 29-MAY-2001;
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Best Local Similarity 100.0%; Pred. No. 0;
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BD073962 2372 bp DNA linear PAT 27-AUG-2002
LOCUS BD073962
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073962.1 GI:22619565
VERSION JP 2001513996-A/1.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 2372)
AUTHORS Chen, J., Agrawal, S. and Zhang, R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 1 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/1
PD 11-SEP-2001
PF 18-AUG-1998 US 2000507794
PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
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PC C12N15/09, A61K31/47, A61K31/7088, A61K48/00, A61P35/00, C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
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LOCUS BD138075
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138075
VERSION BD138075.1 GI:23233020
KEYWORDS JP 2002508944-A/1.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 2372)
AUTHORS Miragليا, L.J., Nero, P., Graham, M.J., Montia, B.P. and Cowseert, L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 1 26-MAR-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Unclassified
PN JP 2002508944-A/1
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
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LOCUS
DEFINITION
Method and reagent of enhancing growth capability and preventing
replicative senescence.
ACCESSION
BD233925
VERSION
BD233925.1 GI:33043695
KEYWORDS
JP 2002530436-A/2.
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
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Hannon, G.J. and Beach, D.H.
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Patent: JP 2002530436-A 2 17-SEP-2002;
JOURNAL
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OS Homo sapiens (human)
PN JP 2002530436-A/2
PD 17-SEP-2002 JP 2000584049
PF 24-NOV-1999 JP 60/109.891.17-FEB-1999 US 60/120549 PI
PR 25-NOV-1998 US 60/109.891.17-FEB-1999 US 60/120549 PI
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PC A61K35/12, A61K7/00, A61K38/22, A61K45/00, A61K48/00, A61P43/00, PC
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RESULT 8
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LOCUS 111727 2372 bp DNA linear PAT 26-JUL-1995

DEFINITION Sequence 1 from Patent US 5411860.
ACCESSION 111727
VERSION 111727.1 GI:909479
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Vogelstein, B. and Kinzler, K. W.
TITLE Amplification of human MDM2 gene in human tumors
JOURNAL Patent: US 5411860-A 1 02-May-1995;
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Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 9

112226

LOCUS 112226 2372 bp DNA linear PAT 26-JUL-1995

DEFINITION Sequence 1 from patent US 5420263.

ACCESSION 112226

VERSION 112226.1 GI:909724

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B.

TITLE Amplification of human MDM2 gene in human tumors

JOURNAL Patent: US 5420263-A 1 30-MAY-1995;

FEATURES Location/Qualifiers

source

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ORIGIN /mol_type="unassigned DNA"

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LOCUS 121256 2372 bp DNA linear PART 07-OCT-1996
DEFINITION Sequence 1 from patent US 5519118.
ACCESSION 121256
VERSION 121256.1 GI:1601610
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
Vogelstein, B. and Kinzler, K.
TITLE Human MDM2 protein involved in human tumors
JOURNAL Patent: US 5519118-A 1 21-MAY-1996;
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RESULT 11
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LOCUS 125341
DEFINITION Sequence 2 from patent US 5550023.
ACCESSION 125341 GI:1605211
VERSION 125341.1
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2372)
AUTHORS Kinzler, K.W. and Vogelstein, B.
TITLE Amplification of human MDW2 gene in human tumors
JOURNAL Patent: US 5550023-A 2 27-AUG-1996;
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ACCESSION	136472		
VERSION	136472.1	GI:2086985	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2372)		
AUTHORS	Burrell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.		
TITLE	Kits for detecting amplification of human MDM2		
JOURNAL	Patent: US 5606044-A 2 25-FEB-1997;		
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RESULT 13
140222 2372 bp DNA linear PAT 13-MAY-1997
LOCUS 140222
DEFINITION Sequence 2 from patent US 5618921.
ACCESSION 140222
VERSION 140222.1 GI:2083227
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B.
TITLES Antibodies for detection of human MDM2 protein
JOURNAL Patent: US 5618921-A 2 08-APR-1997;
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AUTHORS  Sheri, C.J., Quelle, D., Rousset, M.F., Zindy, F. and Weber, J.D.
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AUTHORS: Kinzler, K.W.
AUTHORS: Melzer, P.S.
AUTHORS: George, D.L.
AUTHORS: Vogelstein, B.
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DB 121 CAGCAGAGAGCAGCCGCTCCCTCCCGAATTAGTCGTAAGAGCGCCAGTGCCTGACCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCGCGCGCTGTGTGCTTCCGAGATGATGATCCCGCTG 240
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QY 241 AAGAACTGGGGAATCTTGAAGGAGCCCGGAGCTGAGAGCGGAAAGCCCGGATGTGA 300
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DB 301 GAGAGAGCGAAATGTGCAATACCAATGTCTGTACTGATGATGCTGTACACCT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGACCTGTGTAGACCAAGCCATGCTTTGAAGT 420
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QY 481 TTGGCAGATATATATGACTAAACGATTTATGATGAGAGCAACAATATTGTATAT 540
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QY 661 ACTCAGATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGAATCAAAAG 720
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DB 781 CTACCTCATCTAGAGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
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DB 841 GTGAACGCAAAAGAAAGCCCAATCTGATGATATTTCCCTTCTTGTATGAAGCC 900
QY 901 TGGCTGTGTGTATTAAGGAGATATGTTGTGAAGAGAGTGAAGTGAATCTACAG 960
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QY 961 GAGAGCCATCGAATCCGATCTTGTATGCTGTGTATGTAACATTCAGTATGTTGG 1020
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DB 1441 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
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DB 1801 AAGAGATTTATATTTCTAATATATATATATATATATATATATATATATATAT 1860

QY 1861 CACATATACAAAGTGAAGAAAAGCTCAATTCACATAGATTCCTCTTATATAT 1920
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 DB 1921 TGACCTACTCTTGATGATGAAATGATATCTTATATATTTGACTGAAATAGTACT 1980
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 DB 1981 CATCTTTACACCACTCTCTATTTTAAATATTTCTACTCTGCTTAAATAGAGTAC 2040
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 QY 2281 ACCGTTTACCGAGATGCTGATCTCTGACCTGATCCGCCCACTCGGCTCC 2340
 DB 2281 ACCGTTTACCGAGATGCTGATCTCTGACCTGATCCGCCCACTCGGCTCC 2340
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 DB 2341 CAAAGTCTGGGATTAACAGGCAATGAGCCACCG 2372

RESULT 2
 US-09-956-425-7
 ; Sequence 7, Application US/09956425
 ; Patent No. US2002045192A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kriwacki, Richard
 ; APPLICANT: Bothner, Brian
 ; APPLICANT: Lewis, William
 ; TITLE OF INVENTION: Art and Hdm2 Interaction Domains and Method of Use Thereof
 ; FILE REFERENCE: 1340/1/035
 ; CURRENT APPLICATION NUMBER: US/09-956,425
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 2372
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-956-425-7

Query Match 100.0%; Score 2372; DB 3; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCACCGCCGAGCTTGCTGCTTCTGGGCGCTGTGTGCGCTGTGTGCGAAAGATGGA 60
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QY 181 GAGAGTGAATGATCCCCGAGGCGCCAGGGCGGTGCTCTCCAGATGATCAGTCCCGTG 240
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 DB 301 GGAGAGGCAAAATGAGCAATACCAACATGTCGTACTACTGATGATGATGATGATGATGAT 360
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 DB 361 CACAGATTCAGCTTCGGAACAAAGAGCCCTGGTATGACCAAGCATTCCTTTGAAGT 420
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 DB 481 TTGGCCAGTATATTATGACTAAACGATTAATGATGAGAGCAACAATATTGATATTT 540
 QY 541 GTTCAAATGATCTTAGAGATTTGTTGGGTGCGCAAGCTTCTGTGAAAGAGCA 600
 DB 541 GTTCAAATGATCTTAGAGATTTGTTGGGTGCGCAAGCTTCTGTGAAAGAGCA 600
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 DB 601 GGAATATATATACATGATCTTACAGAACTTGGTATGATCAATGACGAGAAATCATCG 660
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 DB 661 ACTCAGTACATCTGTAGTGAAGAACAGGTGCACTTGAAAGTGGAGTATCAAAAG 720
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 DB 721 AACTGTACAGAGCTTAGAGAGAAACCTTCACTTCACTTGGTTCTTACACAT 780
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 DB 781 CTACCTCATCTAGAGAGAGCAATTTAGTGAACAGAGAAATTCAGATGAATATCTG 840
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 DB 841 GTGAACGACAAAGAAACGCCCAAAATCTGATGATTTCCCTTCTTGTATGAAGCC 900
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 DB 1021 ATCAGGATTCAGTTTCAATCAGATCAGTTAGTGAATTTGAAGTGAATCTCTGACTAG 1080
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 DB 1201 TTTCTTAGTACTATTGAAATGACCTTCATGCAATGAATGAATCCCCCTTCAT 1260
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Db 1261 CACATTCGACAGATGTTGGGCCCTTCGTGAGAAATGTCCTTCAAGATTAAGGGAAG 1320
Qy 1321 ATAAAGGGGAATCTCTGAGAAAGCCAACTGGAAAATCTCAACACAACTGAAGGGCT 1380
Db 1321 ATAAAGGGGAATCTCTGAGAAAGCCAACTGGAAAATCTCAACACAACTGAAGGGCT 1380
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Db 1501 CATCACTCTAGTAGAGCTTAATTTATPACAGCCAGAGAGATGTGAAGGTTGAAAGG 1560
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Qy 1621 CTGTGTGATTTGTCAGAGTCGACCTAAATGTTGCAATGTCATGCAAGCAAGAGAC 1680
Db 1621 CTGTGTGATTTGTCAGAGTCGACCTAAATGTTGCAATGTCATGCAAGCAAGAGAC 1680
Qy 1681 ATCTTATAGCCCTGCTTACATGTGCAAGAGACTAAAGAAAGAAATAGCCCTGCGAG 1740
Db 1681 ATCTTATAGCCCTGCTTACATGTGCAAGAGACTAAAGAAAGAAATAGCCCTGCGAG 1740
Qy 1741 TATGTAGACAACCAATTAATGATGTTGCTAATTTCCCTAGTTGACCTGTCTAT 1800
Db 1741 TATGTAGACAACCAATTAATGATGTTGCTAATTTCCCTAGTTGACCTGTCTAT 1800
Qy 1801 AAGAGAAATTAATTAATTTCTAATTAATAAACCCTAGGAATTTAGACAACTGAATTTAT 1860
Db 1801 AAGAGAAATTAATTAATTTCTAATTAATAAACCCTAGGAATTTAGACAACTGAATTTAT 1860
Qy 1861 CACATATATCAAAAGAGAGAAATGCTCAATTCATATAGATTTCTCTTATAGATATAT 1920
Db 1861 CACATATATCAAAAGAGAGAAATGCTCAATTCATATAGATTTCTCTTATAGATATAT 1920
Qy 1921 TGACCTACTTGGTAGTGAATAGTAATCTACTAATTAATTTGAATATATAGT 1980
Db 1921 TGACCTACTTGGTAGTGAATAGTAATCTACTAATTAATTTGAATATATAGT 1980
Qy 1981 CATCTTTACACCACTCTTAATTTAAATATTTCTACTGCTTTAAATGAGAATAC 2040
Db 1981 CATCTTTACACCACTCTTAATTTAAATATTTCTACTGCTTTAAATGAGAATAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAATAATGTAATAGACATTTAAATGTAATATATTTTTTTT 2100
Db 2041 TTGGTTTTTTTTTTCTTAATAATGTAATAGACATTTAAATGTAATATATTTTTTTT 2100
Qy 2101 AGACGAGGCTGCTCTGTTACCCAGAGCTGAGTGAAGGGTGAATCTGGCTCACTGA 2160
Db 2101 AGACGAGGCTGCTCTGTTACCCAGAGCTGAGTGAAGGGTGAATCTGGCTCACTGA 2160
Qy 2161 AGCTGTGCTCTCCCGGGTTGACACATTTCTGCTGACGCTCCCAATTAAGCTTGAGC 2220
Db 2161 AGCTGTGCTCTCCCGGGTTGACACATTTCTGCTGACGCTCCCAATTAAGCTTGAGC 2220
Qy 2221 TACAGTCACTGCGCACACACCTGGCTAATTTTGTACTTTTATAGTAGAGAGAGGGTTTC 2280
Db 2221 TACAGTCACTGCGCACACACCTGGCTAATTTTGTACTTTTATAGTAGAGAGAGGGTTTC 2280
Qy 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCTGACCTGATTCCTGACCTGATTCGACCTGAC 2340
Db 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCTGACCTGATTCCTGACCTGATTCGACCTGAC 2340
Qy 2341 CAAAGTGTGGGATTAACAGGATGAGCCG 2372
Db 2341 CAAAGTGTGGGATTAACAGGATGAGCCG 2372

Db 2341 CAAAGTGTGGGATTAACAGGATGAGCCG 2372

RESULT 3
US-09-851-771A-1
; Sequence 1, Application US/09851771A
; Patent No. US200201511A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; MODULATION OF HUMAN MDN2 EXPRESSION
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,771A
; FILING DATE: 09-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/048,810
; FILING DATE: 1998-03-26
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-779-2400
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; ANTI-SENSE: No
; PUBLICATION INFORMATION:
; AUTHORS: Oliner,J.D.,Kinzler,K.W.,Meltzer,P.S.,George,D.L.,Vogelstein,B.
; TITLE: Amplification of a gene encoding a p53-associated protein in hum
; JOURNAL: Nature
; VOLUME: 358
; ISSUE: 6381
; PAGES: 80-83
; DATE: 02-JUL-1992
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-851-771A-1

Query Match 100.0%; Score 2372; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACGCGCGAGCTTGCTGCTTCTGGGGCCGTGTGAGCCCTGTGTGCGAAAGATGA 60
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Qy 121 CAGCCAGAGAGCAGCTCCCTCCCGGATTAAGTGCCTTAAGAGGCCCAAGTCCGCGCG 180
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1441 AAAATGAT 1500
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1621 CTTGT 1680
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1801 AAGAGAT 1860
1801 AAGAGAT 1860
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1921 TGACCTACTTGT 1980
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2101 AGACCGAGTCTGT 2160
2101 AGACCGAGTCTGT 2160
2161 AGCTGTGCTTGT 2220
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2221 TACAGTATCTGT 2280
2221 TACAGTATCTGT 2280
2281 ACCGTGTAGGCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
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2341 CAAAGT 2372

Db	1661	ATCTATGSGCGCTTTACATGTGGAAAGAGCTTAAGAAAGAGATTAAGCCCTGCCAG	1740
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Db	1741	TATGTAGCAACCAATTCAAATGATGTGCTAACTTAATTCGCCAGTGAACCTGTCTAT	1800
Qy	1801	AAGGAATTAATTAATTTCTAACTTAATTAACCTTGGAATTTAGCAACCTGAATTAAT	1860
Db	1801	AAGGAATTAATTAATTTCTAACTTAATTAACCTTGGAATTTAGCAACCTGAATTAAT	1860
Qy	1861	CACATATATCAAGAGAGAAAATGCTCAATTCACATAGATTTCTGCTTTGGTAAAT	1920
Db	1861	CACATATATCAAGAGAGAAAATGCTCAATTCACATAGATTTCTGCTTTGGTAAAT	1920
Qy	1921	TGACCTACTTTGGTAGTGGAAATAGTAATCTTAATTTGACTTGAATATGAGCT	1980
Db	1921	TGACCTACTTTGGTAGTGGAAATAGTAATCTTAATTTGACTTGAATATGAGCT	1980
Qy	1981	CATCCTTTACACCAACTCTTAATTTTAATTAATTTCTACTCTGTCTTAATAAGAAATAC	2040
Db	1981	CATCCTTTACACCAACTCTTAATTTTAATTAATTTCTACTCTGTCTTAATAAGAAATAC	2040
Qy	2041	TTGGTTTTTTTTTCTTAATAATTAATTAATTAATTAATTAATTAATTAATTTTGTG	2100
Db	2041	TTGGTTTTTTTTTCTTAATAATTAATTAATTAATTAATTAATTAATTAATTTTGTG	2100
Qy	2101	AGACCGAGTCTTGGCTCTGTATCCAGGCTGGAGTGCAGTGGGATGATCTTGGCTCACTGCA	2160
Db	2101	AGACCGAGTCTTGGCTCTGTATCCAGGCTGGAGTGCAGTGGGATGATCTTGGCTCACTGCA	2160
Qy	2161	AGCTTGGCCCTCCCGGGTTGGCACAATTCCTCTGCTCAGCCTCCCAATTAGCTTGGCC	2220
Db	2161	AGCTTGGCCCTCCCGGGTTGGCACAATTCCTCTGCTCAGCCTCCCAATTAGCTTGGCC	2220
Qy	2221	TACAGTCAATCTGCGCACCAACCTGGCTAATTTTTTGTACTTTAAGTAGAACAAGGGTTTC	2280
Db	2221	TACAGTCAATCTGCGCACCAACCTGGCTAATTTTTTGTACTTTAAGTAGAACAAGGGTTTC	2280
Qy	2281	ACCGTGTTAAGCCAGATAGTGTCTGATCTCCGTCGACCTGTGATCCGCCACCTGGGGCTCC	2340
Db	2281	ACCGTGTTAAGCCAGATAGTGTCTGATCTCCGTCGACCTGTGATCCGCCACCTGGGGCTCC	2340
Qy	2341	CAAGTGTCTGGATTACAGGAGTACGACCG	2372
Db	2341	CAAGTGTCTGGATTACAGGAGTACGACCG	2372
RESULT 5			
US-09-873-367C-450			
; Sequence 450, Application US/09873367C			
; Publication No. US20030165839A1			
GENERAL INFORMATION:			
APPLICANT: Young, Paul			
APPLICANT: Soppet, Daniel			
APPLICANT: Endress, Gregory			
APPLICANT: Augustus, Meena			
APPLICANT: Ehner, Reinhard			
APPLICANT: Carter, Kenneth			
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using			
FILE REFERENCE: 689290-64			
CURRENT APPLICATION NUMBER: US/09/873.367C			
CURRENT FILING DATE: 2003-04-29			
PRIOR APPLICATION NUMBER: U.S. 60/236,891			
PRIOR FILING DATE: 2000-09-29			
PRIOR APPLICATION NUMBER: U.S. 60/236,842			
PRIOR FILING DATE: 2000-09-29			
PRIOR APPLICATION NUMBER: U.S. 60/244,867			
PRIOR FILING DATE: 2000-11-01			
PRIOR APPLICATION NUMBER: U.S. 60/245,084			
PRIOR FILING DATE: 2000-11-01			
; NUMBER OF SEQ ID NOS: 1067			

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; SOFTWARE:Patentin version 3.0
; SEQ ID NO 450
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-450

Query Match      100.0%; Score 2372; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 GCACCGCGCAGCTTGGCTGCTTCTGGGGCCTGTGTGGCCCTGTGTGTGCGAAAGATGGA 60
Db      1 GCACCGCGCAGCTTGGCTGCTTCTGGGGGCGTGTGTGGCCCTGTGTGTGCGAAAGATGGA 60
QY      61 GCAAGAACCCAGCGCCGAGGGGCGGCGCGACCCCTCGACCGAGATCCTGCTTGG 120
Db      61 GCAAGAACCCAGCGCCGAGGGGCGGCGCGACCCCTCGACCGAGATCCTGCTTGG 120
QY      121 CAGCCAGGAGCAGCGTCCCTCCCGGATTTAGTGGCTAGCAGCGCCAGTGGCTGGCCG 180
Db      121 CAGCCAGGAGCAGCGTCCCTCCCGGATTTAGTGGCTAGCAGCGCCAGTGGCTGGCCG 180
QY      181 GAGAGTGAATGATCCCGGAGGCCAGGGCGTCTGTCTTCCGAGTAGTCAGTCCCGTG 240
Db      181 GAGAGTGAATGATCCCGGAGGCCAGGGCGTCTGTCTTCCGAGTAGTCAGTCCCGTG 240
QY      241 AAGGAACTGGGGAGCTTTGAGGGACCCCGGACTCCAGCGCGGAAAACCCCGGATGTGA 300
Db      241 AAGGAACTGGGGAGCTTTGAGGGACCCCGGACTCCAGCGCGGAAAACCCCGGATGTGA 300
QY      301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACCTAGTAGTGTGCTGTAAACACT 360
Db      301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACCTAGTAGTGTGCTGTAAACACT 360
QY      361 CACAGATTTCCAGCTTTCGGAACAAGACCCCTGTGTTAGCAAAAGCCATTGCTTTGAAGT 420
Db      361 CACAGATTTCCAGCTTTCGGAACAAGACCCCTGTGTTAGCAAAAGCCATTGCTTTGAAGT 420
QY      421 TATTAAAGTCTGTGTGTGTCACAAAAGACCTTATATCTATGAAAGAGGTTCTTTTATTC 480
Db      421 TATTAAAGTCTGTGTGTGTCACAAAAGACCTTATATCTATGAAAGAGGTTCTTTTATTC 480
QY      481 TTGGCCAGTATATTATGACTTAAAGATTTATGTATGTAGAGACCAACATATTTGTATTT 540
Db      481 TTGGCCAGTATATTATGACTTAAAGATTTATGTATGTAGAGACCAACATATTTGTATTT 540
QY      541 GTTCAATGATCTTCTAGAGATTTGTTTGGCGTGCAGAGCTTCTGTGAAAGACGACA 600
Db      541 GTTCAATGATCTTCTAGAGATTTGTTTGGCGTGCAGAGCTTCTGTGAAAGACGACA 600
QY      601 GGAATAATATATACCATGATCTACAGGAATTGTGATGATCAATCAGAGAAATCATCGG 660
Db      601 GGAATAATATATACCATGATCTACAGGAATTGTGATGATCAATCAGAGAAATCATCGG 660
QY      661 ACTAGGTAATCTGTAGTGAAGAAACAGGTGTCACTTGAAGGTGGAGTCAATCAAAAGG 720
Db      661 ACTAGGTAATCTGTAGTGAAGAAACAGGTGTCACTTGAAGGTGGAGTCAATCAAAAGG 720
QY      721 ACCTTTGTAAGAAGCTTCAGGAAGAGAAACCTTCATCTTCACTTGGTTTCTAGACCAT 780
Db      721 ACCTTTGTAAGAAGCTTCAGGAAGAGAAACCTTCATCTTCACTTGGTTTCTAGACCAT 780
QY      781 CTACTCTCATCTAGAAGAGAGCAATTATGTGAGACAGAAAGAAATTCAGATGAATATCTG 840
Db      781 CTACTCTCATCTAGAAGAGAGCAATTATGTGAGACAGAAAGAAATTCAGATGAATATCTG 840
QY      841 GTGAAGCAAAAGAAAGCGCAAAATCTGATATGTAATTTCCCTTCTTGGATGAAGCC 900
Db      841 GTGAAGCAAAAGAAAGCGCAAAATCTGATATGTAATTTCCCTTCTTGGATGAAGCC 900
QY      901 TGCTCTGTGTGTAATAAGGAGATATGTTGTGAAGAGACAGTAGACGTAATCTACAG 960

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Db 901 TGGCTGTGTGTAAATGAAGAGATATGTGTGAAGAAGCAGTAGCATGATCTACAG 960
Qy 961 GAGCGCCATCGAATCCGATCTTGATGCTGTGTAAAGTGAACAATCAGGTGTTGGTGG 1020
Db 961 GAGCGCCATCGAATCCGATCTTGATGCTGTGTAAAGTGAACAATCAGGTGTTGGTGG 1020
Qy 1021 ATCAGAGATTCAGTTTCAATCAGTTTCAATGTTGAATTTGAAGTTGAATCTCTGAC 1080
Db 1021 ATCAGAGATTCAGTTTCAATCAGTTTCAATGTTGAATTTGAAGTTGAATCTCTGAC 1080
Qy 1081 AAGATTATAGCTTGTGTGAAGAAGCAAGAACTCTCAGATGAATATGATGATATATC 1140
Db 1081 AAGATTATAGCTTGTGTGAAGAAGCAAGAACTCTCAGATGAATATGATGATATATC 1140
Qy 1141 AAGTACTGTGTATCAGGCAAGGAGAGATGATGATGATGATGATGATGATGATGATG 1200
Db 1141 AAGTACTGTGTATCAGGCAAGGAGAGATGATGATGATGATGATGATGATGATGATG 1200
Qy 1201 TTTCTGTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 TTTCTGTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Qy 1261 CACATTCAGACAGATGTTGGGCTTCTGTGTGAATTTGGTCTCTGATGATGATGATG 1320
Db 1261 CACATTCAGACAGATGTTGGGCTTCTGTGTGAATTTGGTCTCTGATGATGATGATG 1320
Qy 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAGAGCTGAAGAGGCT 1380
Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAGAGCTGAAGAGGCT 1380
Qy 1381 TTGATGTTCTGTATGTAAATTAATGATGATGATGATGATGATGATGATGATGATG 1440
Db 1381 TTGATGTTCTGTATGTAAATTAATGATGATGATGATGATGATGATGATGATGATG 1440
Qy 1441 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db 1441 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Qy 1501 CATCAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Db 1501 CATCAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Qy 1561 AAGAAACCCAAAGCAAGAAAGAGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 AAGAAACCCAAAGCAAGAAAGAGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy 1621 CTGTGTGTATGTTGTCAAGGTGCACTTAAATGTTGCAATGTCATGTCATGTCATG 1680
Db 1621 CTGTGTGTATGTTGTCAAGGTGCACTTAAATGTTGCAATGTCATGTCATGTCATG 1680
Qy 1681 ATCTTATGAGCTGCTTTACATGTCAGAAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
Db 1681 ATCTTATGAGCTGCTTTACATGTCAGAAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
Qy 1741 TATGTAGCAACCAATTCATATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 TATGTAGCAACCAATTCATATGATGATGATGATGATGATGATGATGATGATGATG 1800
Qy 1801 AAGAGATTTATATTTTCTAATCTATATTAACCTAGGAATTTGACAACTGAAATTTAT 1860
Db 1801 AAGAGATTTATATTTTCTAATCTATATTAACCTAGGAATTTGACAACTGAAATTTAT 1860
Qy 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATGATATTTCTTCTTTAGATATAT 1920
Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATGATATTTCTTCTTTAGATATAT 1920
Qy 1921 TGACCTACTTGT 1980
Db 1921 TGACCTACTTGT 1980
Qy 1981 CATCTTTTACCAACTCTTAATTTTAAATATTTTCTACTCTGTCTTAAATGAGAATGAC 2040
Db 1981 CATCTTTTACCAACTCTTAATTTTAAATATTTCTACTCTGTCTTAAATGAGAATGAC 2040

Qy 2041 TTGGTTTTTTTTTTCTTAATATGATATGATGATGATGATGATGATGATGATGATGATG 2100
Db 2041 TTGGTTTTTTTTTTCTTAATATGATATGATGATGATGATGATGATGATGATGATGATG 2100
Qy 2101 AGACCGAGTCTTGTCTGTGTTTCCAGAGGTGAGTGCAGTGGTGTATCTTGGCTACTGCA 2160
Db 2101 AGACCGAGTCTTGTCTGTGTTTCCAGAGGTGAGTGCAGTGGTGTATCTTGGCTACTGCA 2160
Qy 2161 AGCTGTGCTTCCCGGGTGGCAACATTCCTGCTCAGCTCCCAATAGCTGGCC 2220
Db 2161 AGCTGTGCTTCCCGGGTGGCAACATTCCTGCTCAGCTCCCAATAGCTGGCC 2220
Qy 2221 TACAGTATCTGCCACACACACTGCTAATTTTTTTGATGTTAGTGAAGACAGAGTTTC 2280
Db 2221 TACAGTATCTGCCACACACACTGCTAATTTTTTTGATGTTAGTGAAGACAGAGTTTC 2280
Qy 2281 ACCGTGTTAGCCAGATGTTCTGATCTCTGACCTGTTATCGCCCACTCGGCTTC 2340
Db 2281 ACCGTGTTAGCCAGATGTTCTGATCTCTGACCTGTTATCGCCCACTCGGCTTC 2340
Qy 2341 CAAGTGTGAGATTTACAGGATGAGCCACG 2372
Db 2341 CAAGTGTGAGATTTACAGGATGAGCCACG 2372

RESULT 6
US-09-966-724-1
Sequence 1, Application US/09966724
Publication No. US20040170971A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G ST., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,724
FILING DATE: 01-Oct-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/044,619
FILING DATE: 2001-10-01
APPLICATION NUMBER: US 07/867,840
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,40148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

Db 1921 TGACCTACTTGTAGTGGAAATGAACTACTTAATTAATTTGACTTAATATGAGCT 1980
Qy 1981 CATCTTTTACACCAACTCCATTAATTTTAATTTCTACTCTGTCTTAATGAGAATGAC 2040
Db 1981 CATCTTTTACACCAACTCCATTAATTTTAATTTCTACTCTGTCTTAATGAGAATGAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAATATATGATATGACATTTAAATGTAATTTATTTTATTTT 2100
Db 2041 TTGGTTTTTTTTTTCTTAATATATGATATGACATTTAAATGTAATTTATTTTATTTT 2100
Qy 2101 AGACCGAGTCTTGTCTGTCTTACCAAGGCTGAGAGTGGATCTTTGGCTACATGCA 2160
Db 2101 AGACCGAGTCTTGTCTGTCTTACCAAGGCTGAGAGTGGATCTTTGGCTACATGCA 2160
Qy 2161 AGCTGTGCTTCCCGGGGTTGACACATTTCTCTGCTCAGCTCCCAATTAAGTTGGCC 2220
Db 2161 AGCTGTGCTTCCCGGGGTTGACACATTTCTCTGCTCAGCTCCCAATTAAGTTGGCC 2220
Qy 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
Db 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
Qy 2281 ACCGTGTAGCCAGAGATGCTCTGCATCTCTGACCTGTGATCCGCCACCTCCGCTCC 2340
Db 2281 ACCGTGTAGCCAGAGATGCTCTGCATCTCTGACCTGTGATCCGCCACCTCCGCTCC 2340
Qy 2341 CAAAGTGTGGGATTACAGGACATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTACAGGACATGAGCCACCG 2372

RESULT 7

US-10-007-926A-121
; Sequence 121, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOUIGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIEWS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: mouse double minute 2, human homolog of;
; US-10-007-926A-121

Query Match 100.0%; Score 2372; DB 7; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCACCGCGCGAGCTTGGCTTCTTGGGGCTGTGTGGCTCTGTGTGCGAAAATGGA 60
Db 1 GCACCGCGCGAGCTTGGCTTCTTGGGGCTGTGTGGCTCTGTGTGCGAAAATGGA 60
Qy 61 GCAGAGCCGAGCCGAGAGGGGCGCGGACCCCTCTTACCGAGATCTCTGCTTTGG 120
Db 61 GCAGAGCCGAGCCGAGAGGGGCGCGGACCCCTCTTACCGAGATCTCTGCTTTGG 120
Qy 121 CAGCAGAGACGACCGTCCCTCCCGGATTAGTGGTACGAGGCGCCAGTGCCTGGCCG 180

Db 121 CAGCAGAGACGACCGTCCCTCCCGGATTAGTGGTACGAGGCGCCAGTGCCTGGCCG 180
Qy 181 GAGAGTGAATGATCCCCAGAGCCCAAGGCGCTGTGCTCCGACGTAGTCCCGCTG 240
Db 181 GAGAGTGAATGATCCCCAGAGCCCAAGGCGCTGTGCTCCGACGTAGTCCCGCTG 240
Qy 241 AAGGAAACTGGGAGTCTTGAAGGACCCCGCATCTCAAGCGGAAAAACCCGATGTGA 300
Db 241 AAGGAAACTGGGAGTCTTGAAGGACCCCGCATCTCAAGCGGAAAAACCCGATGTGA 300
Qy 301 GGAGCAGGCAATGTGCAATACCAACATGCTGTACCTACGATGTGTGTACCACT 360
Db 301 GGAGCAGGCAATGTGCAATACCAACATGCTGTACCTACGATGTGTGTACCACT 360
Qy 361 CACAGATTCCAGCTTCGGAACAAGAGACCCGTGTAGACCAAGCCATGCTTTTGAAGT 420
Db 361 CACAGATTCCAGCTTCGGAACAAGAGACCCGTGTAGACCAAGCCATGCTTTTGAAGT 420
Qy 421 TATTAAAGTCTGTGTGCACAAAAAGACACTTATATGATAAAGAGGTTCTTTTATTC 480
Db 421 TATTAAAGTCTGTGTGCACAAAAAGACACTTATATGATAAAGAGGTTCTTTTATTC 480
Qy 481 TTGGCCAGTATATATGACTTAAAGATTAATGATGAGAGCAACAATTTGTAATT 540
Db 481 TTGGCCAGTATATATGACTTAAAGATTAATGATGAGAGCAACAATTTGTAATT 540
Qy 541 GTTCAAAATGATCTTCTAGGAGATTTGTTGGCGTGGCAAGCTTCTGTGTAAGAGCACA 600
Db 541 GTTCAAAATGATCTTCTAGGAGATTTGTTGGCGTGGCAAGCTTCTGTGTAAGAGCACA 600
Qy 601 GAAAAATATATACCATGATCTTACAGAACTTGTAGTATGTAATCAGCAGGAATCATCG 660
Db 601 GAAAAATATATACCATGATCTTACAGAACTTGTAGTATGTAATCAGCAGGAATCATCG 660
Qy 661 ACTGAGTACATCTGTGAGTGAAGAACAGGTGTCACCTTGAAGGTGGAGTATCAAAAG 720
Db 661 ACTGAGTACATCTGTGAGTGAAGAACAGGTGTCACCTTGAAGGTGGAGTATCAAAAG 720
Qy 721 ACCTTGTACAAAGCCTTCAGAGAAACCTTCATCTTCACTTTGTTGTTGATGACCAT 780
Db 721 ACCTTGTACAAAGCCTTCAGAGAAACCTTCATCTTCACTTTGTTGTTGATGACCAT 780
Qy 781 CTACCTCATCTAGAGAGAGCAATTAAGTGAAGCAAGAAATTCAGATGAATATATCTG 840
Db 781 CTACCTCATCTAGAGAGAGCAATTAAGTGAAGCAAGAAATTCAGATGAATATATCTG 840
Qy 841 GTGAACGACAAAGAAACGCCACAATCTGATGATTTCCCTTCTTGTGATGAAGCC 900
Db 841 GTGAACGACAAAGAAACGCCACAATCTGATGATTTCCCTTCTTGTGATGAAGCC 900
Qy 901 TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAGAGAGAGTGAAGTATCTACAG 960
Db 901 TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAGAGAGAGTGAAGTATCTACAG 960
Qy 961 GGAGCCCATCGAATCCGATCTTGAATGCTGTGTGAAGTGAACATTCAGGTATGGTGG 1020
Db 961 GGAGCCCATCGAATCCGATCTTGAATGCTGTGTGAAGTGAACATTCAGGTATGGTGG 1020
Qy 1021 ATCAGAGTTCAGTTTCAATCAGATGATTAAGTGAATTTGAAGTGAATCTCCGACTAG 1080
Db 1021 ATCAGAGTTCAGTTTCAATCAGATGATTAAGTGAATTTGAAGTGAATCTCCGACTAG 1080
Qy 1081 AAGATTATAGCTTATAGTGAAGAGCAAGAACTTCAGATGAATATATGAGTATATC 1140
Db 1081 AAGATTATAGCTTATAGTGAAGAGCAAGAACTTCAGATGAATATATGAGTATATC 1140
Qy 1141 AAGTTACTGTGTATCAGGAGGAGAGTGTATACAGATTTCTTGAAGAGATCTCGAAA 1200
Db 1141 AAGTTACTGTGTATCAGGAGGAGAGTGTATACAGATTTCTTGAAGAGATCTCGAAA 1200
Qy 1201 TTTCTTAGCTGACTTATGAAATGCACTTCATGCAATGAAATGAATCCCTTCAT 1260

Db	1201	TTTTCTTGCTGACTATTGGAAATGCACTTCATGCAATGAATGAATCCCCCTTCAT	1268
Qy	1261	CACATTGCAACAGATGTTGGCCCTTCGTGGAATTTGCTCTCGAAGATTAAGGGAAG	1320
Db	1261	CACATTGCAACAGATGTTGGGCCCTTCGTGGAATTTGGCTCTCGAATGAAGGAAG	1320
Qy	1321	ATTAAGGGGAATCTCTGGAAGGCAACTGGAATCTCAACCACTGAAGGGCT	1380
Db	1321	ATTAAGGGGAATCTCTGGAAGGCAACTGGAATCTCAACCACTGAAGGGCT	1380
Qy	1381	TTGATGTTCTGATTTGTAATAAACTATAGTAATGATTTCCAGAGAGTCATGTGTTAGG	1440
Db	1381	TTGATGTTCTGATTTGTAATAAACTATAGTAATGATTTCCAGAGAGTCATGTGTTAGG	1440
Qy	1441	AAAAATGATGATTAATAATACAGAGCTTCACATCAACAAGAAAGTGAAGACTATTCTCAGC	1500
Db	1441	AAAAATGATGATTAATAATACAGAGCTTCACATCAACAAGAAAGTGAAGACTATTCTCAGC	1500
Qy	1501	CATCAACCTTCTAGTAGCATTTATTTATAGCAGCCAAAGAAAGTGAAGATTTGAAGGG	1560
Db	1501	CATCAACCTTCTAGTAGCATTTATTTATAGCAGCCAAAGAAAGTGAAGATTTGAAGGG	1560
Qy	1561	AAGAAACCCAGACAAAGAAAGAGTGGAAATCAGTTTGGCCCTTAATGCAATGAC	1620
Db	1561	AAGAAACCCAGACAAAGAAAGAGTGGAAATCAGTTTGGCCCTTAATGCAATGAC	1620
Qy	1621	CTGTGTGATTTGTCAAGSTGCACCTMAAAATGTTGATTCATGTCCATGGCAAAACAGAC	1680
Db	1621	CTGTGTGATTTGTCAAGSTGCACCTMAAAATGTTGATTCATGTCCATGGCAAAACAGAC	1680
Qy	1681	ATCTTATGCGCTGCTTACATGTGCAAGAGCTPAAGAAAGAAATPAAGCCCTGGCCAG	1740
Db	1681	ATCTTATGCGCTGCTTACATGTGCAAGAGCTPAAGAAAGAAATPAAGCCCTGGCCAG	1740
Qy	1741	TATGTAGAACAACAAATGAAATGAGTGAACCTTAATTCCTCCAGTGTGACCTGTGAT	1800
Db	1741	TATGTAGAACAACAAATGAAATGAGTGAACCTTAATTCCTCCAGTGTGACCTGTGAT	1800
Qy	1801	AAGAAATTAATATATTTCTPAACCTATPAACCTAGAAATTTAGACAACCTGAATTTAAT	1860
Db	1801	AAGAAATTAATATATTTCTPAACCTATPAACCTAGAAATTTAGACAACCTGAATTTAAT	1860
Qy	1861	CACATATATCAAAGTGAAGAAATGCTCAATTCACATGATTTCTTCTTATGATPAT	1920
Db	1861	CACATATATCAAAGTGAAGAAATGCTCAATTCACATGATTTCTTCTTATGATPAT	1920
Qy	1921	TGACCTTCTTTGGTAGTGAATTAAGAAATCTPAATTAATTTGAATTAAGTGAAT	1980
Db	1921	TGACCTTCTTTGGTAGTGAATTAAGAAATCTPAATTAATTTGAATTAAGTGAAT	1980
Qy	1981	CATCCTTTTACCAAACTCTAATTTTAAATTAATTTCTACTCTGTCTTAAATGAGAAGTAC	2040
Db	1981	CATCCTTTTACCAAACTCTAATTTTAAATTAATTTCTACTCTGTCTTAAATGAGAAGTAC	2040
Qy	2041	TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTAATTTTTTTTG	2100
Db	2041	TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTAATTTTTTTTG	2100
Qy	2101	AGACCGAGTCTTGCTCTGTTAACCAAGCTGGAAGTGAAGTGGGTATCTTGGCTCACTGCA	2160
Db	2101	AGACCGAGTCTTGCTCTGTTAACCAAGCTGGAAGTGAAGTGGGTATCTTGGCTCACTGCA	2160
Qy	2161	AGCTCTGCGCCCTCCCGGGTTGCAACCAATCTTCCCTGAGCTCCCAATTAAGCTTGGCC	2220
Db	2161	AGCTCTGCGCCCTCCCGGGTTGCAACCAATCTTCCCTGAGCTCCCAATTAAGCTTGGCC	2220
Qy	2221	TACAGTCAATCTGCAACAACCTGGCTPAATTTTTTTGTACTTTTGTAGTGAAGACAGGTTTTC	2280
Db	2221	TACAGTCAATCTGCAACAACCTGGCTPAATTTTTTTGTACTTTTGTAGTGAAGACAGGTTTTC	2280
Qy	2281	ACCGTTTAAAGCAGAGATGATCGATCTCCGACCTGTGTATTCGCGCCACCTCGGCTCC	2340
Db	2281	ACCGTTTAAAGCAGAGATGATCGATCTCCGACCTGTGTATTCGCGCCACCTCGGCTCC	2340

Qy	2341	CAAGTCTGGATTACAGGATGAGCCACCG	2372	
Db	2341	CAAGTCTGGATTACAGGATGAGCCACCG	2372	
RESULT 8				
US-10-005-344-1				
; Sequence 1, Application US/10005544				
; Publication No. US20030203862n1				
GENERAL INFORMATION:				
APPLICANT: Loren J. Miraglia				
APPLICANT: Pamela Nero				
APPLICANT: Mark J. Graham				
APPLICANT: Brett P. Monia				
APPLICANT: Erich Koller				
APPLICANT: Mingyi Chiang				
APPLICANT: Mano Manoharan				
TITLE OF INVENTION: Antisense Modulation of mdm2 expression.				
FILE REFERENCE: ISPH-0622				
CURRENT APPLICATION NUMBER: US/10/005,344				
CURRENT FILING DATE: 2001-12-04				
PRIOR APPLICATION NUMBER: US 09/048,810				
PRIOR FILING DATE: 1998-03-26				
PRIOR APPLICATION NUMBER: US 09/280,805				
PRIOR FILING DATE: 1999-03-26				
NUMBER OF SEQ ID NOS: 379				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 1				
; LENGTH: 2372				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (312)...(1787)				
US-10-005-344-1				
Query Match 100.0%; Score 2372; DB 7; Length 2372;				
Best Local Similarity 100.0%; Pred. No. 0;				
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	GCACCGCGCAGAGCTGTGCTGCTTCTGTGGGCGCTGTGTGGCCCTGTGTGTGGAAAGATGA	60	
Db	1	GCACCGCGCAGAGCTGTGCTGCTTCTGTGGGCGCTGTGTGGCCCTGTGTGTGGAAAGATGA	60	
Qy	61	GCAAGAAAGCCGAGCCCGAGGGGCGGCCGCAACCCCTTGACCGAGATCTGTGCTTTCC	120	
Db	61	GCAAGAAAGCCGAGCCCGAGGGGCGGCCGCAACCCCTTGACCGAGATCTGTGCTTTCC	120	
Qy	121	CAGCCAGAGACCGTCCCTCCCGGATTTGTGGGTGCGAGCGGCCGAGTGCCTGGGCCG	180	
Db	121	CAGCCAGAGACCGTCCCTCCCGGATTTGTGGGTGCGAGCGGCCGAGTGCCTGGGCCG	180	
Qy	181	GAGAGTGAATGATCCCGAGGCCCAAGGGGCTGTGCTTCGCGAGTCAGTCCCCGTG	240	
Db	181	GAGAGTGAATGATCCCGAGGCCCAAGGGGCTGTGCTTCGCGAGTCAGTCCCCGTG	240	
Qy	241	AAGGAAATCTGGGAGTCTTTGAGGAGCCCGCATCTCCAAGGCGGAAAAACCCGGATGTGA	300	
Db	241	AAGGAAATCTGGGAGTCTTTGAGGAGCCCGCATCTCCAAGGCGGAAAAACCCGGATGTGA	300	
Qy	301	GGAGCAGGAAATGTGCAATACCAACATGTCTGTACTCAATGATGATGTGTATACCACT	360	
Db	301	GGAGCAGGCAAAATGTGCAATACCAACATGTCTGTACTCAATGATGATGTGTATACCACT	360	
Qy	361	CACAGATTCAGCTTGGGAAACAAGAGACCTCTGTATTACCAAAAGCCATTCTTTGAAGT	420	
Db	361	CACAGATTCAGCTTGGGAAACAAGAGACCTCTGTATTACCAAAAGCCATTCTTTGAAGT	420	
Qy	421	TATTAAGTCTGTGTGTGCAAAAAACACTTAATATAGAAAGAGTTCTTTTATC	480	
Db	421	TATTAAGTCTGTGTGTGCAAAAAACACTTAATATAGAAAGAGTTCTTTTATC	480	

481 TTGGCCAGTATATATATGACTAAACGATATATGATGAGAACAAACAATATGTATTT 540
481 TTGGCCAGTATATATATGACTAAACGATATATGATGAGAACAAACAATATGTATTT 540
QY 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGTGCAGAGCTTCTGTGTAAAGACACA 600
Db 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGTGCAGAGCTTCTGTGTAAAGACACA 600
QY 601 GGAATAATATACATGATCTACAGGAACTTGATGTGCAATGAGAGAAATCATGCG 660
Db 601 GGAATAATATACATGATCTACAGGAACTTGATGTGCAATGAGAGAAATCATGCG 660
QY 661 ACTCAGGATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTATCAAAAG 720
Db 661 ACTCAGGATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTATCAAAAG 720
QY 721 ACCTTGTACAGAGCTTCAGAGAGAAACCTTCATCTTCAATTTGGTTTCTAGACCAT 780
Db 721 ACCTTGTACAGAGCTTCAGAGAGAAACCTTCATCTTCAATTTGGTTTCTAGACCAT 780
QY 781 CTACCTCATCTAGAGAGAGACATTAATGAGACAGAAAGAAATTCAGATGAATATCTG 840
Db 781 CTACCTCATCTAGAGAGAGACATTAATGAGACAGAAAGAAATTCAGATGAATATCTG 840
QY 841 GTGAACGACAAAGAAAGACCAACATCTGATGATTTCCCTTCTTGTGTAAGACC 900
Db 841 GTGAACGACAAAGAAAGACCAACATCTGATGATTTCCCTTCTTGTGTAAGACC 900
QY 901 TGGCTGTGTGTAAAGAGAGATATGTGTGAAGAGACATGACATGATCTACAG 960
Db 901 TGGCTGTGTGTAAAGAGAGATATGTGTGAAGAGACATGACATGATCTACAG 960
QY 961 GGAAGCCATCCAGATCCGATCTTGTGCTGTGTGAAGACATTCAGGTGTTGGTTGG 1020
Db 961 GGAAGCCATCCAGATCCGATCTTGTGCTGTGTGAAGACATTCAGGTGTTGGTTGG 1020
QY 1021 ATCAGAGATTCAGTTTCAATCAGTTTGAAGTGAATTTGAAGTGAATCTCCAGCTCAG 1080
Db 1021 ATCAGAGATTCAGTTTCAATCAGTTTGAAGTGAATTTGAAGTGAATCTCCAGCTCAG 1080
QY 1081 AAGATTATAGCTTATGATGAGAGAGACAAAGCTTCAGATGAGATGATGATGATTC 1140
Db 1081 AAGATTATAGCTTATGATGAGAGAGACAAAGCTTCAGATGAGATGATGATGATTC 1140
QY 1141 AAGTTACTGTGTATCAGGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 1200
Db 1141 AAGTTACTGTGTATCAGGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 TTTCTTGTGCTGATGATGAGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 TTTCTTGTGCTGATGATGAGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATTTGGCTTCCTGAAGTAAAGGGAAG 1320
Db 1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATTTGGCTTCCTGAAGTAAAGGGAAG 1320
QY 1321 ATAAAGGGGAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAGCTGAGAGGCT 1380
Db 1321 ATAAAGGGGAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAGCTGAGAGGCT 1380
QY 1381 TTGATGTTCTGATTTGTAAGAACTATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 TTGATGTTCTGATTTGTAAGAACTATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 AAAATGAT 1500
Db 1441 AAAATGAT 1500
QY 1501 CATCACTCTGTAGAT 1560
Db 1501 CATCACTCTGTAGAT 1560
QY 1561 AAGAAACCAAGACAAAGAGAGAGTGTGGAATCTAGTTGGCCCTTAATGCAATTAAC 1620

1561 AAGAAACCAAGACAAAGAGAGAGTGTGGAATCTAGTTGGCCCTTAATGCAATTAAC 1620
QY 1621 CTGTGTGATTTGTCAAGGTGCAACCTTAAATATGTTGTCAATTTGTCAATGCAAGAC 1680
Db 1621 CTGTGTGATTTGTCAAGGTGCAACCTTAAATATGTTGTCAATTTGTCAATGCAAGAC 1680
QY 1681 ATCTTATGAGCTGCTTATCATATGTCAGAAAGACTTAAAGAAAGAAATGAGCCCTG 1740
Db 1681 ATCTTATGAGCTGCTTATCATATGTCAGAAAGACTTAAAGAAAGAAATGAGCCCTG 1740
QY 1741 TATGTAGCAACCAATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1741 TATGTAGCAACCAATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 AAGAGAT 1860
Db 1801 AAGAGAT 1860
QY 1861 CACATATATCAAGAGAGAAATGCTCAATTCATATGATGATGATGATGATGATGATGAT 1920
Db 1861 CACATATATCAAGAGAGAAATGCTCAATTCATATGATGATGATGATGATGATGATGAT 1920
QY 1921 TGACCTACTTGTGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 1921 TGACCTACTTGTGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 CATCTTATACCAACCTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 2040
Db 1981 CATCTTATACCAACCTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 2040
QY 2041 TTGGTTTTTTTTTTCTTAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
Db 2041 TTGGTTTTTTTTTTCTTAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
QY 2101 AGACGAGCTTGTCTCTGTATCCAGAGCTGAGTGCAGTGGTATCTTGGCTCACTGCA 2160
Db 2101 AGACGAGCTTGTCTCTGTATCCAGAGCTGAGTGCAGTGGTATCTTGGCTCACTGCA 2160
QY 2161 AGCTTGCCCTCCCGGTTTGACACATTTCTGCTGACCTCCCAATTAAGCTTGGCC 2220
Db 2161 AGCTTGCCCTCCCGGTTTGACACATTTCTGCTGACCTCCCAATTAAGCTTGGCC 2220
QY 2221 TACAGTATCTGACCAACCACTGCTGATTTTGTATTTGTATGATGATGATGATGATGAT 2280
Db 2221 TACAGTATCTGACCAACCACTGCTGATTTTGTATTTTGTATGATGATGATGATGATGAT 2280
QY 2281 ACCGTGTTAGCCAGATGATCTGATCTGACCTGATGATGATGATGATGATGATGATGAT 2340
Db 2281 ACCGTGTTAGCCAGATGATGATCTGATCTGACCTGATGATGATGATGATGATGATGAT 2340
QY 2341 CAAAGTGTGGGATTTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTTACAGGATGAGCCACCG 2372

RESULT 9
US-10-422-536-136
; Sequence 136, Application US/10422536
; Publication No. US20040014100A1
; GENERAL INFORMATION:
; APPLICANT: Kinsella, Todd
; APPLICANT: Lorens, James
; APPLICANT: Pray, Todd
; APPLICANT: Bennett, Mark
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
; FILE REFERENCE: A-71433-1/AMP/CYO
; CURRENT APPLICATION NUMBER: US/10/422,536
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/187,130
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/800,770

PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: US 10/232,758
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 168
SOFTWARE: Patentin version 3.2
SEQ ID NO 136
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
US-10-422-536-136

Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACACGCGGAGACTTGGCTGCTTCTGGGCTGTGTGGCCCTGTGTGTGGAAAGATGGA 60
DB 1 GCACGCGCGGAGACTTGGCTGCTTCTGGGCTGTGTGGCCCTGTGTGTGGAAAGATGGA 60
QY 61 GCAGAAAGCCGAGCCCGAGGGGGGCGCGGAGCCCTCTGACCGAGATCTGTGCTTTGG 120
DB 61 GCAGAAAGCCGAGCCCGAGGGGGGCGCGGAGCCCTCTGACCGAGATCTGTGCTTTGG 120
QY 121 CAGCCAGAGACACCGTCCCTCCCGGATTAGTGCCTGACGAGGCGCCAGTGCCTGGCCG 180
DB 121 CAGCCAGAGACACCGTCCCTCCCGGATTAGTGCCTGACGAGGCGCCAGTGCCTGGCCG 180
QY 181 GAGAGTGGAAATATCCCGAGGCGCCAGGCGCTGTGCTTCCGAGTATGATCCCGTGG 240
DB 181 GAGAGTGGAAATATCCCGAGGCGCCAGGCGCTGTGCTTCCGAGTATGATCCCGTGG 240
QY 241 AAGAAACTGGGGAAGTCTTGAAGGAGCCCGGACTCCAAAGCGGAAACCCCGATGTGA 300
DB 241 AAGAAACTGGGGAAGTCTTGAAGGAGCCCGGACTCCAAAGCGGAAACCCCGATGTGA 300
QY 301 GGAGAGGCGAAATGTGCAATACCAATGTCTGTACTTGTGTGTGTGTGTGTGTGTGT 360
DB 301 GGAGAGGCGAAATGTGCAATACCAATGTCTGTACTTGTGTGTGTGTGTGTGTGTGT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGCCCTGTTAGAACCAAGCCATTTGTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGCCCTGTTAGAACCAAGCCATTTGTTGAAGT 420
QY 421 TATTAAGCTGT 480
DB 421 TATTAAGCTGT 480
QY 481 TTGGCCAGTATATATGACTTAACATATATATATATATATATATATATATATATAT 540
DB 481 TTGGCCAGTATATATGACTTAACATATATATATATATATATATATATATATATAT 540
QY 541 GTTCAATGATCTTCTGAGAGATTTGTTGGGCTGCAAGCTTCTCTGTGAAGAGACA 600
DB 541 GTTCAATGATCTTCTGAGAGATTTGTTGGGCTGCAAGCTTCTCTGTGAAGAGACA 600
QY 601 GGAATAAT 660
DB 601 GGAATAAT 660
QY 661 ACTCAGTAT 720
DB 661 ACTCAGTAT 720
QY 721 ACCCTGTAT 780
DB 721 ACCCTGTAT 780
QY 781 CTAACCTAT 840
DB 781 CTAACCTAT 840
QY 841 GTGAAGCAAGAAAGAGCCCAATCTGATATATATATATATATATATATATATATAT 900
DB 841 GTGAAGCAAGAAAGAGCCCAATCTGATATATATATATATATATATATATATATAT 900

DB 841 GTGAAGCAAGAAAGAGCCCAATCTGATATATATATATATATATATATATATATAT 900
QY 901 TGGCTCTGT 960
DB 901 TGGCTCTGT 960
QY 961 GGAGCCAT 1020
DB 961 GGAGCCAT 1020
QY 1021 ATCAGATTCAGTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1080
DB 1021 ATCAGATTCAGTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1080
QY 1081 AAGATTTAT 1140
DB 1081 AAGATTTAT 1140
QY 1141 AAGTTACTGTGTAT 1200
DB 1141 AAGTTACTGTGTAT 1200
QY 1201 TTTCTTATGCTAT 1260
DB 1201 TTTCTTATGCTAT 1260
QY 1261 CACATTTGCAACAT 1320
DB 1261 CACATTTGCAACAT 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCAATCTGAAATCTCAACAGCTGAAGAGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCAATCTGAAATCTCAACAGCTGAAGAGGCT 1380
QY 1381 TTGATGTTCTGATTTGTAATATATATATATATATATATATATATATATATATAT 1440
DB 1381 TTGATGTTCTGATTTGTAATATATATATATATATATATATATATATATATATAT 1440
QY 1441 AAAATGAT 1500
DB 1441 AAAATGAT 1500
QY 1501 CATCACTTCTAT 1560
DB 1501 CATCACTTCTAT 1560
QY 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTGCTTATATATATATATATAT 1620
DB 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTGCTTATATATATATATATAT 1620
QY 1621 CTTGTGTAT 1680
DB 1621 CTTGTGTAT 1680
QY 1681 ATCTTATGCTGCTTAT 1740
DB 1681 ATCTTATGCTGCTTAT 1740
QY 1741 TATGTAGAACAACAT 1800
DB 1741 TATGTAGAACAACAT 1800
QY 1801 AAGAAATTAAT 1860
DB 1801 AAGAAATTAAT 1860
QY 1861 CACAT 1920
DB 1861 CACAT 1920
QY 1921 TGACCTACTTGT 1980
DB 1921 TGACCTACTTGT 1980

QY 1981 CATCTTACGACCACTCTTAATTTTAAATATTTCTACTGCTTAAATGAGATAC 2040
DB 1981 CATCTTACGACCACTCTTAATTTTAAATATTTCTACTGCTTAAATGAGATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATATATGATATGACATTTAAATGTAATTTTATTTT 2100
DB 2041 TTGGTTTTTTTTTTCTTAATATATGATATGACATTTAAATGTAATTTTATTTT 2100
QY 2101 AGACCGAGCTCTGCTCTGTACCCAGGCTGAGTGCATGAGTGTATCTTGGCTCA 2160
DB 2101 AGACCGAGCTCTGCTCTGTACCCAGGCTGAGTGCATGAGTGTATCTTGGCTCA 2160
QY 2161 AGCTCTGCTCTCCCGGGTTCGACACATTTCTCTGCTCAGCTCCCAATGAGTTC 2220
DB 2161 AGCTCTGCTCTCCCGGGTTCGACACATTTCTCTGCTCAGCTCCCAATGAGTTC 2220
QY 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTAGTAGAGAGGTTTC 2280
DB 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTAGTAGAGAGGTTTC 2280
QY 2281 ACCGTGTAGCCAGATGCTCTCCATCTCTGACTCTGATCCGCCACCTCGGCTCC 2340
DB 2281 ACCGTGTAGCCAGATGCTCTCCATCTCTGACTCTGATCCGCCACCTCGGCTCC 2340
QY 2341 CAAAGTCTGGGATTACAGGCGATGAGCCACCG 2372
DB 2341 CAAAGTCTGGGATTACAGGCGATGAGCCACCG 2372

RESULT 10

US-10-232-951-34
; Sequence 34, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Brian
; APPLICANT: Pray, Todd
; APPLICANT: Bennett, Mark
; APPLICANT: Parlati, Francesco
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Assays
; TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
; FILE REFERENCE: 021044-006800US
; CURRENT APPLICATION NUMBER: US/10/232,951
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2
; OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
; OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
; OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
; OTHER INFORMATION: Mdm2 cDNA
US-10-232-951-34

Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGTGCGAAAATGGA 60
DB 1 GCACCGCGGAGCTTGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGTGCGAAAATGGA 60
QY 61 GCAAGAGCGGAGCGGAGGGGGCGCGGACCCCTGACCGAGATCTCGTGGCTTTCG 120
DB 61 GCAAGAGCGGAGCGGAGGGGGCGCGGACCCCTGACCGAGATCTCGTGGCTTTCG 120
QY 121 CAGCCAGAGACGCTCCCTCCCGGATTAAGTCGATCAGAGCGCCAGTGCCTGGCCCG 180
DB 121 CAGCCAGAGACGCTCCCTCCCGGATTAAGTCGATCAGAGCGCCAGTGCCTGGCCCG 180

DB 121 CAGCCAGAGACCGCTCCCTCCCGGATTAAGTCGATCAGAGCGCCAGTGCCTGGCCCG 180
QY 181 GAGAGTGAATGATCCCGGAGGCCACAGGGCGTGTGCTTCGCGAGTGTAGTCCCGTG 240
DB 181 GAGAGTGAATGATCCCGGAGGCCACAGGGCGTGTGCTTCGCGAGTGTAGTCCCGTG 240
QY 241 AAGGAACTGGGAGTCTTGAAGGAGCCCGGACTCCAGAGCGGAAAAACCCGAGTGTGA 300
DB 241 AAGGAACTGGGAGTCTTGAAGGAGCCCGGACTCCAGAGCGGAAAAACCCGAGTGTGA 300
QY 301 GGAGCAGCAATGTGCAATACCAATGTCTGATACCTACATGATGTGTATACCACT 360
DB 301 GGAGCAGCAATGTGCAATACCAATGTCTGATACCTACATGATGTGTATACCACT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGACCTGTTAGACCAAGCCATGCTTTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCTGTTAGACCAAGCCATGCTTTTGAAGT 420
QY 421 TATTAAAGTCTGTGTGTCACAAAAAGACCTTAATATGATAAAGAGTCTTTTATTC 480
DB 421 TATTAAAGTCTGTGTGTCACAAAAAGACCTTAATATGATAAAGAGTCTTTTATTC 480
QY 481 TTGGCCAGTATATTATGACTTAACGATTAATGATGAGAGCAACAATTTGTATTT 540
DB 481 TTGGCCAGTATATTATGACTTAACGATTAATGATGAGAGCAACAATTTGTATTT 540
QY 541 GTTCAAAATGATCTCTAGAGATTTGTTGGCGTGGCCAGCTCTCTGTGAAGAGCACA 600
DB 541 GTTCAAAATGATCTCTAGAGATTTGTTGGCGTGGCCAGCTCTCTGTGAAGAGCACA 600
QY 601 GAAAAATATATACCATGATCTACAGAACTTGTGATGATCAATCAGCAGGAATCATCG 660
DB 601 GAAAAATATATACCATGATCTACAGAACTTGTGATGATCAATCAGCAGGAATCATCG 660
QY 661 ACTGAGTCACTCTGTGATGAGAAACAGGTGTCACCTTGAAGGTGGAGTATCAAAAG 720
DB 661 ACTGAGTCACTCTGTGATGAGAAACAGGTGTCACCTTGAAGGTGGAGTATCAAAAG 720
QY 721 ACCTTGTACAAGAGCTTCAGAGAGAAACCTTCAATCTTCACATTTGGTTTCTAGACAT 780
DB 721 ACCTTGTACAAGAGCTTCAGAGAGAAACCTTCAATCTTCACATTTGGTTTCTAGACAT 780
QY 781 CTACCTCATCTAGAGAGAGCAATTAGTGAAGACAGAAAGAAATTCAGATGATATCTG 840
DB 781 CTACCTCATCTAGAGAGAGCAATTAGTGAAGAGCAAAATTCAGATGATATCTG 840
QY 841 GTGAACGACAAAGAAAGGCGCACAAATCTGATGATATTTCTTTCTTTGATGAAGCC 900
DB 841 GTGAACGACAAAGAAAGGCGCACAAATCTGATGATATTTCTTTCTTTGATGAAGCC 900
QY 901 TGGCTGTGTATATAGGAGATATGTGTGAAGAGCAGTAGCAGTATCTACAG 960
DB 901 TGGCTGTGTATATAGGAGATATGTGTGAAGAGCAGTAGCAGTATCTACAG 960
QY 961 GGAAGCCATGCAATCCGATCTTGAATGCTGTGTGATGAGCAATTCAGGTATGGTTGG 1020
DB 961 GGAAGCCATGCAATCCGATCTTGAATGCTGTGTGATGAGCAATTCAGGTATGGTTGG 1020
QY 1021 ATCAGGATTCAGTTCAATCAGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 ATCAGGATTCAGTTCAATCAGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 AAGATTATAGCTTATAGTAAGAGCAAGAACTCTCAGATGAGATGATGATGATGATG 1140
DB 1081 AAGATTATAGCTTATAGTAAGAGCAAGAACTCTCAGATGAGATGATGATGATGATG 1140
QY 1141 AAGTTACTGTATACGAGGAGGAGAGTGTATACAGATTTCAATTTGAAGAGATCTGAAA 1200
DB 1141 AAGTTACTGTATACGAGGAGGAGAGTGTATACAGATTTCAATTTGAAGAGATCTGAAA 1200
QY 1201 TTTCTTACTGACTATTTGAATATGCACTTCAATGATGAAATGAATCCCCCTTCAT 1260
DB 1201 TTTCTTACTGACTATTTGAATATGCACTTCAATGATGAAATGAATCCCCCTTCAT 1260

QY 1261 CACATTGCAACAGATGTTGGGCTTCTGAGAAATGGCTTCTGAAAGATTAAGGGAAG 1320
DB 1261 CACATTGCAACAGATGTTGGGCTTCTGAGAAATGGCTTCTGAAAGATTAAGGGAAG 1320
QY 1321 ATAAAAGGGAATCTCTGAGAAAGCCAACTGAGAAATCTCAACAAAGCTGAAGGGCT 1380
DB 1321 ATAAAAGGGAATCTCTGAGAAAGCCAACTGAGAAATCTCAACAAAGCTGAAGGGCT 1380
QY 1381 TTGATGTCCTGATGTTAAATAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1440
DB 1381 TTGATGTCCTGATGTTAAATAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1440
QY 1441 AAAATGATGATTAATTAACAAGCTTCAATCAACAAGAAAGTGAAGTATCTCAGC 1500
DB 1441 AAAATGATGATTAATTAACAAGCTTCAATCAACAAGAAAGTGAAGTATCTCAGC 1500
QY 1501 CATCAACTTCTAGTATGATTAATTAATGAGAGCCAAAGAGATGTAAGAGGTTGAAGG 1560
DB 1501 CATCAACTTCTAGTATGATTAATTAATGAGAGCCAAAGAGATGTAAGAGGTTGAAGG 1560
QY 1561 AAGAAACCCCAACAAAGAAAGAGTGTGAATCTAGTGTGCTTAAATGCTTGAAG 1620
DB 1561 AAGAAACCCCAACAAAGAAAGAGTGTGAATCTAGTGTGCTTAAATGCTTGAAG 1620
QY 1621 CTGTGTGATTTGTCAAGGTGAGCTTAAATGTTGATGCTTGAAGTGAAGTGAAG 1680
DB 1621 CTGTGTGATTTGTCAAGGTGAGCTTAAATGTTGATGCTTGAAGTGAAGTGAAG 1680
QY 1681 ATCTTATGAGCTTCTTATCATGTCGAAAGAGCTTAAAGAAAGTAAAGCTGCTGAG 1740
DB 1681 ATCTTATGAGCTTCTTATCATGTCGAAAGAGCTTAAAGAAAGTAAAGCTGCTGAG 1740
QY 1741 TATGTAAGCAACCAATTAATGATGTTGCTTAACTTAACTTAACTTAACTTAACT 1800
DB 1741 TATGTAAGCAACCAATTAATGATGTTGCTTAACTTAACTTAACTTAACTTAACT 1800
QY 1801 AAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
DB 1801 AAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
QY 1861 CACATATATCAAAAGTGAAGAAATGCTCAATCAATGATGTTCTTCTTAAATTAAT 1920
DB 1861 CACATATATCAAAAGTGAAGAAATGCTCAATCAATGATGTTCTTCTTAAATTAAT 1920
QY 1921 TGACCTACTTGTGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1980
DB 1921 TGACCTACTTGTGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1980
QY 1981 CATCTTTACCAAGCTCTTAACTTAAATTAATTAATTAATTAATTAATTAATTAAT 2040
DB 1981 CATCTTTACCAAGCTCTTAACTTAAATTAATTAATTAATTAATTAATTAATTAAT 2040
QY 2041 TTGGTTTTTTTTTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2100
DB 2041 TTGGTTTTTTTTTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2100
QY 2101 AGACCGAGTCTTCTCTGTTAACTCAAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160
DB 2101 AGACCGAGTCTTCTCTGTTAACTCAAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160
QY 2161 AGCTTGTGCTTCTCTGTTAACTCAAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2220
DB 2161 AGCTTGTGCTTCTCTGTTAACTCAAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2220
QY 2221 TACAGTCACTGCAACCAAGCTGCTAATTTTGTACTTTTGTAGTGAAGTGAAGTGAAG 2280
DB 2221 TACAGTCACTGCAACCAAGCTGCTAATTTTGTACTTTTGTAGTGAAGTGAAGTGAAG 2280
QY 2281 ACCGTGTTAGCGAGATGTTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTG 2340
DB 2281 ACCGTGTTAGCGAGATGTTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTG 2340
QY 2340 ACCGTGTTAGCGAGATGTTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTG 2340
DB 2340 ACCGTGTTAGCGAGATGTTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTG 2340

QY 2341 CAAAGTGTGAGTATTAAGGATGAGCCAGC 2372
DB 2341 CAAAGTGTGAGTATTAAGGATGAGCCAGC 2372

RESULT 11
US-10-052-482-173
; Sequence 173, Application US/10052482
; Publication No. US20040072264A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71087/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/052,482
; PRIORITY FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 173
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-482-173

Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCTGTGTGCTGTGTGCTGTGTG 60
DB 1 GCAACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCTGTGTGCTGTGTGCTGTGTG 60
QY 61 GCAACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCTGTGTGCTGTGTGCTGTGTG 120
DB 61 GCAACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCTGTGTGCTGTGTGCTGTGTG 120
QY 121 CAGCAGAGGAGCAGCTTCCCTCCCGGATTAAGTGTGCTGTGTGCTGTGTGCTGTGTG 180
DB 121 CAGCAGAGGAGCAGCTTCCCTCCCGGATTAAGTGTGCTGTGTGCTGTGTGCTGTGTG 180
QY 181 GAGAGTGAATGATCTCCGAGGCTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTG 240
DB 181 GAGAGTGAATGATCTCCGAGGCTGCTGTGTGCTGTGTGCTGTGTGCTGTGTGCTGTGTG 240
QY 241 AAGGAACTGGGAGTCTTGAAGGACCCCGGATTAAGTGTGCTGTGTGCTGTGTGCTGTGTG 300
DB 241 AAGGAACTGGGAGTCTTGAAGGACCCCGGATTAAGTGTGCTGTGTGCTGTGTGCTGTGTG 300
QY 301 GGAGCAGGCAATGTCATTAATCAATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 301 GGAGCAGGCAATGTCATTAATCAATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 CACAGATTCAGCTTGGAAACAGAGACCTGCTGTGTGATGATGATGATGATGATGATGATG 420
DB 361 CACAGATTCAGCTTGGAAACAGAGACCTGCTGTGTGATGATGATGATGATGATGATGATG 420
QY 421 TATTAAGTCTGTGTGTGCAAAAAGACCTTAATTAATGATGATGATGATGATGATGATGATG 480
DB 421 TATTAAGTCTGTGTGTGCAAAAAGACCTTAATTAATGATGATGATGATGATGATGATGATG 480
QY 481 TTGGCAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 481 TTGGCAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 541 GTTCAATGATCTTGAAGATTTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 GTTCAATGATCTTGAAGATTTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 GGAATAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 GGAATAATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

|||||
Db 601 GGAATAATATACCATGATCTACAGGAACCTGGTAGTCAATCAGACAGAAATCATCGG 660
Qy 661 ACTGAGTACATCTGTGAGTGAAGACAGTGTCACTTGAAGTGGAGTATCAAAAG 720
Db 661 ACTGAGTACATCTGTGAGTGAAGACAGTGTCACTTGAAGTGGAGTATCAAAAG 720
Qy 721 ACCTGTACAGAGCTTCAAGAGAGAAACCTTCACTTCACTTGGTTTCTAGACCAT 780
Db 721 ACCTGTACAGAGCTTCAAGAGAGAAACCTTCACTTCACTTGGTTTCTAGACCAT 780
Qy 781 CTACCTCATCTAGAGAGAGAGCAATTTAGTGAACAGAGAAATTCAGATGATATCTG 840
Db 781 CTACCTCATCTAGAGAGAGAGCAATTTAGTGAACAGAGAAATTCAGATGATATCTG 840
Qy 841 GTGAACGCAAGAAAGAAAGCCCAATCTGATGATGATTTCCCTTCTTGAAGAAC 900
Db 841 GTGAACGCAAGAAAGAAAGCCCAATCTGATGATGATTTCCCTTCTTGAAGAAC 900
Qy 901 TGGCTCTGTGTATTAAGAGAGATATGTGTAAGAGAGAGTACAGTGAATCTACAG 960
Db 901 TGGCTCTGTGTATTAAGAGAGATATGTGTAAGAGAGAGTACAGTGAATCTACAG 960
Qy 961 GGAAGCATCGAATCCGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGTTG 1020
Db 961 GGAAGCATCGAATCCGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGTTG 1020
Qy 1021 ATCAGGATTCAGTTCAGATCAGTTCAGTGAATTTGAAGTGAATCTCCGACCTAG 1080
Db 1021 ATCAGGATTCAGTTCAGATCAGTTCAGTGAATTTGAAGTGAATCTCCGACCTAG 1080
Qy 1081 AAGATTATAGCTTGTAGTGAAGAGAGAGAGAGAGTCTCAGATGATGATGATATC 1140
Db 1081 AAGATTATAGCTTGTAGTGAAGAGAGAGAGAGAGTCTCAGATGATGATGATATC 1140
Qy 1141 AAGTACTGTGTATCAGGAGAGAGAGAGTATCAGATTCATTTGAAGAGATCTGAAA 1200
Db 1141 AAGTACTGTGTATCAGGAGAGAGAGAGTATCAGATTCATTTGAAGAGATCTGAAA 1200
Qy 1201 TTTCTTGTAGTCACTATTTGAAGATGATCCTTCACTGAGTGAATTTGAAGAGAG 1260
Db 1201 TTTCTTGTAGTCACTATTTGAAGATGATCCTTCACTGAGTGAATTTGAAGAGAG 1260
Qy 1261 CACATTGCAAGATGTTGGGCTTCTGAGAGATTTGGCTCTGAGTGAATTTGAAGAG 1320
Db 1261 CACATTGCAAGATGTTGGGCTTCTGAGAGATTTGGCTCTGAGTGAATTTGAAGAG 1320
Qy 1321 ATTAAGGGGAAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 ATTAAGGGGAAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 TTGATGTTCTGTATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 TTGATGTTCTGTATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1441 AAAATGATGATTAATTTCAAGAGTCTCAATCAAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 AAAATGATGATTAATTTCAAGAGTCTCAATCAAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 CATCACTTCTAGTATTTATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 CATCACTTCTAGTATTTATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Qy 1561 AAGAAACCAAG 1620
Db 1561 AAGAAACCAAG 1620
Qy 1621 CTGTGTATTTGTCAAGAGTCACTAAAGATGATGATTTGATGATGATGATGATG 1680
Db 1621 CTGTGTATTTGTCAAGAGTCACTAAAGATGATGATTTGATGATGATGATGATG 1680
Qy 1681 ATCTTATGCTGTCTTATCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ATCTTATGCTGTCTTATCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740

Db 1681 ATCTTATGCTGTCTTATCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 TATGTAG 1800
Db 1741 TATGTAG 1800
Qy 1801 AAGAGATTAATTAATTTCTAATCTATTAATTAATTAATTAATTAATTAATTAAT 1860
Db 1801 AAGAGATTAATTAATTTCTAATCTATTAATTAATTAATTAATTAATTAATTAAT 1860
Qy 1861 CACATATATCAAG 1920
Db 1861 CACATATATCAAG 1920
Qy 1921 TGACCTACTTGTGTAGTGAATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1980
Db 1921 TGACCTACTTGTGTAGTGAATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1980
Qy 1981 CATCTTACAG 2040
Db 1981 CATCTTACAG 2040
Qy 2041 TTGCTTTTCTTTCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 2100
Db 2041 TTGCTTTTCTTTCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 2100
Qy 2101 AGACGAGTCTTGTCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2160
Db 2101 AGACGAGTCTTGTCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2160
Qy 2161 AGCTGTGCTTGTCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2220
Db 2161 AGCTGTGCTTGTCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2220
Qy 2221 TACAGTATCTGAG 2280
Db 2221 TACAGTATCTGAG 2280
Qy 2281 ACCGTGTAG 2340
Db 2281 ACCGTGTAG 2340
Qy 2341 CAAAGTGTGAGATTAAG 2400
Db 2341 CAAAGTGTGAGATTAAG 2400

RESULT 12
US-10-489-802-7
; Sequence 7, Application US/10489802
; Publication No. US20040248198A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital, Inc.
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Art and Hm2 Interaction Domains and
; TITLE OF INVENTION: Method of Use Thereof
; FILE REFERENCE: 44158/243642
; CURRENT APPLICATION NUMBER: US/10/489,802
; PRIOR APPLICATION NUMBER: 2004-03-16
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-802-7

Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	GCACCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGTCGGAAGATGGA	60	
Db	1	GCACCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGTCGGAAGATGGA	60	
Qy	61	GCAAGAGCCGAGCCCGAGGGGCGCGGACCCCTCTGACCGAGATCCTGTGCTTTG	120	
Db	61	GCAAGAGCCGAGCCCGAGGGGCGCGGACCCCTCTGACCGAGATCCTGTGCTTTG	120	
Qy	121	CAGCCAGAGGACCCGCTCCCGGATTAGTGCCTGACAGGCGCCAGTGCCTGCGCCG	180	
Db	121	CAGCCAGAGGACCCGCTCCCGGATTAGTGCCTGACAGGCGCCAGTGCCTGCGCCG	180	
Qy	181	GAGAGTGAATGATCCCGGAGGCGGAGGCTGTGCTTCCGAGATGACATGCCCCCG	240	
Db	181	GAGAGTGAATGATCCCGGAGGCGGAGGCTGTGCTTCCGAGATGACATGCCCCCG	240	
Qy	241	AMGAAACTGGGGAGCTTGTAGGGGACCCCGGACTCCAGCGGAAACCCCGGATGTGA	300	
Db	241	AMGAAACTGGGGAGCTTGTAGGGGACCCCGGACTCCAGCGGAAACCCCGGATGTGA	300	
Qy	301	GGAGCAGCAATGTGCAATACCAATGTGTACTCTA CTGATGCTGTAAACCACT	360	
Db	301	GGAGCAGCAATGTGCAATACCAATGTGTACTCTA CTGATGCTGTAAACCACT	360	
Qy	361	CACAGATTCAGCTTCGGAACAAGACCCCTGTGTAACCAAGCATTGCTTTGAAT	420	
Db	361	CACAGATTCAGCTTCGGAACAAGACCCCTGTGTAACCAAGCATTGCTTTGAAT	420	
Qy	421	TATTAAAGCTGTGGTGCACAAAAAGACCTTATCTATGAAAGGTTCTTTTATC	480	
Db	421	TATTAAAGCTGTGGTGCACAAAAAGACCTTATCTATGAAAGGTTCTTTTATC	480	
Qy	481	TTGGCCAGTATATATGACTAAACGATATATATGAGGAAGCAACAATATGTATAT	540	
Db	481	TTGGCCAGTATATATGACTAAACGATATATATGAGGAAGCAACAATATGTATAT	540	
Qy	541	GTTCAAATGATCTTCTAGAGAGTTGTTGGCGTGCAGCTTCTGTGAAAGAGACA	600	
Db	541	GTTCAAATGATCTTCTAGAGAGTTGTTGGCGTGCAGCTTCTGTGAAAGAGACA	600	
Qy	601	GGAATAATATATACAGATCTACAGGAACCTGTGTAGTCAATACAGCAGATCATCG	660	
Db	601	GGAATAATATATACAGATCTACAGGAACCTGTGTAGTCAATACAGCAGATCATCG	660	
Qy	661	ACTCAGTATCATCTGTAGTGAAGACAGGTGTCACTTGAAGTGGAGTATCAAAAG	720	
Db	661	ACTCAGTATCATCTGTAGTGAAGACAGGTGTCACTTGAAGTGGAGTATCAAAAG	720	
Qy	721	ACCTGTACAGAGCTTCAAGAAAGAAACCTTCACTTCACTTGTGTTCTAGACAT	780	
Db	721	ACCTGTACAGAGCTTCAAGAAAGAAACCTTCACTTCACTTGTGTTCTAGACAT	780	
Qy	781	CTACCTCATCTAGAGAGAGCAATTAAGTGAACAAGAAATTCAGATGAATATATCG	840	
Db	781	CTACCTCATCTAGAGAGAGCAATTAAGTGAACAAGAAATTCAGATGAATATATCG	840	
Qy	841	GTTGAACGACAAAGAAAGCCCAATCTGATGATATTTCCCTTCTTTGATGAAGCC	900	
Db	841	GTTGAACGACAAAGAAAGCCCAATCTGATGATATTTCCCTTCTTTGATGAAGCC	900	
Qy	901	TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAAGCAGTACAGTATCTACAG	960	
Db	901	TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAAGCAGTACAGTATCTACAG	960	
Qy	961	GGAACCCATCGAATCCGATCTTGTAGTGTGTAGTGAATTCAGTCAAGTGTGTTGG	1020	
Db	961	GGAACCCATCGAATCCGATCTTGTAGTGTGTAGTGAATTCAGTCAAGTGTGTTGG	1020	
Qy	1021	ATCAGAGTTCAGTTCAATCAGTATGATGATGAATTTGAAGTGAATCTTCGACTCG	1080	
Db	1021	ATCAGAGTTCAGTTCAATCAGTATGATGATGAATTTGAAGTGAATCTTCGACTCG	1080	

Qy	1081	AAAGATTATAGCCTTAGTGAAGAGGACAGAACTCTCAGATGAAGTATGAGTATATC	1140	
Db	1081	AAAGATTATAGCCTTAGTGAAGAGGACAGAACTCTCAGATGAAGTATGAGTATATC	1140	
Qy	1141	AAAGTACTGTATCAGGAGGGAGAGTATACAGATTCATTTGAAAGAGATCTGAAA	1200	
Db	1141	AAAGTACTGTATCAGGAGGGAGAGTATACAGATTCATTTGAAAGAGATCTGAAA	1200	
Qy	1201	TTTCCTTAGCTGATTAATGGAATGCACTTCAATGCAATGAATGAATCCCCCTTCAT	1260	
Db	1201	TTTCCTTAGCTGATTAATGGAATGCACTTCAATGCAATGAATGAATCCCCCTTCAT	1260	
Qy	1261	CACATTTGACAGATGTTGGGCCCTTCGGAATTTGGCTTCCTGAAATTAAGGAAAG	1320	
Db	1261	CACATTTGACAGATGTTGGGCCCTTCGGAATTTGGCTTCCTGAAATTAAGGAAAG	1320	
Qy	1321	ATPAAGGGGAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGGGCT	1380	
Db	1321	ATPAAGGGGAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGGGCT	1380	
Qy	1381	TTGATGTTCTGATTTGTAATAAACTATAGTAATGATTCAGAGTCAATGTTGAG	1440	
Db	1381	TTGATGTTCTGATTTGTAATAAACTATAGTAATGATTCAGAGTCAATGTTGAG	1440	
Qy	1441	AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAAAGTGAAGCTATTCACG	1500	
Db	1441	AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAAAGTGAAGCTATTCACG	1500	
Qy	1501	CATCAACTCTAGTACATTTATTAAGAGCCAGAAAGATGGAAGGTTGAAAGGG	1560	
Db	1501	CATCAACTCTAGTACATTTATTAAGAGCCAGAAAGATGGAAGGTTGAAAGGG	1560	
Qy	1561	AAAGAACCCAGACAAAGAGAGGTGGAATCTAGTTGCCCTTAATGCAATTGAAC	1620	
Db	1561	AAAGAACCCAGACAAAGAGAGGTGGAATCTAGTTGCCCTTAATGCAATTGAAC	1620	
Qy	1621	CTTGATGATTTGTCAAGGTGCACTTAATAATGTTGTCATTTCCATGCGAAACAGAC	1680	
Db	1621	CTTGATGATTTGTCAAGGTGCACTTAATAATGTTGTCATTTCCATGCGAAACAGAC	1680	
Qy	1681	ATCTATGGCCGCTTTCATGTGCAAGAGCTAAAGAAAGTAAGCCCTGCCAG	1740	
Db	1681	ATCTATGGCCGCTTTCATGTGCAAGAGCTAAAGAAAGTAAGCCCTGCCAG	1740	
Qy	1741	TATGTAGCAACCAATTCATATGCTAATTTCCCTAGTTGACCTGTCTAT	1800	
Db	1741	TATGTAGCAACCAATTCATATGCTAATTTCCCTAGTTGACCTGTCTAT	1800	
Qy	1801	AAAGAAATTAATATTTCTAACTATATAACCTAGGAATTTAGACAACCTGAATTTAT	1860	
Db	1801	AAAGAAATTAATATTTCTAACTATATAACCTAGGAATTTAGACAACCTGAATTTAT	1860	
Qy	1861	CACATATACAAAGGAGAAATGCTCAATTCATATGATTTCTTCTTAAGTATAT	1920	
Db	1861	CACATATACAAAGGAGAAATGCTCAATTCATATGATTTCTTCTTAAGTATAT	1920	
Qy	1921	TGACCTACTTGGTGTGGAATAGTAATCTTAATAATTTGACTGAAATATATAGT	1980	
Db	1921	TGACCTACTTGGTGTGGAATAGTAATCTTAATAATTTGACTGAAATATATAGT	1980	
Qy	1981	CATCTTTACACCACTCTTAATTAATATATTTCTACTGTCTTAATGAGAATAC	2040	
Db	1981	CATCTTTACACCACTCTTAATTAATATATTTCTACTGTCTTAATGAGAATAC	2040	
Qy	2041	TTGGTTTTTTTTTCTTAATATGATATGACATTTAATGTAATCTTAATTTTGTG	2100	
Db	2041	TTGGTTTTTTTTTCTTAATATGATATGACATTTAATGTAATCTTAATTTTGTG	2100	
Qy	2101	AGACGAGTCTTGCTCTGTATCCAGGCTGAGTGCAGATGGGTGATCTTGGCTCACTGA	2160	
Db	2101	AGACGAGTCTTGCTCTGTATCCAGGCTGAGTGCAGATGGGTGATCTTGGCTCACTGA	2160	

QY 2161 AGCTCTGCCCTCCCGGGTTGCAACATCTCTGCTCCAGCCTCCCAATTAGCTTGGCC 2220
DB 2161 AGCTCTGCCCTCCCGGGTTGCAACATCTCTGCTCCAGCCTCCCAATTAGCTTGGCC 2220
QY 2221 TAGAGTCACTGCGCAACACACTGCTAATTTTGTATCTTTTGTATAGAGAGAGGTTTC 2280
DB 2221 TAGAGTCACTGCGCAACACACTGCTAATTTTGTATCTTTTGTATAGAGAGAGGTTTC 2280
QY 2281 ACCGTGTAGGCGAGATGCTGATCTGATCTCTGACCTGCTGATCCGCCACCTGCGCTCC 2340
DB 2281 ACCGTGTAGGCGAGATGCTGATCTCTGATCTCTGACCTGCTGATCCGCCACCTGCGCTCC 2340
QY 2341 CAAAGTCTGGGATTTACAGGATAGACCAACCG 2372
DB 2341 CAAAGTCTGGGATTTACAGGATAGACCAACCG 2372

RESULT 13
US-10-723-860-2235
; Sequence 2235, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsaba
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882, 0193, NUS01
; CURRENT APPLICATION NUMBER: US/10/723, 860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429, 739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2235
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2235

Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGCGCTGTGAGCCCTGTGTCGAAAGATGGA 60
DB 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGCGCTGTGAGCCCTGTGTCGAAAGATGGA 60
QY 61 GCAGAGACCGAGCGCCGAGGGCGCGCGACCCCTGTGACCGAGATCCTGCTGCTTTCG 120
DB 61 GCAGAGACCGAGCGCCGAGGGCGCGCGACCCCTGTGACCGAGATCCTGCTGCTTTCG 120
QY 121 CAGCCAGAGACGACCGTCCCTCCCGAGATTAGTGCATGAGCGCCAGTCCCTGCGCCG 180
DB 121 CAGCCAGAGACGACCGTCCCTCCCGAGATTAGTGCATGAGCGCCAGTCCCTGCGCCG 180
QY 181 GAGAGTGAATATATCCCGAGGCGCGAGCGCTGCTTCCGAGATGATGATCCCGCG 240
DB 181 GAGAGTGAATATATCCCGAGGCGCGAGCGCTGCTTCCGAGATGATGATCCCGCG 240
QY 241 AAGAAACTGGGAGATCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGATGTA 300
DB 241 AAGAAACTGGGAGATCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGATGTA 300
QY 301 GAGAGAGCGAAATGTGCAATACCAATGTCTGTACTTACTGATGCTGTGACCACT 360
DB 301 GAGAGAGCGAAATGTGCAATACCAATGTCTGTACTTACTGATGCTGTGACCACT 360
QY 361 CACAGATTCAGACTTCGAGCAAGAGACCGCTGTTAGACCAAGCCATGCTTTGAAT 420
DB 361 CACAGATTCAGACTTCGAGCAAGAGACCGCTGTTAGACCAAGCCATGCTTTGAAT 420
QY 421 TATTAAGTCTGTGTGACAAAGAAAGACATTAATGTAAGAGGTTCTTTTATC 480

DB 421 TATTAAGTCTGTGTGACAAAGAAAGACATTAATGTAAGAGGTTCTTTTATC 480
QY 481 TTGGCAGATATATATGACTTAAAGATTAATGTATGAGCAACAATATGTATAT 540
DB 481 TTGGCAGATATATATGACTTAAAGATTAATGTATGAGCAACAATATGTATAT 540
QY 541 GTTCAATATGATCTTCTAGAGATTTGTTGGCGTCCAGAGCTTCTGTGAAAGACA 600
DB 541 GTTCAATATGATCTTCTAGAGATTTGTTGGCGTCCAGAGCTTCTGTGAAAGACA 600
QY 601 GGAATAATATATCAATATCTAGAGAACTTGTAATAGTAATCAAGAGAAATCATCG 660
DB 601 GGAATAATATATCAATATCTAGAGAACTTGTAATAGTAATCAAGAGAAATCATCG 660
QY 661 ACTCAGGATCATCTGTAGTGAAGACAGTGTCACTTGAAGTGGAGTATCAAAAG 720
DB 661 ACTCAGGATCATCTGTAGTGAAGACAGTGTCACTTGAAGTGGAGTATCAAAAG 720
QY 721 ACCTTGATCAAGACCTTCAAGAGAAACCTTCATCTTCAATTTGGTTTCTAGACAT 780
DB 721 ACCTTGATCAAGACCTTCAAGAGAAACCTTCATCTTCAATTTGGTTTCTAGACAT 780
QY 781 CTACCTCATCTAGAGAGAGCAATTTAGTGAAGAGAAATTTCAATGATATATCTG 840
DB 781 CTACCTCATCTAGAGAGAGCAATTTAGTGAAGAGAAATTTCAATGATATATCTG 840
QY 841 GTGAACGACAAAGAAACGCCCAAAATCTGATAGATTTCCCTTCTTATGAAAGCC 900
DB 841 GTGAACGACAAAGAAACGCCCAAAATCTGATAGATTTCCCTTCTTATGAAAGCC 900
QY 901 TGGCTGTGTGTATATAGAGAGATGTGTGAAAGAGAGTACAGTAAATCTACAG 960
DB 901 TGGCTGTGTGTATATAGAGAGATGTGTGAAAGAGAGTACAGTAAATCTACAG 960
QY 961 GAGGCCATGCAATCCGATCTTGATGCTGTGTATGAGAACATTCAGGTATGTTGG 1020
DB 961 GAGGCCATGCAATCCGATCTTGATGCTGTGTATGAGAACATTCAGGTATGTTGG 1020
QY 1021 ATCAGGATTCAGTTTACATCAGTTTATGATGATTTGAAGTTGAATCTCTGACCTCAG 1080
DB 1021 ATCAGGATTCAGTTTACATCAGTTTATGATGATTTGAAGTTGAATCTCTGACCTCAG 1080
QY 1081 AAGATTATAGCTTATGTAAGAGAGCAAGAACTCTCAGATGAGATGATGATATATC 1140
DB 1081 AAGATTATAGCTTATGTAAGAGAGCAAGAACTCTCAGATGAGATGATGATATATC 1140
QY 1141 AAGTTATCTGTATATCAGAGGAGAGATGATACAGATTCATTTGAAGAAATCTGAAA 1200
DB 1141 AAGTTATCTGTATATCAGAGGAGAGATGATACAGATTCATTTGAAGAAATCTGAAA 1200
QY 1201 TTTCTTTCGATGATATGAGAAATGCACTTCATGCAATGAAATGAAATCCCGCTTCAT 1260
DB 1201 TTTCTTTCGATGATATGAGAAATGCACTTCATGCAATGAAATGAAATCCCGCTTCAT 1260
QY 1261 CACATTTGCAACAGATGTTGGCCCTTCCGTGAGAAATTTGCTTCTGAAATTAAGGAAAG 1320
DB 1261 CACATTTGCAACAGATGTTGGCCCTTCCGTGAGAAATTTGCTTCTGAAATTAAGGAAAG 1320
QY 1321 AATAAGGGGAAATCTCTGAGAAAGCAATCTGAGAAATCTCAACACACCTGAGAGGCT 1380
DB 1321 AATAAGGGGAAATCTCTGAGAAAGCAATCTGAGAAATCTCAACACACCTGAGAGGCT 1380
QY 1381 TTGATGTTCTGATTTGTAAGAAATCTATAGTAATGATTTCCAGAGAGTCAATGTTGAGG 1440
DB 1381 TTGATGTTCTGATTTGTAAGAAATCTATAGTAATGATTTCCAGAGAGTCAATGTTGAGG 1440
QY 1441 AAAATGATGATTAATTAACAAGGTTCAATCAAGAAAGTGAAGCTATTTCTCAGC 1500
DB 1441 AAAATGATGATTAATTAACAAGGTTCAATCAAGAAAGTGAAGCTATTTCTCAGC 1500
QY 1501 CATCAATTCATAGTATATTTATAGCAAGCAAGAAAGATGTAAGGTTTGAAGGG 1560

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Db 1501 CATCACTTCTAGTACATTATTATATAGCAGCCAGAGAGTGAAGATTGAAAGG 1560
Qy 1561 AAGAAACCCAGACAAAGAGAGAGTGTGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
Db 1561 AAGAAACCCAGACAAAGAGAGAGTGTGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
Qy 1621 CTGTGTGATTTGTCAAGGTGACCTTAATAATGTTGATTTGCATGGCAAAACAGAC 1680
Db 1621 CTGTGTGATTTGTCAAGGTGACCTTAATAATGTTGATTTGCATGGCAAAACAGAC 1680
Qy 1681 ATCTATGCGCTGCTTTACATGTGCAAGAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
Db 1681 ATCTATGCGCTGCTTTACATGTGCAAGAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
Qy 1741 TATGTAGACCAACCAATTCAATGATGTGCTAATTATTTCCCTAGTTGACCTGTCTAT 1800
Db 1741 TATGTAGACCAACCAATTCAATGATGTGCTAATTATTTCCCTAGTTGACCTGTCTAT 1800
Qy 1801 AAGAGAAATATATATTTCTAATACTATTAACCCCTAGGAATTTAGACAACCTGAATTTAT 1860
Db 1801 AAGAGAAATATATATTTCTAATACTATTAACCCCTAGGAATTTAGACAACCTGAATTTAT 1860
Qy 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCAATGATGATTTCTTCTTTAGTAAAT 1920
Db 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCAATGATGATTTCTTCTTTAGTAAAT 1920
Qy 1921 TACACCTCTTGTGTAGTGAATATGTAATTAATTAATTTGACTTGAATATGTAGCT 1980
Db 1921 TACACCTCTTGTGTAGTGAATATGTAATTAATTAATTTGACTTGAATATGTAGCT 1980
Qy 1981 CATTCTTTACACCACTCTTAATTTTAAATTTTAAATTTTAACTGCTTAAATGAAATAC 2040
Db 1981 CATTCTTTACACCACTCTTAATTTTAAATTTTAAATTTTAACTGCTTAAATGAAATAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAATAATATGTAATGATGATTAATTAATTAATTTTAAATTTT 2100
Db 2041 TTGGTTTTTTTTTTCTTAATAATATGTAATGATGATTAATTAATTAATTTTAAATTTT 2100
Qy 2101 AGACGAGCTTGTCTGTGTTACCCAGGCTGAGTGAAGTGTGATCTTGGCTCACTGCA 2160
Db 2101 AGACGAGCTTGTCTGTGTTACCCAGGCTGAGTGAAGTGTGATCTTGGCTCACTGCA 2160
Qy 2161 AGCTGCGCTCCCGGGGTGACCATTTCTCTGCTGACGCTCCCATTAAGCTTGGCC 2220
Db 2161 AGCTGCGCTCCCGGGGTGACCATTTCTCTGCTGACGCTCCCATTAAGCTTGGCC 2220
Qy 2221 TACAGTCACTCTGCCACCACTGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
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RESULT 14
US-10-843-641A-450
; Sequence 450, Application US/10843641A
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
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Qy 121 CAGCAGAGAGCAGCTGCTCCCGGATTAAGTGCATGACAGGCGCCAGTGCCTGCGCG 180
Db 121 CAGCAGAGAGCAGCTGCTCCCGGATTAAGTGCATGACAGGCGCCAGTGCCTGCGCG 180
Qy 181 GAGAGTGAATATATCCCGAGGCGGCGGCTGCTTCCGAGTATGATGATCCCGTG 240
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RESULT 15
US-11-069-642-136
; Sequence 136, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-069-642-136

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: August 4, 2006, 13:38:17
Job time : 2943 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 20:42:58 ; Search time 322 Seconds
(without alignments)
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Title: US-09-966-724b-2

Perfect score: 2372

Sequence: 1 GCACCGCGCGAGCTTGCTG.....ATTACGAGCATGAGCCACCG 2372

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters: 4386554

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

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3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB_seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2372	100.0	2372	US-10-511-937-615	Sequence 615, App
2	984.4	41.5	34088	US-11-266-748A-23848	Sequence 23848, A
3	962.4	40.6	1000	US-11-266-748A-114799	Sequence 114799, A
4	962.4	40.6	1000	US-11-266-748A-119930	Sequence 119930, A
5	962.4	40.6	1000	US-11-266-748A-281679	Sequence 281679, A
6	962.4	40.6	1000	US-11-266-748A-308319	Sequence 308319, A
7	962.4	40.6	1000	US-11-266-748A-390721	Sequence 390721, A
8	962.4	40.6	1000	US-11-266-748A-481439	Sequence 481439, A
9	777.6	32.8	1000	US-11-266-748A-221947	Sequence 221947, A
10	777.6	32.8	1000	US-11-266-748A-287544	Sequence 287544, A
11	777.6	32.8	1000	US-11-266-748A-338973	Sequence 338973, A
12	777.6	32.8	1000	US-11-266-748A-398267	Sequence 398267, A
13	777.6	32.8	1000	US-11-266-748A-469313	Sequence 469313, A
14	773.4	32.6	1540	US-11-266-748A-29783	Sequence 29783, A
15	594.8	25.1	631	US-11-266-748A-17558	Sequence 17558, A
16	481.8	20.3	674	US-11-266-748A-219905	Sequence 219905, A
17	418.6	17.6	75976	US-10-539-228-229	Sequence 229, App
18	226.2	9.5	68689	US-11-266-748A-23956	Sequence 23956, A
19	226.2	9.5	29454	US-10-540-898-951	Sequence 951, App
20	226.2	9.5	180227	US-10-539-228-308	Sequence 308, App
21	226	9.5	267156	US-11-266-748A-32012	Sequence 32012, A
22	226	9.5	684973	US-11-266-748A-12013	Sequence 12013, A
23	225.4	9.5	1000	US-11-266-748A-204803	Sequence 204803, A
24	225.2	9.5	30328	US-11-266-748A-25024	Sequence 25024, A

25	223.4	9.4	59753	8	US-11-266-748A-25122	Sequence 25122, A
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27	221.4	9.3	100445	6	US-10-539-228-170	Sequence 170, App
28	221.4	9.3	254396	6	US-10-540-898-534	Sequence 534, App
29	221	9.3	118456	8	US-11-266-748A-58957	Sequence 58957, A
30	220.6	9.3	778	8	US-11-266-748A-212538	Sequence 212538, A
31	220.6	9.3	155379	8	US-11-266-748A-59410	Sequence 59410, A
32	220.6	9.3	155379	8	US-11-266-748A-59410	Sequence 59410, A
33	220.4	9.3	24825	8	US-11-266-748A-22745	Sequence 22745, A
34	220.4	9.3	355211	6	US-10-540-898-242	Sequence 242, App
35	220.2	9.3	148828	6	US-11-266-748A-24893	Sequence 24893, A
36	220.2	9.3	390183	6	US-10-540-898-937	Sequence 937, App
37	219.8	9.3	109661	6	US-10-540-898-795	Sequence 795, App
38	219.8	9.3	113456	8	US-11-266-748A-58942	Sequence 58942, A
39	219.8	9.3	201239	8	US-11-266-748A-22854	Sequence 22854, A
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43	219.6	9.3	11283	8	US-11-266-748A-30885	Sequence 30885, A
44	219.6	9.3	99291	6	US-10-539-228-744	Sequence 744, App
45	219.6	9.3	150000	8	US-11-266-748A-23591	Sequence 23591, A

ALIGNMENTS

RESULT 1						
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Sequence 615, Application US/10511937						
Publication No. US200600883661						
GENERAL INFORMATION:						
APPLICANT: EXPRESSION DIAGNOSTICS, INC.						
APPLICANT: Wohlgemuth, Jay						
APPLICANT: Fry, Kirk						
APPLICANT: Woodward, Robert						
APPLICANT: Ly, Ngoc						
APPLICANT: Prentice, James						
APPLICANT: Morris, Macdonald						
APPLICANT: Rosenberg, Steven						
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING						
FILE REFERENCE: AND MONITORING TRANSPLANT REJECTION						
CURRENT APPLICATION NUMBER: US/10/511, 937						
CURRENT FILING DATE: 2004-10-19						
PRIOR APPLICATION NUMBER: PCT/US2003/012946						
PRIOR FILING DATE: 2003-04-24						
PRIOR FILING DATE: 2002-04-24						
PRIOR APPLICATION NUMBER: US 10/131, 831						
PRIOR FILING DATE: 2002-12-20						
NUMBER OF SEQ ID NOS: 3117						
SOFTWARE: PatentIn version 3.2						
SEQ ID NO 615						
LENGTH: 2372						
TYPE: DNA						
ORGANISM: Homo sapiens						
US-10-511-937-615						
Query Match						
Best Local Similarity 100.0%; Score 2372; DB 6; Length 2372;						
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	GCACCGCGCGAGCTTGCTTGCGGGGCTGTGTGCGCCCTGTGTGCGGAAGATGGA	60			
DB	1	GCACCGCGCGAGCTTGCTTGCGGGGCTGTGTGCGCCCTGTGTGCGGAAGATGGA	60			
QY	61	GCAAGAGCGAGCGCCGAGGGGCGCGCGACCCCTTGACCGAGATCTTGCTTTG	120			
DB	61	GCAAGAGCGCGAGCGCGAGGGGCGCGCGACCCCTTGACCGAGATCTTGCTTTG	120			
QY	121	CAGCAGGAGGACGCTCCCTCCCGGATTAGTGGTACGAGCGCCAGTGGCGGCGG	180			
DB	121	CAGCAGGAGGACGCTCCCTCCCGGATTAGTGGTACGAGCGCCAGTGGCGGCGG	180			

181 GAGAGTGAATGATCCCCGAGGCCGCGTCTGCTCCGAGTAGTCAGTCCCCGCTG 240
181 GAGAGTGAATGATCCCCGAGGCCGCGTCTGCTCCGAGTAGTCAGTCCCCGCTG 240
241 AAGGAACTGGGGAGTCTTGAAGGACCCCGCACTCAAGCGGAAACCCTGGATGTGA 300
241 AAGGAACTGGGGAGTCTTGAAGGACCCCGCACTCAAGCGGAAACCCTGGATGTGA 300
301 GGACAGGCAATGTCGAATCCAACTGCTGTACTGATGAGTGTGCTGAACCACT 360
301 GGACAGGCAATGTCGAATCCAACTGCTGTACTGATGAGTGTGCTGAACCACT 360
361 CACAGATCCAGCTTCGGAACAAGAGACCTGCTTGAACAAGCCATTCCTTTGAAGT 420
361 CACAGATCCAGCTTCGGAACAAGAGACCTGCTTGAACAAGCCATTCCTTTGAAGT 420
421 TATTAAAGTCTGTGGTGCACAAAAAGACCTTATATATGAAAGAGGTTCTTTTATC 480
421 TATTAAAGTCTGTGGTGCACAAAAAGACCTTATATATGAAAGAGGTTCTTTTATC 480
481 TTGGCCAGTATATATGACTAAAGATATATATGAGAGAGCAACAATTTGATAT 540
481 TTGGCCAGTATATATGACTAAAGATATATATGAGAGAGCAACAATTTGATAT 540
541 GTTCAAAATGATCTCTAGAGATTTGTTGGCGTCCAGCTTCTCTGTAAGAGACA 600
541 GTTCAAAATGATCTCTAGAGATTTGTTGGCGTCCAGCTTCTCTGTAAGAGACA 600
601 GGAATAATATATCAATGATCTACAGAACTTGTAGTGTCAATGACAGAAATCATCG 660
601 GGAATAATATATCAATGATCTACAGAACTTGTAGTGTCAATGACAGAAATCATCG 660
601 GGAATAATATATCAATGATCTACAGAACTTGTAGTGTCAATGACAGAAATCATCG 660
601 GGAATAATATATCAATGATCTACAGAACTTGTAGTGTCAATGACAGAAATCATCG 660
661 ACTGAGTACATCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGAGTATCAAAAG 720
661 ACTGAGTACATCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGAGTATCAAAAG 720
721 ACCTGTACAAGAGCTTCAGAAAGAAACCTTCATCTTCATCTTGTGTAAGCAT 780
721 ACCTGTACAAGAGCTTCAGAAAGAAACCTTCATCTTCATCTTGTGTAAGCAT 780
781 CTACCTCATCTGAAGAGAGCAATTAAGTGAACAAGAAATTCAGATGATATCTG 840
781 CTACCTCATCTGAAGAGAGCAATTAAGTGAACAAGAAATTCAGATGATATCTG 840
841 GTGAACGACAAAGAAACGCGCAAAATCGATGATATTCCTTTCTTTGATGAAGCC 900
841 GTGAACGACAAAGAAACGCGCAAAATCGATGATATTCCTTTCTTTGATGAAGCC 900
901 TGGCTCTGTGTATTAAGGAGATATGTTGTAAGAAAGACAGTACAGTATCTACG 960
901 TGGCTCTGTGTATTAAGGAGATATGTTGTAAGAAAGACAGTACAGTATCTACG 960
961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTGAAGTGAACATTCAGGTGA 1020
961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTGAAGTGAACATTCAGGTGA 1020
1021 ATCAGAGTTCAGTTCAATCACTTTAGTGTGAATTTGAAGTGAATCTTCGACTCG 1080
1021 ATCAGAGTTCAGTTCAATCACTTTAGTGTGAATTTGAAGTGAATCTTCGACTCG 1080
1081 AAGATTATAGCTTGTGTGAAGAGCAAGAACTCTCAATGAGAGTGAAGATATATC 1140
1081 AAGATTATAGCTTGTGTGAAGAGCAAGAACTCTCAATGAGAGTGAAGATATATC 1140
1141 AAGTACTGTGTATCAGGAGGAGATGATACATTTGTAAGAAAGATCTGAAA 1200
1141 AAGTACTGTGTATCAGGAGGAGATGATACATTTGTAAGAAAGATCTGAAA 1200
1201 TTTCTTACTGACTATTTGAAATGCACTTCATGCAATGAATGAATCCCTTCAT 1260
1201 TTTCTTACTGACTATTTGAAATGCACTTCATGCAATGAATGAATCCCTTCAT 1260

1261 CACATTCGACAGATGTTGGGCCCTTCGTGAGAAATGCGCTTCCTGAAGATTAAGGAAAG 1320
1261 CACATTCGACAGATGTTGGGCCCTTCGTGAGAAATGCGCTTCCTGAAGATTAAGGAAAG 1320
1321 ATAAAGGGAATTCCTGAGAAAGCCCAACCTGAAACCTGAACAAGCTGAAGGGCT 1380
1321 ATAAAGGGAATTCCTGAGAAAGCCCAACCTGAAACCTGAACAAGCTGAAGGGCT 1380
1381 TTGATGTTCTGATTTGTAATAAACTATAGTATGATTTCCAGAGAGTCATGTGTGAGG 1440
1381 TTGATGTTCTGATTTGTAATAAACTATAGTATGATTTCCAGAGAGTCATGTGTGAGG 1440
1441 AAAATGATTAATAATTAACAAGCTTCACATCAACAAGAAAGTGAAGATTAATTCACG 1500
1441 AAAATGATTAATAATTAACAAGCTTCACATCAACAAGAAAGTGAAGATTAATTCACG 1500
1501 CATCACTTCATAGTATGATTTTATATGACCAAGAAAGATGTAAGAGTTGAAAGG 1560
1501 CATCACTTCATAGTATGATTTTATATGACCAAGAAAGATGTAAGAGTTGAAAGG 1560
1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAC 1620
1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAC 1620
1621 CTGTGTGATTTGTCAAGTGCACCTTAAATGTTGCTTATGCTGCAAGCAAGAC 1680
1621 CTGTGTGATTTGTCAAGTGCACCTTAAATGTTGCTTATGCTGCAAGCAAGAC 1680
1681 ATCTTATGCTGCTTATCATGTGCAAGAAAGCTTAAGAAAGAAATGAAGCCGCGCAG 1740
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1741 TATGTAGCAACCAATTCATGATGATTTGCTTATTTCCCTGATTTGACCTGTAT 1800
1801 AAGAGATTAATATTTCTAATATATTAACCTTGAAGAAATTAAGACACTGAATTAAT 1860
1801 AAGAGATTAATATTTCTAATATATTAACCTTGAAGAAATTAAGACACTGAATTAAT 1860
1861 CACATTAATCAAAAGTGAAGAAATGCTCAATTCATGATGATTTCTCTTATGATAT 1920
1861 CACATTAATCAAAAGTGAAGAAATGCTCAATTCATGATGATTTCTCTTATGATAT 1920
1921 TGACCTACTTGTGTGGAATGATGATTAATCTTATTAATTTGACTTGAATATAGCT 1980
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1981 CATCTTTACCAACAATCTTAATTTTAATAATTTCTACTGTCTTAATGAGAAATAC 2040
1981 CATCTTTACCAACAATCTTAATTTTAATAATTTCTACTGTCTTAATGAGAAATAC 2040
2041 TTGGTTTTTTTTTTCTTAATATGATATGACATTTAAATGTAATTTATTTT 2100
2041 TTGGTTTTTTTTTTCTTAATATGATATGACATTTAAATGTAATTTATTTT 2100
2101 AGACCGAGCTTGTCTGTATCCAGGCTGAGTGCAGTGGGTGATCTTGCTCACTGA 2160
2101 AGACCGAGCTTGTCTGTATCCAGGCTGAGTGCAGTGGGTGATCTTGCTCACTGA 2160
2161 AGCTGTGCTTCCCGGGGTGCAACATTCCTGCTCAGCTCCCAATTAAGCTTGGC 2220
2161 AGCTGTGCTTCCCGGGGTGCAACATTCCTGCTCAGCTCCCAATTAAGCTTGGC 2220
2221 TACAGTCACTGCAACAACCTGCTAATTTTGTACTTTTATGAGAGAGGTTTC 2280
2221 TACAGTCACTGCAACAACCTGCTAATTTTGTACTTTTATGAGAGAGGTTTC 2280
2281 ACCGTGTAGCCAGAGATGCTGATCTCCGATCCGATCCGCGCACTCGGCTTC 2340
2281 ACCGTGTAGCCAGAGATGCTGATCTCCGATCCGATCCGCGCACTCGGCTTC 2340
2341 CAAAGTGTGGATTAACAGGCATGAGCAACG 2372

Db 2341 CAAAGTGTGGATTACAGGCATGAGCCACCG 2372

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RESULT 2
US-11-266-748A-23848
/ Sequence 23848, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcription Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ PRIOR FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 48396
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 23848
/ LENGTH: 34088
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (787)..(787)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (820)..(832)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (834)..(840)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (851)..(851)
/ OTHER INFORMATION: n is a, c, g, or t
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/ LOCATION: (861)..(877)
/ OTHER INFORMATION: n is a, c, g, or t
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/ LOCATION: (899)..(900)
/ OTHER INFORMATION: n is a, c, g, or t
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/ NAME/KEY: misc_feature
/ LOCATION: (912)..(919)
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/ NAME/KEY: misc_feature
/ LOCATION: (921)..(928)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
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/ LOCATION: (937)..(960)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (967)..(970)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (981)..(981)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1027)..(1028)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1052)..(1077)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1075)..(1087)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1085)..(1093)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1190)..(1198)
/ OTHER INFORMATION: n is a, c, g, or t
/ US-11-266-748A-23848
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Query Match 41.5%; Score 984.4; DB 8; Length 34088;
Best Local Similarity 99.0%; Pred. No. 1.4e-165;
Matches 1022; Conservative 0; Mismatches 6; Indels 4; Gaps 3;

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QY 1200 ATTCCCTAGCTGATATTTGGAATGCACTTCAGTCAATGAATGAAATCCCTCCCTTCCA 1259
Db 33059 ATTTCATTGAAAGCATATTTGGAATGCACTTCAGTCAATGAATGAAATCCCTCCCTTCCA 33118
QY 1260 TCACATTCGCAAGAGTGTGGCCCTTCGTGGAATTTGGCTTCGAAATGAAAGGANA 1319
Db 33119 TCACATTCGCAAGAGTGTGGCCCTTCGTGGAATTTGGCTTCGAAATGAAAGGANA 33178
QY 1320 GATAAAGGGGAAATCTGAGAAAGCCAACTGAAAACTCAACAAGCTGGAAGAGGC 1379
Db 33179 GATAAAGGGGAAATCTGAGAAAGCCAACTGAAAACTCAACAAGCTGGAAGAGGC 33238
QY 1380 TTTGATGTTCTGATTTGAAAAAACTATAGTAATGATTCAGAGAGTCATGTGTTGAG 1439
Db 33239 TTTGATGTTCTGATTTGAAAAAACTATAGTAATGATTCAGAGAGTCATGTGTTGAG 33298
QY 1440 GAAATGATGATTAATAATTAACAAGCTTCACATGACAAAGAAAGTGAAGACTATTTCTGAG 1499
Db 33299 GAAATGATGATTAATAATTAACAAGCTTCACATGACAAAGAAAGTGAAGACTATTTCTGAG 33358
QY 1500 CCATCAACTTCTAGTAGCATTATTTATAGACGCCAAGAGATGTGAAAAGGTTTGAAGG 1559
Db 33359 CCATCAACTTCTAGTAGCATTATTTATAGACGCCAAGAGATGTGAAAAGGTTTGAAGG 33418
QY 1560 GAAAGAAACCAAGACAAAGAAAGAGGTGGAATTTAGTTGCCCTTTATGCTTGA 1619
Db 33419 GAAAGAAACCAAGACAAAGAAAGAGGTGGAATTTAGTTGCCCTTTATGCTTGA 33478
QY 1620 CTTGTGTGATTTTGTCAAGGTGACCTTAATAATGTTGATTCATGTCAGCAAAACAGGA 1679
Db 33479 CTTGTGTGATTTTGTCAAGGTGACCTTAATAATGTTGATTCATGTCAGCAAAACAGGA 33538
QY 1680 CATCTTATGCGCTGCTTTACATGTGCAAAAGAAAGCTTAAGAAAGAAATGAGCCCTGCCA 1739
Db 33539 CATCTTATGCGCTGCTTTACATGTGCAAAAGAAAGCTTAAGAAAGAAATGAGCCCTGCCA 33598
QY 1740 GTATGTAGCAACAATCAATGATGTGTGCTAATTTCCCTAGTTGACCTGTGTA 1799
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Db 33599 GATAGTACACCAACCAATCAATGATGTGCTAATTTCCCTAGTGAACCTGTCTA 33658
Qy 1800 TAAAGAAATTAATATTTCTTACCTATATTAACCTAGGAATTTAGCAACCGAAATTTAT 1859
Db 33659 TAAAGAAATTAATATTTCTTACCTATATTAACCTAGGAATTTAGCAACCGAAATTTAT 33718
Qy 1860 TCACATATATCAAGATGAGAAATATGCTCAATTCACATAGATTTCTCTTTAGTATTA 1919
Db 33719 TCACATATATCAAGATGAGAAATATGCTCAATTCACATAGATTTCTCTTTAGTATTA 33778
Qy 1920 TTGACCTACTTTGGTAGTGAATAGTGAATCTTATCTAATTTGACTTGAATATGATGC 1979
Db 33779 TTGACCTACTTTGGTAGTGAATAGTGAATCTTATCTAATTTGACTTGAATATGATGC 33838
Qy 1980 TCATCTCTTACACCACTCCCTAATTTTAAATTTCTACTCTGTCTTAAATGAGAACTA 2039
Db 33839 TCATCTCTTACACCACTCCCTAATTTTAAATTTCTACTCTGTCTTAAATGAGAACTA 33898
Qy 2040 CTTGG-TTTTTTTTCTTAATATGATATGACATTTAAATGTAATTTATTTATTTT 2098
Db 33899 CTTGGTTTTTTTTTTTTCTTAATATGATATGACATTTAAATGTAATTTATTTT 33958
Qy 2099 TGAACCCAGTCTTGCTCTGTTTACCAGGCTGAGAGTGAAGTGC 2157
Db 33959 TGAACCCAGTCTTGCTCTGTTTACCAGGCTGAGAGTGAAGTGAAGTGC 34018
Qy 2158 GCAAGCTCTGCCCTCCCGGCTTGCACCACTTCTCTCCCTCAAGCTCCCAATTAAGCTTG 2217
Db 34019 GCAAGCTCTGCC--TCCCGGCTTGCACCACTTCTCTCCCTCAATTAAGCTTG 34076
Qy 2218 GCTTACAGTCAT 2229
Db 34077 GCTTACAGTCAT 34088

RESULT 3
US-11-266-748A-114799
Sequence 114799, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patencin version 3.3
SEQ ID NO 114799
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-114799

Query Match 40.6%; Score 962.4; DB 8; Length 1000;
Best Local Similarity 99.5%; Pred. No. 9.1e-162;
Matches 997; Conservative 0; Mismatches 1; Indels 4; Gaps 3;
Qy 1230 TCATGCAATGAATGATCCCTCCATCACTTGAACAAGATGTGGCCCTTCGT 1289
Db 1 TCATGCAATGAATGATCCCTCCATCACTTGAACAAGATGTGGCCCTTCGT 60
Qy 1290 GAGAAATGGCTTCTGGAAGATTAAGGAAAGATTAAGGGGAAATCTGAGAAAGCCAAA 1349
Db 61 GAGAAATGGCTTCTGGAAGATTAAGGAAAGATTAAGGGGAAATCTGAGAAAGCCAAA 120
Qy 1350 CTGAAAATCTACACAAGCTGAAAGAGGCTTTGATGTCTCTGATTTGTAATAAACTATA 1409
Db 121 CTGAAAATCTACACAAGCTGAAAGAGGCTTTGATGTCTCTGATTTGTAATAAACTATA 180
Qy 1410 GTGAATGATTCGAGAGTCAATGTTGAGGAAATATGATTAATAATTAACAAGCTTCA 1469
Db 181 GTGAATGATTCGAGAGTCAATGTTGAGGAAATATGATTAATAATTAACAAGCTTCA 240
Qy 1470 CAATCACAAGAAAGTGAAGATATCTCAGCATCACTTCTAGTACATTTATTAAGC 1529
Db 241 CAATCACAAGAAAGTGAAGATATCTCAGCATCACTTCTAGTACATTTATTAAGC 300
Qy 1530 AGCCAAGAGATGTGAAGAGTTTGAAGGAGAAACCCAGACAAAGAAAGAGATGTG 1589
Db 301 AGCCAAGAGATGTGAAGAGTTTGAAGGAGAAACCCAGACAAAGAGAGATGTG 360
Qy 1590 GAATCTGTTGGCCCTTAAGTGAACCTTGATGATTTGTCAAGTGCACCTTAA 1649
Db 361 GAATCTGTTGGCCCTTAAGTGAACCTTGATGATTTGTCAAGTGCACCTTAA 420
Qy 1650 AATGTTGATTTGTCATGCAAGCAAAACAGACATCTTAATGAGCTCTTACATGTGCAAG 1709
Db 421 AATGTTGATTTGTCATGCAAGCAAAACAGACATCTTAATGAGCTCTTACATGTGCAAG 480
Qy 1710 AAGCTAAAGAAAGAAATTAAGCCCTGCCAGATATGAGACAAACAATTCAAATGATGTG 1769
Db 481 AAGCTAAAGAAAGAAATTAAGCCCTGCCAGATATGAGACAAACAATTCAAATGATGTG 540
Qy 1770 CTAATTTATTTCCCTAGTTGACCTGTCTATTAAGAAATTAATTTCTAATATATA 1829
Db 541 CTAATTTATTTCCCTAGTTGACCTGTCTATTAAGAAATTAATTTCTAATATATA 600
Qy 1830 CCTAGGAATTTAGCAACCTGAATTTATTCATATATCAATGAGAAATGCTTCA 1889
Db 601 CCTAGGAATTTAGCAACCTGAATTTATTCATATATCAATGAGAAATGCTTCA 660
Qy 1890 ATTCAATGATTTCTCTTTAGTATTAATGACCTTATGTTGATGAGATATGAT 1949
Db 661 ATTCAATGATTTCTCTTTAGTATTAATGACCTTATGTTGATGAGATATGAT 720
Qy 1950 ACTTACTATTAATTTGACTTGAATATGATGCTTATCCCTTAAACAACCTTAATTTTAA 2009
Db 721 ACTTACTATTAATTTGACTTGAATATGATGCTTATCCCTTAAACAACCTTAATTTTAA 780
Qy 2010 TAATTTACTCTGCTTAAATGAGAACTACTGG-TTTTTTTTTTCTTAATATGATATA 2068
Db 781 TAATTTACTCTGCTTAAATGAGAACTACTGGTTTTTTTTTTCTTAATATGATATA 840
Qy 2069 TGACATTTAAATGTAATTTATTTTGTGAGACGAGTCTGCTGTATCCAGGC 2128
Db 841 TGACATTTAAATGTAATTTATTTTGTGAGACGAGTCTGCTGTATCCAGGC 900
Qy 2129 TGAAGTGAAGTGC-GTGAATTTGGCTCAGTCAAGCTCTGCCCTCCGGGTTGGACCA 2187
Db 901 TGAAGTGAAGTGCAGTCAAGTCTGCTCAGTCAAGCTCTGCC--TCCGGGTTGGACCA 958
Qy 2188 TTCTCCTGCTCAGCTCCCAATTTAGCTTGGCTTACAGTCAT 2229
Db 959 TTCTCCTGCTCAGCTCCCAATTTAGCTTGGCTTACAGTCAT 1000

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches 997; Conservative	99.5%;	0; Mismatches 1;	Indels 4;	Gaps 3		
1230 TCATGCAATGAAATGATCCCTTCATCATCATGTCAGATGTTGGCCCTTGGT	1000	TCATGCAATGAAATGATCCCTTCATCATCATGTCAGATGTTGGCCCTTGGT	1281			
1230 TCATGCAATGAAATGATCCCTTCATCATCATGTCAGATGTTGGCCCTTGGT	941	TCATGCAATGAAATGATCCCTTCATCATCATGTCAGATGTTGGCCCTTGGT	941			
1230 GAGAAATGGCTCTCTGAGATGATGAGGAAAGATGAGGAAATCTCTGAGAAAGCCAA	1344	GAGAAATGGCTCTCTGAGATGATGAGGAAAGATGAGGAAATCTCTGAGAAAGCCAA	1344			
940 GAGAAATGGCTCTCTGAGATGATGAGGAAAGATGAGGAAATCTCTGAGAAAGCCAA	881	GAGAAATGGCTCTCTGAGATGATGAGGAAAGATGAGGAAATCTCTGAGAAAGCCAA	881			
1350 CTGGAAGAACTCAACAGAGCTGTAAGAGGCTTGAATGTTCCGATGTTGTAAGAACTATA	1400	CTGGAAGAACTCAACAGAGCTGTAAGAGGCTTGAATGTTCCGATGTTGTAAGAACTATA	1400			
880 CTGGAAGAACTCAACAGAGCTGTAAGAGGCTTGAATGTTCCGATGTTGTAAGAACTATA	821	CTGGAAGAACTCAACAGAGCTGTAAGAGGCTTGAATGTTCCGATGTTGTAAGAACTATA	821			
1410 GTGAATGATTCAGAGAGTCATGTTGTAAGGAAATGATGATGTAATTAACAAGCTTCA	1461	GTGAATGATTCAGAGAGTCATGTTGTAAGGAAATGATGATGTAATTAACAAGCTTCA	1461			
820 GTGAATGATTCAGAGAGTCATGTTGTAAGGAAATGATGATGTAATTAACAAGCTTCA	761	GTGAATGATTCAGAGAGTCATGTTGTAAGGAAATGATGATGTAATTAACAAGCTTCA	761			
1470 CAATACAGAAAGTGAAGACATTTCTCAGCCATCACTCTTAGTAGCATTTATTATAGC	1522	CAATACAGAAAGTGAAGACATTTCTCAGCCATCACTCTTAGTAGCATTTATTATAGC	1522			
760 CAATACAGAAAGTGAAGACATTTCTCAGCCATCACTCTTAGTAGCATTTATTATAGC	701	CAATACAGAAAGTGAAGACATTTCTCAGCCATCACTCTTAGTAGCATTTATTATAGC	701			
1530 AGCCAGAAGATGTGAAGAGTTTGAAGGGAAGAAACCAAGACAAAGAGAGAGGTG	1588	AGCCAGAAGATGTGAAGAGTTTGAAGGGAAGAAACCAAGACAAAGAGAGAGGTG	1588			
700 AGCCAGAAGATGTGAAGAGTTTGAAGGGAAGAAACCAAGACAAAGAGAGAGGTG	641	AGCCAGAAGATGTGAAGAGTTTGAAGGGAAGAAACCAAGACAAAGAGAGAGGTG	641			
1590 GAATCTAGTTGGCCCTTATGCAATGAACTTGTGTGATTTGTCAAGGTGACCTTAA	1644	GAATCTAGTTGGCCCTTATGCAATGAACTTGTGTGATTTGTCAAGGTGACCTTAA	1644			
640 GAATCTAGTTGGCCCTTATGCAATGAACTTGTGTGATTTGTCAAGGTGACCTTAA	581	GAATCTAGTTGGCCCTTATGCAATGAACTTGTGTGATTTGTCAAGGTGACCTTAA	581			
1650 AATGGTTCATGTCATGAGCAAAACAGGACATTTATGAGCTGCTTATCATGTCGAAG	1700	AATGGTTCATGTCATGAGCAAAACAGGACATTTATGAGCTGCTTATCATGTCGAAG	1700			
580 AATGGTTCATGTCATGAGCAAAACAGGACATTTATGAGCTGCTTATCATGTCGAAG	521	AATGGTTCATGTCATGAGCAAAACAGGACATTTATGAGCTGCTTATCATGTCGAAG	521			

QY	1710	AAGCTAAAGAAAGAGATTAACCCCTGCCAGTAGTGTGCAACAATTCAATGATGTG	1768
Db	520	AAGCTAAAGAAAGAAATTAAGCCCTGCCAGTAGTGTGCAACAACAATTCAATGATGTG	461
QY	1770	CTAACTTAATTTCCCTAGTTGACCTGTCATTAAGAGATTATATATTCTTAATATTA	1829
Db	460	CTAACTTAATTTCCCTAGTTGACCTGTCATTAAGAGATTATATATTCTTAATATTA	401
QY	1830	CCCTAGAAATTTAGACAACCTGAATTATTCACATATATCAAAATGAGAAATGCCCTCA	1889
Db	400	CCCTAGAAATTTAGACAACCTGAATTATTCACATATATCAAAATGAGAAATGCCCTCA	341
QY	1890	ATTGACATGATTTCTTCTCTTTAGTATTAATGTGACCTTCTTGTAATGTGAT	1949
Db	340	ATTGACATGATTTCTTCTCTTTAGTATTAATGTGACCTTCTTGTAATGTGAT	281
QY	1950	ACTTACATATAATTGACCTGAAATATGTAGTCATCCCTTACACAACCTCCCAATTTTAAA	2009
Db	280	ACTTACATATAATTGACCTGAAATATGTAGTCATCCCTTACACAACCTCCCAATTTTAAA	221
QY	2010	TAAATTTCACTGTCCTTAAATGAGAAGTACTGG-TTTTTTTTTCTTAATATATGATA	2068
Db	220	TAAATTTCACTGTCCTTAAATGAGAAGTACTGGTTTTTTTTTTCTTAATATATGATA	161
QY	2069	TGACATTTAAATGTACTTATTTATTTTTTTGAGACCGAGCTGTGCTCTGTTAACCAAGC	2128
Db	160	TGACATTTAAATGTACTTATTTATTTTTTTGAGACCGAGCTGTGCTCTGTTAACCAAGC	101
QY	2129	TGAGGTGAGTGG-GTGAATCTTGCTCACTGCAAGCTCTGCCCCCGGATTGCACCA	2187
Db	100	TGAGGTGAGTGGGGTATCTTGCTCACTGCAAGCTCTGCC--TCCCGGGTTGCACCA	43
QY	2188	TTCTCCGCTCAGAGCTCCCAATTAGTGTGGCCCAAGTAT	2229
Db	42	TTCTCCGCTCAGAGCTCCCAATTAGTGTGGCCCAAGTAT	1

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RESULT 5
US-11-266-748A-281679
; Sequence 281679, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Hartson, Paul
; APPLICANT: Johnstson, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,216
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 281679
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-281679

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Query Match	40.6%	Score 962.4	DB 8	Length 1000	
Best Local Similarity	99.5%	Pred. No. 9.1e-162			
Matches 997	Conservative 0	Mismatches 1	Indels 4	Gaps 3	
QY	1230	TCATGCAATGAAATGAATATCCCTCCCTTCATCATATTCGACAGATGTTGGCCCTTCGT	1288		
Db	1	TCATGCAATGAAATGAATATCCCTCCCTTCATCATATTCGACAGATGTTGGCCCTTCGT	60		
QY	1290	GAGAAATTGGCTTCCTGGAAGATPAAAGGGAAGATPAAAGGGAAATCTCTGAGAAAAGCCAA	1349		
Db	61	GAGAAATTGGCTTCCTGGAAGATPAAAGGGAAGATPAAAGGGAAATCTCTGAGAAAAGCCAA	120		
QY	1350	CTGGA AAAA CTCAACA CAGCTGTAAGAGGGCTTTGATGTCTCATGTGTAA AAAA ACTATA	1408		
Db	121	CTGGA AAAA CTCAACA CAGCTGTAAGAGGGCTTTGATGTCTCATGTGTAA AAAA ACTATA	180		
QY	1410	GTGAATGATTCACAGAGCTCATGTGTTGAGAAAATGATGATAAATTAACA CAGCTTCA	1466		
Db	181	GTGAATGATTCACAGAGCTCATGTGTTGAGAAAATGATGATAAATTAACA CAGCTTCA	240		
QY	1470	CAATCACAGAAAAGTGAAGACATATCTCAGCCATCAACTTCAGTAGAATTAATTAATG	1522		
Db	241	CAATCACAGAAAAGTGAAGACATATCTCAGCCATCAACTTCAGTAGAATTAATTAATG	300		
QY	1530	AGCCAGAGAAGATGTGA AAA GAGTTTGAAAAGGAGAAACCCAGACAAAAGAGAGGTG	1588		
Db	301	AGCCAGAGAAGATGTGA AAA GAGTTTGAAAAGGAGAAACCCAGAGCAAAGAGAGGTG	360		
QY	1590	GAATCTAATTTGCCCTTCCTTAATGCCATGACACTTGTGTGATTTGTTCAGAGCTGACCTAA	1644		
Db	361	GAATCTAATTTGCCCTTCCTTAATGCCATGACACTTGTGTGATTTGTTCAGAGCTGACCTAA	420		
QY	1650	AATGGTTGCATTTGTCATGCGCAAAAACAGACACATCTTAATGSGCTGCTTTACATGTGCAAG	1708		
Db	421	AATGGTTGCATTTGTCATGCGCAAAAACAGACACATCTTAATGSGCTGCTTTACATGTGCAAG	480		
QY	1710	AAGCTAAAGAAAAGGAATPAGCCCTGCCCCAGATGTAGACAAACCAATTCAAATGATTTGT	1766		
Db	481	AAGCTAAAGAAAAGGAATPAGCCCTGCCCCAGATGTAGACAAACCAATTCAAATGATTTGT	540		
QY	1770	CTAACTTAATTTCCCTAGTGTGACCTGTCTATPAGAAGATTAATTAATTTCTAATCTATATA	1822		
Db	541	CTAACTTAATTTCCCTAGTGTGACCTGTCTATPAGAAGATTAATTAATTTCTAATCTATATA	600		
QY	1830	CCCTAGGAATTTAGACAACTTGAAATTTATTCACATATATCAAAAGTGAAGAAATGCTTCA	1888		
Db	601	CCCTAGGAATTTAGACAACTTGAAATTTATTCACATATATCAAAAGTGAAGAAATGCTTCA	660		
QY	1890	ATTGACATAGATTTCTCTCTTAATTAATTAATGACCTACTTGTGTAGTGGAAATATGTAAT	1944		
Db	661	ATTGACATAGATTTCTCTCTTAATTAATTAATGACCTACTTGTGTAGTGGAAATATGTAAT	720		
QY	1950	ACTTACTTAATTTGACTTGAATATGATGATCATCTTCCTTACACCAACTCTAATTTTAA	2008		
Db	721	ACTTACTTAATTTGACTTGAATATGATGATCATCTTCCTTACACCAACTCTAATTTTAA	780		
QY	2010	TAAATTTCTACTCTGTCTTAATGAGAGTACTTGG- TTTT TTTT TTTCTTAATAATGATATA	2066		
Db	781	TAAATTTCTACTCTGTCTTAATGAGAGTACTTGG TTTT TTTT TTTCTTAATAATGATATA	840		
QY	2069	TGACATTTAAATGTAACCTTAATTAATTTTGTGAGCCGAGCTGTGCTGTAACCGAGG	2122		
Db	841	TGACATTTAAATGTAACCTTAATTAATTTTGTGAGCCGAGCTGTGCTGCTGTAACCGAGG	900		
QY	2129	TGAGATGCAAGTGG- GTGATCTTGAGCTCACTGCAAGCTCTGCCCTCCCGGGATTGCAACCA	2187		
Db	901	TGAGATGCAAGTGGCGTGTACTTGGCTCACTGCAAGCTCTGCC- -TCCCGGGATTGCAACCA	958		
QY	2188	TTCTCTGCTCAGGCTCCCAATPAGCTTGCGCTACAGTCAT 2229			
Db	959	TTCTCTGCTCAGGCTCCCAATPAGCTTGCGCTACAGTCAT 1000			

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RESULT 6
US-11-266-748A-308319/C
; Sequence 308319, Application US//11266748A
; Publication No. US20060134653A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US//11266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 308319
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-308319

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Query Match	40.6%	Score 962.4	DB 8	Length 1000
Beet Local Similarity	99.5%	Pred. No. 9.1e-162		
Matches 997	Conservative	0	Mismatches 1	Indels 4
			Gaps	3
QY	1230	TCATGCATGAAATGAATCCCCCTTCATCATTCGCAACAGATGTGGCCCTTCGT	1289	
Db	1000	TCATGCATGAAATGAATCCCCCTTCATCATTCGCAACAGATGTGGCCCTTCGT	941	
QY	1230	GAGAAATTGGCTTCTGGAAGATAAAGGAAATATTAAGGGAAATCTGTGAAAGCCAA	1349	
Db	940	GAGAAATTGGCTTCTGGAAGATAAAGGAAATATTAAGGGAAATCTGTGAAAGCCAA	881	
QY	1350	CTGGAATACTCAACACAGCTGAAGAGGGCTTTGATGTCTCTGATTGTAATAAACTATA	1409	
Db	880	CTGGAATACTCAACACAGCTGAAGAGGGCTTTGATGTCTCTGATTGTAATAAACTATA	821	
QY	1410	GTGAATGATTTCCAGAGATCATGTGTGTGAGAAATGATGATAAATATACCAAGCTCA	1469	
Db	820	GTGAATGATTTCCAGAGATCATGTGTGTGAGAAATGATGATAAATATACCAAGCTCA	761	
QY	1470	CAATCACAGAAAGTAGAAGCTATTTCTCAGCATCACTTCTAGTAGCATTTTATAGC	1529	
Db	760	CAATCACAGAAAGTAGAAGCTATTTCTCAGCATCACTTCTAGTAGCATTTTATAGC	701	
QY	1530	AGCCAGAAGATGTGAAAAGATTGAAAGGGAAGAAACCCAAACAAAGAAAGAGTGTG	1589	
Db	700	AGCCAGAAGATGTGAAAAGATTGAAAGGGAAGAAACCCAAACAAAGAAAGAGTGTG	641	
QY	1590	GAATCTAGTTGGCCCTTAATGCAATTGAACCTTGTGTGATTGTTCAGAGTCGACTTAA	1649	
Db	640	GAATCTAGTTGGCCCTTAATGCAATTGAACCTTGTGTGATTGTTCAGAGTCGACTTAA	581	
QY	1650	AATGTTGCATTTGTCCATGCGAAACAGACATCTTATGCGCTGCTTACATGTGCAAG	1709	
Db	580	AATGTTGCATTTGTCCATGCGAAACAGACATCTTATGCGCTGCTTACATGTGCAAG	521	

QY 1710 AAGCTAAAGAAAAGAAATAGCCCTGCGCAGATATGAGCAACCAATTCMAATGATTG 1769
DB 520 AAGCTAAAGAAAAGAAATAGCCCTGCGCAGATATGAGCAACCAATTCMAATGATTG 461
QY 1770 CTAACTTATTTCCCTAGTTGACCTGTCTATAAGAAATATATTTCTAACTATATA 1829
DB 460 CTAACTTATTTCCCTAGTTGACCTGTCTATAAGAAATATATTTCTAACTATATA 401
QY 1830 CCTAGGAATTTAGAACACCTGAAATTTATTCATATATCAAAAGGAGAAAATGCTCA 1889
DB 400 CCTAGGAATTTAGAACACCTGAAATTTATTCATATATCAAAAGGAGAAAATGCTCA 341
QY 1890 ATTCAATAGATTTCTCTTATGATATATGACCTACTTGTGTAGGAATATGGAAT 1949
DB 340 ATTCAATAGATTTCTCTTATGATATATGACCTACTTGTGTAGGAATATGGAAT 281
QY 1950 ACTTACTATATTTGAATTTATGATATGATGCTCACTCTTACCACTCTTATTTTAA 2009
DB 280 ACTTACTATATTTGAATTTATGATATGATGCTCACTCTTACCACTCTTATTTTAA 221
QY 2010 TAAATTTCTACTCTGTCTTAAATGAGAGTACTTG- TTTTCTTCTTAAATATGATA 2068
DB 220 TAAATTTCTACTCTGTCTTAAATGAGAGTACTTG- TTTTCTTCTTAAATATGATA 161
QY 2069 TGAATTTAAATGTACTTATTTTGTGAGACCGAGTCTGCTGTTAACCGAGC 2128
DB 160 TGAATTTAAATGTACTTATTTTGTGAGACCGAGTCTGCTGTTAACCGAGC 101
QY 2129 TGAATGTAGAGG- GTGATCTTGAGTCACTGCAAGCTGCTCCCTCCGGTTCGACCA 2187
DB 100 TGAATGTAGAGGCGGTGATCTTGAGTCACTGCAAGCTGCTCC- TCCGGTTCGACCA 43
QY 2188 TTCTCTGCTAGGCTCCCAATTAGCTTGCGCTTACAT 2229
DB 42 TTCTCTGCTAGGCTCCCAATTAGCTTGCGCTTACAT 1

RESULT 7

US-11-266-748A-390721
Sequence 390721, Application US/11266748A
Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patent version 3.3
SEQ ID NO 390721
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens

US-11-266-748A-390721

Query Match	40.6%;	Score 962.4;	DB 8;	Length 1000;
Best Local Similarity	99.5%;	Pred. No. 9.1e-162;		
Matches 997;	Conservative 0;	Mismatches 1;	Indels 4;	Gaps 3;
QY 1230 TCATCAATGAATGAATGATCCCCCTTCATCATGCAATTCGACAGATGTTGGCCCTTCG 1289				
DB 1 TCATCAATGAATGAATGATCCCCCTTCATCATGCAATTCGACAGATGTTGGCCCTTCG 60				
QY 1290 GAGAAATGGCTTCTGAGATATAAGGAAATATAAGGGAAATCTCTGAGAAAGCCAA 1349				
DB 61 GAGAAATGGCTTCTGAGATATAAGGAAATATAAGGGAAATCTCTGAGAAAGCCAA 120				
QY 1350 CTGGAATACTCAACACAGCTGAAGAGGCTTGTATGTTCTGATTTGAAAAAACTATA 1409				
DB 121 CTGGAATACTCAACACAGCTGAAGAGGCTTGTATGTTCTGATTTGAAAAAACTATA 180				
QY 1410 GTGAATGATTCAGAGAGTCATGTGTGAGAAATGATTAATTAACAAGCTTCA 1469				
DB 181 GTGAATGATTCAGAGAGTCATGTGTGAGAAATGATTAATTAACAAGCTTCA 240				
QY 1470 CAATCAAGAAAGTGAAGATATTTCTAGCATCACTTCTAGTATATTTATAG 1529				
DB 241 CAATCAAGAAAGTGAAGATATTTCTAGCATCACTTCTAGTATATTTATAG 300				
QY 1530 AGCCAAAGATGTGAAGATTTGAAGGAAAGAAACCCAAAGCAAGAGAGTGTG 1589				
DB 301 AGCCAAAGATGTGAAGATTTGAAGGAAAGAAACCCAAAGCAAGAGAGTGTG 360				
QY 1590 GAATGTAGTTGGCCCTTAAAGCCATTAACCTTGTGATTTGTCAAGTGTGACCTAA 1649				
DB 361 GAATGTAGTTGGCCCTTAAAGCCATTAACCTTGTGATTTGTCAAGTGTGACCTAA 420				
QY 1650 AATGTTGATTTGTCATAGGCAAAACAGACATCTTATAGGCTGTTCATGTCGAAG 1709				
DB 421 AATGTTGATTTGTCATAGGCAAAACAGACATCTTATAGGCTGTTCATGTCGAAG 480				
QY 1710 AAGCTAAAGAAAAGAAATAGCCCTGCGCAGATATGAGCAACCAATTCMAATGATTG 1769				
DB 481 AAGCTAAAGAAAAGAAATAGCCCTGCGCAGATATGAGCAACCAATTCMAATGATTG 540				
QY 1770 CTAACTTATTTCCCTAGTTGACCTGTCTATAAGAAATATATTTCTAACTATATA 1829				
DB 541 CTAACTTATTTCCCTAGTTGACCTGTCTATAAGAAATATATTTCTAACTATATA 600				
QY 1830 CCTAGGAATTTAGAACACCTGAAATTTATTCATATATCAAAAGGAGAAAATGCTCA 1889				
DB 601 CCTAGGAATTTAGAACACCTGAAATTTATTCATATATCAAAAGGAGAAAATGCTCA 660				
QY 1890 ATTCAATAGATTTCTCTTATGATATATGACCTTCTTGTGATGGAATATGGAAT 1949				
DB 661 ATTCAATAGATTTCTCTTATGATATATGACCTTCTTGTGATGGAATATGGAAT 720				
QY 1950 ACTTACTATATTTGAATTTATGATATGATGCTCACTTACCACTCTTATTTTAA 2009				
DB 721 ACTTACTATATTTGAATTTATGATATGATGCTCACTTACCACTCTTATTTTAA 780				
QY 2010 TAAATTTCTACTCTGTCTTAAATGAGAGTCTG- TTTTCTTCTTAAATATGATA 2068				
DB 781 TAAATTTCTACTCTGTCTTAAATGAGAGTCTG- TTTTCTTCTTAAATATGATA 840				
QY 2069 TGAATTTAAATGTAACTTATATTTTGTGAGACGAGTCTGCTGTTACCGAGC 2128				
DB 841 TGAATTTAAATGTAACTTATATTTTGTGAGACGAGTCTGCTGTTACCGAGC 900				
QY 2129 TGAATGTAGAGG- GTGATCTTGAGTCACTGCAAGCTTGGCTCCCGGTTGACCA 2187				
DB 901 TGAATGTAGAGGCGGTGATCTTGAGTCACTGCAAGCTTGGC- TCCGGTTCGACCA 958				
QY 2188 TTCTCTGCTAGGCTCCCAATTAGCTTGCGCTTACAT 2229				
DB 959 TTCTCTGCTAGGCTCCCAATTAGCTTGCGCTTACAT 1000				

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RESULT 8
US-11-266-748A-481439/c
; Sequence 481439, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 481439
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-481439

Query Match      40.6%; Score 962.4; DB 8; Length 1000;
Best Local Similarity 99.5%; Pred. No. 9,1e-162;
Matches 997; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

QY 1230 TCATGCATGAATGAATCCCTTCATCATCATGTAAGAGATGTTGGCCCTTGT 1289
DB 1000 TCATGCATGAATGAATCCCTTCATCATCATGTAAGAGATGTTGGCCCTTGT 941

QY 1290 GAGAAATGGCTTCTGAAGATTAAGGAAAGTAAGGGAAATCTTGAGAAACCAA 1349
DB 940 GAGAAATGGCTTCTGAAGATTAAGGAAAGTAAGGGAAATCTTGAGAAACCAA 881

QY 1350 CTGGAATACTCAACCAAGCTGAAAGAGGCTTGAATGTTCTCGATTTGAAAAAACTATA 1409
DB 880 CTGGAATACTCAACCAAGCTGAAAGAGGCTTGAATGTTCTCGATTTGAAAAAACTATA 821

QY 1410 GTGAATGATTCAGAGAGTCATGTGTGAGAAAAATGATTAATAACACAACTTCA 1469
DB 820 GTGAATGATTCAGAGAGTCATGTGTGAGAAAAATGATTAATAACACAACTTCA 761

QY 1470 CAATCACAAGAAAGTGAAGACTATTCTCAGCCATCACTTCTAGTAGCATTTATATAGC 1529
DB 760 CAATCACAAGAAAGTGAAGACTATTCTCAGCCATCACTTCTAGTAGCATTTATATAGC 701

QY 1530 AGCCAAAGAAATGTGAAGAGTTTGAAGAGGAAAGAAACCAAGACAAAGAGAGTGTG 1589
DB 700 AGCCAAAGAAATGTGAAGAGTTTGAAGAGGAAAGAAACCAAGACAAAGAGAGTGTG 641

QY 1590 GAATTAATGTTGCCCTTAATGCCATTTGAACCTTGATGATTTGTCAAGGTGACCTTAA 1649
DB 640 GAATTAATGTTGCCCTTAATGCCATTTGAACCTTGATGATTTGTCAAGGTGACCTTAA 581

QY 1650 AATGTTGATGTGCATGCAAAACAGACATCTTATGCGCTTTCATGTGCAAG 1709
DB 581 AATGTTGATGTGCATGCAAAACAGACATCTTATGCGCTTTCATGTGCAAG 1709
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DB 580 AATGTTGATGTGCATGCAAAACAGACATCTTATGCGCTTTCATGTGCAAG 521
QY 1710 AAGCTAAGAAAGAAATTAAGCCCTGCCAGTATGAGACAACTTAATGATGTG 1769
DB 520 AAGCTAAGAAAGAAATTAAGCCCTGCCAGTATGAGACAACTTAATGATGTG 461
QY 1770 CTAACTATTTCCCTTAATGAGACCTGTCTATPAAGAAATATATATTTCTACTATATA 1829
DB 460 CTAACTATTTCCCTTAATGAGACCTGTCTATPAAGAAATATATATTTCTACTATATA 401
QY 1830 CCTTAGAATTTAGACAACTGAAATTTATTCATATATATCAAGTGAAGAAAGCCCTCA 1889
DB 400 CCTTAGAATTTAGACAACTGAAATTTATTCATATATCAAGTGAAGAAAGCCCTCA 341
QY 1890 ATTGACATGATTTCTCTCTTATGATTAATGACCTTGTGTAAGTGAAT 1949
DB 340 ATTGACATGATTTCTCTCTTATGATTAATGACCTTGTGTAAGTGAAT 281
QY 1950 ACTTACTATATTTGACTTGAATATGATGCTCATCTTTACACCACTCTTAATTTTAA 2009
DB 280 ACTTACTATATTTGACTTGAATATGATGCTCATCTTTACACCACTCTTAATTTTAA 221
QY 2010 TAATTTCTACTCTGTCTTAATGAGAGTACTGG-TTTTTTTTTTCTTAATATGATA 2068
DB 220 TAATTTCTACTCTGTCTTAATGAGAGTACTGGTTTTTTTTTTCTTAATATGATA 161
QY 2069 TGACATTTAATGTAATGATTAATTTTTTTGAGACCGAGCTTGCTGTATCCAGGC 2128
DB 160 TGACATTTAATGTAATGATTAATTTTTTTGAGACCGAGCTTGCTGTATCCAGGC 101
QY 2129 TGAAGTGAAGTGG-GTGATCTTGGCTCAGTCAAGCTTGCCCTCCCGGCTTGACCA 2187
DB 100 TGAAGTGAAGTGGGTATATCTTGGCTCAGTCAAGCTTGCC--TCCGGGTGACACA 43
QY 2188 TTCTCTGCTCAGCTCCCAATTTAGCTTGCCCTCAAGTCA 2229
DB 42 TTCTCTGCTCAGCTCCCAATTTAGCTTGCCCTCAAGTCA 1

RESULT 9
US-11-266-748A-221947
; Sequence 221947, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 221947
; LENGTH: 1000
; TYPE: DNA
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Db 781 GCTCACTCAAGCTCTGCC--TCCCGGGTCCGACCATCTCTCCCTCAGCCTCCCAAT 838
OY 2211 TAGCTGGCCACAGTCACTGATCTGCGACCAACCTGGCTATTTTGTGACTTTTGTAGAG 2270
Db 839 TAGCTGGCCACAGTCACTGATCTGCGACCAACCTGGCTATTTTGTGACTTTTGTAGAG 898
OY 2271 ACAGGGTTTCAACCGTGTAGCCAGAGTGTCTGATCTCTGACCTCGTGTATCCGCCAC 2330
Db 899 ACAGGGTTTCAACCGTGTAGCCAGAGTGTCTGATCTCTGACCTCGTGTATCCGCCAC 958
OY 2331 CTCGGCTTCCCAAGTGTGGGATTCAGGAGTGAAGCCACCG 2372
Db 959 CTCGGCTTCCCAAGTGTGGGATTCAGGAGTGAAGCCACCG 1000

RESULT 11

US-11-266-748A-338973/c
; Sequence 338973, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 338973
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-338973

Query Match 32.8%; Score 777.6; DB 8; Length 1000;
Best Local Similarity 99.0%; Pred. No. 4.9e-129;
Matches 814; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

OY 1553 TGAAGGGAAGAAACCAAGAAAGAAAGAGAGTGTGATCTAGTTGGCCCTTAATGCC 1612
Db 820 TGAGACAGAGAAACCAAGAAAGAAAGAGAGTGTGATCTAGTTGGCCCTTAATGCC 761
OY 1613 CATTAACCTTGTGATTTGTCAAGGTGACCTTAATAATGTGTCATTCATGGCA 1672
Db 760 CATTAACCTTGTGATTTGTCAAGGTGACCTTAATAATGTGTCATTCATGGCA 701
OY 1673 AACAGACATCTTATGCGCTGCTTTACATGTGCCAAAGAAAGCTAAAGAAAGATTAAGCC 1732
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US-11-266-748A-398267
; Sequence 398267, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 398267


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; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-398267

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Best Local Similarity 99.0%; Pred. No. 4,9e-129;
Matches 814; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

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DB      301  AACAGAGACTTTATGAGCCCTGCTTTACATGTGCAAGAAAGCTAAGAAAGAAATAGGC 360
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QY      1853 AATTTATTCACATATATCAAAAGTGAGAAATGCTCAATTCATAGATTTCTCTCTT 1912
DB      481  AATTTATTCACATATATCAAAAGTGAGAAATGCTCAATTCATAGATTTCTCTCTT 540
QY      1913 AGTATATATGACCTACTTTGGTAGTGAATAGTGAATCTACTATATATTTGACTTGAAT 1972
DB      541  AGTATATATGACCTACTTTGGTAGTGAATAGTGAATCTACTATATATTTGACTTGAAT 600
QY      1973 ATGTAGCTCATCTTTACACCAACCTCTTAATTTTAATATTTCTACTCTCTTAAAG 2032
DB      601  ATGTAGCTCATCTTTACACCAACCTCTTAATTTTAATATTTCTACTCTCTTAAAG 660
QY      2033 AGAAGTACTTGG-TTTTTTTTTCTTAATATATATATATATATATATATATATATATAT 2091
DB      661  AGAAGTACTTGGTTTTTTTTTTTTCTTAATATATATATATATATATATATATATATAT 720
QY      2092 TTTTTTTTGAACCGAGTCTTGCTGTAAACCGAGCTGAGAGTGAAGTGA-GTGATCTTG 2150
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QY      2331 CTGGGCTCTCCAAAGTGTGGATTTACAGGCAATGAGCCACCG 2372
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RESULT 13
US-11-266-748A-469313/C
; Sequence 469313, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
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; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent version 3.3
; SEQ ID NO 469313
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-469313

Query Match      32.8%; Score 777.6; DB 8; Length 1000;
Best Local Similarity 99.0%; Pred. No. 4,9e-129;
Matches 814; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

QY      1553 TGAAGAGGAAGAAACCCAGACAAAGAGAGATGAGATCTAGTTGGCCCTTAATGC 1612
DB      820  TGAAGAGGAAGAAACCCAGACAAAGAGAGATGAGATCTAGTTGGCCCTTAATGC 761
QY      1613 CATTTGAACCTTGATTTGTCAAGGTGCACTTAATAAATGTTGATGTCATGGCA 1672
DB      760  CATTTGAACCTTGATTTGTCAAGGTGCACTTAATAAATGTTGATGTCATGGCA 701
QY      1673 AACAGAGACTTTATGAGCCCTGCTTTACATGTGCAAGAAAGCTAAGAAAGAAATAGGC 1732
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QY      1733 CTGCCAGATGTAGCAACAACCAATTCAAATGATTGCTACTTAATTTCCCTAGTTGAC 1792
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QY      1793 CTGCTATAAGAGAAATATATATATTTCTAATCTATATAACCTAGGAATTTAGACAACCTGA 1852
DB      580  CTGCTATAAGAGAAATATATATATTTCTAATCTATATAACCTAGGAATTTAGACAACCTGA 521
QY      1853 AATTTATTCACATATATCAAAAGTGAGAAATGCTCTCAATTCATATGATTTCTCTCTT 1912
DB      520  AATTTATTCACATATATCAAAAGTGAGAAATGCTCTCAATTCATATGATTTCTCTCTT 461
QY      1913 AGTATATATGACCTCTTTGGTAGTGAATAGTGAATCTACTTAATTTGACTTGAAT 1972
DB      460  AGTATATATGACCTCTTTGGTAGTGAATAGTGAATCTACTTAATTTGACTTGAAT 401
QY      1973 ATGTAGCTCATCTTTACACCAACTCTAATTTTAATATTTTCACTGCTTAAAG 2032
DB      400  ATGTAGCTCATCTTTACACCAACTCTAATTTTAATATTTTCACTGCTTAAAG 341
QY      2033 AGAAGTACTTGG-TTTTTTTTTCTTAATATATATATATATATATATATATATATATAT 2091
DB      340  AGAAGTACTTGGTTTTTTTTTTTTCTTAATATATATATATATATATATATATATATAT 281
QY      2092 TTTTTTTTGAACCGAGTCTTGCTGTAAACCGAGCTGAGAGTGAAGTGA-GTGATCTTG 2150
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; SOFTWARE: Patentin version 3.3
; SEQ ID NO 17558
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-17558

Query Match 25.1%; Score 594.8; DB 8; Length 631;
Best Local Similarity 99.5%; Pred. No. 1.2e-96;
Matches 607; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

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5	904.2	38.1	3062	6	AK168690 Mus muscu
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ALIGNMENTS

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VERSION CR857268.1 GI:55725399
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Pongo.
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Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fodor, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZP469A1622) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneID=DKFZP469A1622
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
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Db	1152	TGTGTATCAGGACGAGGAGAGTGTATCAAGATTCATTTGAAGAAAGATCTCGAAATTTCCCT	1211
QY	1208	AGCTGACATTTGGAAGAAATGACCTTCATGCATGTGAATGAATACCCGCCCTTCATCACAATTG	1267
Db	1212	AGCTGACATTTGGAAGAAATGACCTTCATGCATGTGAATGAATACCCGCCCTTCATCACAATTG	1271
QY	1268	CAACGATGTTGGGCCCTTCGTGTGAAGATTTGGCTTCTGGAAGATTAAGGAAAGATTAAGG	1327
Db	1272	CAACGATGTTGGGCCCTTCGTGTGAAGATTTGGCTTCTGGAAGATTAAGGAAAGATTAAGG	1331
QY	1338	GGAATTCCTGAGAAAGCCAAACCTGGAATACTCAACACAGCTGAGAGAGGCTTTGATGT	1387
Db	1342	GGAATTCCTGAGAAAGCCAAACCTGGAATACTCAACACAGCTGAGAGAGGCTTTGATGT	1391
QY	1388	TTCCTGATTTGTAAGAAAACCTATAGGATGTATCCAGAGAGTCATGCTGTGAGGAAATGA	1447
Db	1392	TTCCTGATTTGTAAGAAAACCTATAGGATGTATCCAGAGAGTCATGCTGTGAGGAAATGA	1451
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Db	1512	TTCTAGTAGCATTTATTTATAGCAGCCCAAGAAAGATGTGAAGAGTTGAAGGGAGAAAC	1571
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Db	1572	CCAGAGCAAAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGGCATTGAACCTTGTGT	1631
QY	1628	GATTTGTCAAGSTGCACCTTAAGAAATGGTGCATTTGCATGCGCAAAAACAGACATCTTAT	1687
Db	1632	GATTTGTCAAGSTGCACCTTAAGAAATGGTGCATTTGCATGCGCAAAAACAGACATCTTAT	1691
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Db	1752	ACACCAATTCAAATGATTTGCTTACTTATTTCCCTAGTTGACCTGTCTATTAAGAGAA	1811
QY	1808	TTATATATTTCTAATCTATATAACCTGAGATTTAGCAACCTGAAATTTATTCACATAT	1867
Db	1812	TTATATATTTCTAATCTATATAACCTTGAAGATTTAGCAACCTGAAATTTATTCACATAT	1871
QY	1868	ATCAAGATGAGAAATGCTCAATTTCAATGATTTTCTTCTTTAGTATTAATGAACCTA	1927


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Db      1932 CTTTGTGATGGAATAGTAATGTAATCTTACTATATTTGACTGGAATGTAGCTACCTT 1991
Qy      1968 TACACCAATCTCTTAATTTAAATTTTACTCTGTCTTAAATGAGAAGTACTGGT 2047
Db      1992 TACCCCTACCCCTTAATTTTAAATTTTACTCTGTCTTAAATGAGAAGTACT- GTTG 2050
Qy      2048 TTTTCTTTCTTAATATGATATGACATTTTAAATGTAATCTTATTTTGTAGACCGA 2107
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Qy      2108 GTCTGCTCTGTATCCACAGGCTGAGTGAAGTG- GTGATCTTGGCTCACTGCAAGCTT 2166
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Qy      2167 GCCCTCCCGGCTGCAACCATTTCTCTGCTCAGGCTCCCAATTAGCTTGCGCTACAGT 2226
Db      2171 GCC--TCCGGGTTACACCATTTCTCTCTGCTCAGCTTCCCAAGTACCTTGACATACAGT 2228
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Db      2229 CGCCTGCCACACACCTGCTAATTTTGTACTTTTGTAGAGAGAGGCTTTCACCCGTG 2288
Qy      2287 TTAGCCAGAGATGCTCTGATCTCTGACCTGATGATCCGCCCACTCGGCTCCCAAGT 2346
Db      2289 TTAGCCAGAGATGCTCTGATCTCTGACCTGATGATCCGCCCACTCGGCTCCCAAGT 2348
Qy      2347 GCTGGGATTACAGGATGAGCCACCG 2372
Db      2349 GCTGGGATTACAGGATGAGCCACCG 2374

RESULT 2
AK088638
LOCUS   AK088638      2999 bp      mRNA      linear      HTC 02-SEP-2005
DEFINITION Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN
full-length enriched library, clone:E430022B10 product:transformed
mouse 3T3 cell double minute 2, full insert sequence.
ACCESSION AK088638
VERSION   AK088638.1 GI:26353679
KEYWORDS HTC; CAP trapper.
SOURCE    Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS   Carninci, P. and Hayashizaki, Y.
TITLE     High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
PUBMED   10349636
REFERENCE
AUTHORS   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
PUBMED   11042159
REFERENCE
AUTHORS   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuura, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE     RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)

```

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PUBMED 11076861
REFERENCE
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE     Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
PUBMED   11076861
REFERENCE
AUTHORS   The PANTOM Consortium, the RIKEN Genome Exploration Research Group
Phase I and II Team.
TITLE     Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
PUBMED   12000000
REFERENCE
AUTHORS   RIKEN Genome Exploration Research Group, Genome Science Group
(Genome Network Core Team) and the PANTOM Consortium.
TITLE     Antisense transcription in the mammalian transcriptome
JOURNAL   Science 309, 1564-1566 (2005)
PUBMED   15641566
REFERENCE
AUTHORS   The PANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
TITLE     The Transcriptional Landscape of the Mammalian Genome
JOURNAL   Science 309, 1559-1563 (2005)
PUBMED   15591563
REFERENCE
AUTHORS   Adachi, J., Aizawa, K., Akimura, T., Aikawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kondo, M.,
Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nomura, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE     Direct Submission
JOURNAL   Submitted (16-APR-2002) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp.
URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome-gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
FEATURES
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25. 1694
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Query Match	42.2%	Score 1001;	DB 6;	Length 2999;
Best Local Similarity	79.4%;	Pred. No. 4.3e-170;		
Matches 1303;	Conservative	0;	Mismatches 290;	Indels 48; Gaps 8;

OY	305	AAGGCAATGTCATTAACAATCTGTGTACTACTAGAGTGTGTGAACAACCTACA	364
Db	218	CAGCGCAATGTGCATTAACCAATCTGTGTCTACCGAGGTCTGCAGACACTACA	277
OY	365	GATTCAGCTTCGGAACAAGACCCCTGATTAGACCAAAAGCCATTGCTTTGAAGTTAT	424
Db	278	GATTCACACTTCGGAACAAGACCTCTGGTTAGACAAAACATGTCTTTGAAGTTGT	337
OY	425	AAAGCTGTGTGTGCAAAAAAGACACTATTCTATGAAAGAGTTCTTTTATCTGG	484
Db	338	AAAGTCCTGTGTGAGGCAAAACGACACTTACCTATGAAAGAGTTATATTATTAATGG	397
OY	485	CCAGTATTATTATGACTAAACGATTATATGATGAGAGAACAACTATTGTATATTGTTT	544
Db	398	CCAGTATTATTATGACTAAAGGTTATATGACGAAGAAGACGACGACATTGTGTATTGTT	457
OY	545	AAATATCTCTTCTAGAGAGATTGTTGGCGTGGCAAGCTTCTGTGAAAGAGACAAGAA	604
Db	458	AAATATCTCTCTAGAGAGATGTGTGTGGATCCGAGTTCTCTGGAAGAGACAGAA	517
OY	605	AATATATACCATGATCTACAGGAACCTGGTATGATCATACGACGGAATCATCGAGCTC	664
Db	518	AATATATGCAATGATCTACAGAAATTTAGTGTGCTTAAGTACGA-----AGACTC	568
OY	665	AGGTACATCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGTCAAAAGAACCT	724
Db	569	TGGCACATCTGTGAGTGAAGACAGTGTCAAGCTGAAGGTGGAGTGTCAAAAGATCC	628
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Db	689	CTCATCTTGAAGAGATCATTTAGTAGACACAAAGAAACAAGATGAGCTACCTGGGA	748
OY	845	ACGACAAAGAAAACGCCACAAATCTGATATGTAATTTCCCTTTCCTTTGATGAAAGCTGGC	904
Db	749	GCGGACCGGAAGCCCC-----GCAGGTCCCTGTCTTGTGATCCGAGGCTGGG	796
OY	905	TCTGTGTGTAATAAGGAGATATGTTTG-----AAAGAGACATGAGGAC	949
Db	797	TCTGTGTGAGCTGAGGAGATGTGCAGCGCGGACAGACAGACATGAGCAGACAGAG	856
OY	950	TGAATCTACAGGAGCGCATCGAATCCGGATCTTGAATGCTGTGTAAAGTGAACATTCAG	1008
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OY	1010	TGATTGGTTGGATCGAGATTCAGTTTCAGATCAATTTAGTGAAGTAAATTTGAAGTTGATC	1068
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OY	1070	TCTGCATCAGAAAGATTATAGCCTTATAGTAAAGAGACAAGACCTTCAGATGAAAGATGA	1122
Db	977	TCTGCATCTCGAAAGATTACAGCCTGATGACAAAGGACGAGCTCTCAGATGAGAGATGA	1033
OY	1130	TGAGGTATATCAATTTCTGTGTATTCAGGACGAGGAGAGTGAATACAGATTTTGAAGA	1188

Db	1037	TGAGGTCTATCGGGTCA	CGTCTATTCAGACAGGAGAAAGGATACAGACTCTTTTGAAGG	1096
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Db	1097	AGATCTGAGATTTCT	TAGCTGACTATTTGAAAGTGTACTCTCATGCAATGAATGAATCC	1156
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Db	1217	TAAAGGGAAGATTA	AGGGGAAATCTCTGAGAAAGCCAAACTGGAAAACTCAACACAGC	1276
QY	1370	TGAAGAGGGCTTTG	ATGTTCTCTGATTTGTATTAATAAACTATATGTGATGATTTCCAGAGTTC	1429
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Db	1337	ATGTGCTGAGAGGA	CAGCGAGGAGGAGGCCGGAACAACGCCCTGTGCCAGGAGATGTGA	1396
QY	1487	AGACTATTTCTAG	CGCATCACTTTAGTAGCATTTATTTATAGCAGCCAGAAAGATGTGAA	1546
Db	1387	CGACTATTTCCAA	CCATCGACTTCCAGACGACTTTGTTATAGCAGCCAGAAAGGCTGTGA	1456
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QY	1607	TAAATGCCATTGA	ACCTGTGTGATTTGTCAAGGTTCGACCTTAATAATGTGTGCATTTGTCCA	1666
Db	1514	GAAATGCCATCA	CCATCGTGTGATCTCCAGGGGCGGCTTAATAATGTGTGCATTTGTCCA	1573
QY	1667	TGGCAAAACAGSA	CATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAGAAAGGAA	1726
Db	1574	CGGCAAGCTGACA	CCCTCATGTATGTTTCACTGTGCAAAAGAGCTTAATAATAAGAA	1633
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QY	1844	ACAACCTGAATTT	ATATTCACATATATCAAAAGTGAAGAA--TGCCCTCAATTCACATAGATT	1902
Db	1752	ACAACATGGTATT	ATTTTATTAACATTTAAAGCCAGAAAACTGTCTTATGTGCACATPAAAT	1811
QY	1903	TCTTCTCTTTAG	TATTAATGA 1923	
Db	1812	TCACCTATTAATTT	ATCTCTGGA 1832	

RESULT 3	
LOCUS	AK004719
DEFINITION	AK004719 3028 bp mRNA linear HTC 02-SEP-2005
ACCESSION	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:120001ip22 product:transformed mouse 3T3 cell double minute 2, full insert sequence.
VERSION	AK004719
KEYWORDS	AK004719.1 GI:12836100
SOURCE	HTC; CAP trapper.
ORGANISM	Mus musculus (house mouse)
	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE	
AUTHORS	1 Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning

JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsuai, T., Taahito, H., Itoh, M., Suni, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection. *Nature* 409, 685-690 (2001)

JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 5 The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. *Nature* 420, 563-573 (2002)

JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 6 RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium. Antisense Transcription in the Mammalian Transcriptome. *Science* 309, 1564-1566 (2005)

JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 7 The FANTOM Consortium, Riken Genome Exploration Research Group and the Genome Science Group (Genome Network Project Core Group). The Transcriptional Landscape of the Mammalian Genome. *Science* 309, 1559-1563 (2005)

JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 8 (bases 1 to 3028) Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Iwata, M., Kaekawa, T., Kato, H., Kawai, Y., Kojima, Y., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Saeki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraishi, T., Sogabe, Y., Suuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamata, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

TITLE
 JOURNAL
 COMMENT
 Submitted (10-July-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

TITLE
 JOURNAL
 COMMENT
 Direct Submission
 Submitted (10-July-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

TITLE
 JOURNAL
 COMMENT
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

TITLE
 JOURNAL
 COMMENT
 Please visit our web site for further details.

TITLE
 JOURNAL
 COMMENT
 URL: http://genome-gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.

TITLE
 JOURNAL
 COMMENT
 Location/Qualifiers

TITLE
 JOURNAL
 COMMENT
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Db      778 GCGGACCGGAGAGCGCC-----GCAAGTCCCTGTCCTTGTATCCGAGCTGG 825
Oy      905 TCTGTGTATTAAGGGAGATGTTGNG-----AAAGACAGTACGAG 949
Db      826 TCTGTGTAGCTGAGGGAGATGTGAGCGGCGGACGACGACGACTACAGAGCAG 885
Oy      950 TGAATCTACAGGAGCGCCATCGAATCCGATCTTGATCGGTGTAAGTGAACATTCAG 1009
Db      886 CGAGTCCACAGAGCGCCCTCGCANTCAGATCTTGCATGCGGTAACTGAGCATTCTGG 945
Oy      1010 TGATTTGGTGAATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1069
Db      946 TGATTTGGTGAATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1005
Oy      1070 TCTGAGCTCAGAGATTTAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1129
Db      1006 TCTGAGCTCAGAGATTTAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1065
Oy      1130 TGAGGTATATCAAGTTACTGTGTATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1189
Db      1066 TGAGGTATATCGGGTCAAGTCTATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1125
Oy      1190 AGATTCCTGAATTTCTTAACTGACTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1249
Db      1126 AGATTCCTGAATTTCTTAACTGACTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1185
Oy      1250 CCCCCCTCATCAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1309
Db      1186 TCCCTTCATCAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1245
Oy      1310 TAAAGGAGAGATTAAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1369
Db      1246 TAAAGGAGAGATTAAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1305
Oy      1370 TGAAGAGAGAGATTTGATTTCTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1429
Db      1306 AGAAGAGAGAGATTTGATTTCTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1365
Oy      1430 ATGTCCT---GAGGAGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1486
Db      1366 ATGTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425
Oy      1487 AGACTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1546
Db      1426 CGACTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1485
Oy      1547 AGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1606
Db      1486 AGAGTT---GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1542
Oy      1607 TAAATCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1666
Db      1543 GAATTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1602
Oy      1667 TGGCAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1726
Db      1603 CGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1662
Oy      1727 TAAAGCTGCGCAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1786
Db      1663 CAAGCCCTGCGCAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1722
Oy      1787 GTTGAACCTG---TCAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1843
Db      1723 GCTGACCTGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1780
Oy      1844 ACAACCTGAATTTTATCATATATCAATATCAATATCAATATCAATATCAATATCAATAT 1902
Db      1781 ACAACCTGAATTTTATCATATATCAATATCAATATCAATATCAATATCAATATCAATAT 1840
Oy      1903 TCTTCTCTTAACTATATGA 1923

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Db      1841 TCACCTATTAATTTATCTGGA 1861
RESULT 4
AKI60069
LOCUS
DEFINITION
AKI60069
2870 bp mRNA linear HTC 21-SEP-2005
Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched
library, clone:1420047L17 product:transformed mouse 3T3 cell double
minute 2, full insert sequence.
AKI60069
ACCESSION
AKI60069.1 GI:74213595
VERSION
AKI60069.1
KEYWORDS
HTC; CAP trapper.
MUS musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murine; Mus.
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Direct Submision
 Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa, 230-0045, Japan (E-mail: genome-ree@sc.riken.jp).
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Takashi Ishikawa (Department of Surgery
 2 Yokohama City University 3-9 Fukuura, Kanagawa-ku, Yokohama
 236-0004 Japan) whose assistance we gratefully acknowledge.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 location/Qualifiers

FEATURES
 source

1..2870

/organism="Mus musculus"

/mol_type="RNA"

/strain="C57BL/6J"

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/db_xref="taxon:10090"

/clone="1420047117"

/cell_type="neuroblast-like cell"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

86..1555

/note="unnamed protein product; putative
 transformed mouse 3T3 cell double minute 2 (MG2) [MG1:96952
 GB|BC050902, evidence: BLASTN, 99%, match=2866]"

/codon_start=1

/protein_id="BAE35604.1"

/db_xref="GI:74213596"

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 SISTRRENTDILRGRHRRRRSPDGLICLAPBRCSSSSSSSSSTSTPS
 HODDDGVSEHSGDCLDDSDVSVDQSVFVEVSELSDEYSLSDBEHSLSDBDEYRV
 TVYQTSKSDTDSFEGDPEISLADYWKCTSCNEMNPLPSHCRCTWLENNMPLDCK
 DKVEISGKLENSQAEQEDVPDQKLTNDAPCAEBSERKAEQTPLOSDD
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Query Match 42.1%; Score 997.8; DB 6; Length 2870;
 Best Local Similarity 79.3%; Pred. No. 1.6e-169;
 Matches 1301; Conservative 0; Mismatches 292; Indels 48; Gaps 8;

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 79 CAGGCAATGTCATACCAACATGTCGTACTGATGCTGATGCTGATGCTGATGCTGCA 138

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 139 GATTCACGCTTCGGAACAGAGACCCCTGTTAGACCAAGCATTCCTTTGAATTAAT 198

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Db	610	GCGGACCGGAAAGGCC-----GCAAGTCCTGTCTTCTTGAATCCGAGCTGG	657
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Db	658	TCTGTGTAGCTGAGAGGATGTGTGACGGCGGACAGACAGCATGACACAGACAG	717
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Oy		1844	ACAACCTGAATTTATTTACATATATCAATGAGAGAA-ATGCTCAATTCACATAGATT	1902
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Oy		1903	TCCTTCCTTTAGTATTAATTGA	1923
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AKI68690				
LOCUS				
DEFINITION				
AKI68690		3062 bp	mRNA	linear HTC 21-Sep-2005
VERSION				Mus musculus 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:1920045f06 product:transformed mouse 3T3 cell double minute 2, full insert sequence.
KEYWORDS				
AKI68690				
SOURCE				
ORGANISM				
AKI68690.1 GI:74219907				
HTC; CAP trapper.				
Mus musculus (house mouse)				
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
Sciurognathi; Muroidae; Muridae; Mus.				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komio, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.				
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
Genome Res. 10 (10), 1617-1630 (2000)				
11042159				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
Komio, H., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Shino, H., Akiyama, J., Nishi, K., Kitsumagi, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kasaiwaigi, K., Fujiwabe, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneida, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.				
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
Genome Res. 10 (11), 1757-1771 (2000)				
11076861				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Komio, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Konodo, S., Yamataka, I.,				
4				

CONSRMT	Sato, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Sato, R., Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Pleischmann, W., Gaasterland, T., Giesi, C., King, B., Koehli, H., Kuell, P., Lewis, S., Matsuo, Y., Nika, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarini, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carinelli, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Flecher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hofman, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, U., Mazzarelli, J., Momberte, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shabata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wymshew-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
PUBMED	Nature 409 (6821), 685-690 (2001)
REFERENCE	11217851
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, T., Bono, H., Kondo, S., Nika, I., Oshio, N., Sato, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarini, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapi, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bratt, D., Brucic, V., Chochia, C., Cordani, L.E., Cousins, S., Dalla, E., Dargatz, T.A., Flecher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T., Gariboldi, M., Giesi, C., Godik, A., Gough, J., Grimmond, S., Gustinich, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kana, A., Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konaga, A., Kurochkin, I.V., Lee, Y., Lendard, B., Lyons, P.A., Maglott, D.R., Maltas, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Petosa, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Raveisi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sadelin, A., Schneider, C., Semp, C.A., Setou, M., Shimada, M., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Veardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wymshew-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shabata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 420 (6915), 563-573 (2002)
PUBMED	12466851
REFERENCE	
AUTHORS	
CONSRMT	Carinci, P., Kasukawa, T., Katayama, S., Gough, J., Fith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lendard, B., Wells, C., Kodaira, R., Shimokawa, K., Bajic, V.B., Bremner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Adkins, V., Allen, J.E., Ambesi-Imbondato, A., Apweiler, R., Aurali, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Chiribol, F., Clutterbuck, D.R., Cline, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernarid, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Flecher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Gustinich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Isikawa, T., Jaki, M., Kanapi, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kohli, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S.,
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420 (6915), 563-573 (2002)
PUBMED	12466851
REFERENCE	
AUTHORS	
CONSRMT	Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsen, R., Nishiguchi, S., Nishikawa, S., Noji, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavani, M.J., Pavani, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sadelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semp, C.A., Sano, S., Sessa, L., Sheng, Y., Shabata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Zhu, S., Zimmer, A., Wei, C.L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, B.T., Brucic, V., Quackenbush, J., Wahlestedt, C., Matlick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, T., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Niimura, Y., Nishio, T., Okada, M., Plessey, C., Shabata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watabiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
JOURNAL	The transcriptomic landscape of the mammalian genome
PUBMED	Science 309 (5740), 1559-1563 (2005)
REFERENCE	16141072
AUTHORS	
CONSRMT	Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakashima, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Fith, M., Ravasi, T., Pang, K.C., Hallinan, J., Matlick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Fagiolini, M.A., Sadelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lendard, B. and Wahlestedt, C.
TITLE	Riken Genome Exploration Research Group
JOURNAL	Antisense transcription in the mammalian transcriptome
PUBMED	Science 309 (5740), 1564-1566 (2005)
REFERENCE	16141073
AUTHORS	8 (bases 1 to 3062)
CONSRMT	Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Niimura, Y., Nishiguchi, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shabata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Science Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ location/Qualifiers
SOURCE	1.3062 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM DB:1920045U06" /db_xref="taxon:10090" /clone="1920045U06" /tissue_type="liver" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="13 days embryo" 1.3062 /note="putative transformed mouse 373 cell double minute 2 (MGD MG1:96952 GB BC050902, evidence: BLASTN, 100%, match=2392)"
misc_feature	

ORIGIN

Query Match 38.1%; Score 904.2; DB 6; Length 3062;
 Best Local Similarity 76.3%; Pred. No. 1.2e-152;
 Matches 1288; Conservative 0; Mismatches 288; Indels 111; Gaps 10;

QY 305 CAGGCAAAATGCAATACCAACATGCTGTACTATGATGATGCTGTACACCTTCA 364
 DB 242 CAGGCCATGTGCAATACCAACATGCTGTACTATGATGATGCTGTACACCTTCA 301
 QY 365 GATTCCAGCTTGGAAAGAGAGACCT----- 391
 DB 302 GATTCCAGCTTGGAAAGAGAGACTGTGTGTATTTCTGCTGAGTGTGAATATA 361
 QY 392 -----GTTAGACCAAGCCATGCTTTTGAATATTAAGTCTGTGTG 438
 DB 362 GCTGTGTTTACAGGTTTACCAACCAATGCTTTTGAATGTTTAAAGTCCGTGAG 421
 QY 439 CACAAAAAGACATTATATATGAAAGAGTTCTTTTATCTTGGCCAGTATATATGA 498
 DB 422 CGCAAAAGACATTACATATGAAAGAGATTATTTATTTATTTGGCCAGTATATGA 481
 QY 499 CTAAGACATTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 558
 DB 482 CTAAGAGGTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
 QY 559 GAGATTTGTTGGCGTCCAGCTTCTGTGAAAGAGACAGGAAATATATATACATGA 618
 DB 542 GAGATGTTTGGAGTCCCGAGTTTCTGTGAAAGAGACAGGAAATATATATGATGA 601
 QY 619 TCTACAGAACTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 678
 DB 602 TCTACAGAAATTTAGTGTGTATGATGATGATGATGATGATGATGATGATGATGAT 652
 QY 679 GTGAGAACAGGTGTACCTTGAAGGTGGAGTGTACAAAGAGACCTTGTATCAAGCTTC 738
 DB 653 GTGAGAGAGAGCTGACGCTGAAG-----ATCTTTGAGAGGCGAC 695
 QY 739 AGGAAGAGAAACCTTCATCTTCACTTTGTTTCTAGACCATCTCATCTATAGAGGA 798
 DB 696 CAGAGAGAAACCTTCATCTTCTGTATTTATTTCTAGACTGTCTACCTCATCTAGAGGA 755
 QY 799 GAGCAATTAGTGAAGACAGAAAGAAATTCAGATGATATCTGTGTGAAGACAGAAAGAAAC 858
 DB 756 GATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 815
 QY 859 GCCACAATCTGATATGATTTTCTTCTTCTTGTATGAAAGCTGCTGTGTGTATTA 918
 DB 816 GCC-----GAGGTCCCTGTCTTGTATCCAGGCTGTGTGTGTGTGA 863
 QY 919 GGGAGATATGTTG-----AAAGAAAGAGTAGAGTAGATCTACAGGGA 963
 DB 864 GGGAGATATGACCGCGCGAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 923
 QY 964 CGCCATCGAATCCGATCTTGAATGCTGTGTGAAGTGAATTCAGATGATGATGATGAT 1023
 DB 924 CGCCCTCGCATCAGGATCTTGAATGCTGTGTGAAGTGAATTCAGATGATGATGATGAT 983
 QY 1024 AGGATTCAGTTTCTGATCAGTTTACCTGGAATTTGAAGTTGAAGTCTGTGACCTGGAAG 1043
 DB 984 AGGATTCAGTTTCTGATCAGTTTACCTGGAATTTGAAGTTGAAGTCTGTGACCTGGAAG 1043
 QY 1084 ATTATAGCTTATAGTGAAGAGACAAAGACTCTGATGATGATGATGATGATGATGATGAT 1143
 DB 1044 ATTATAGCTTATAGTGAAGAGACAAAGACTCTGATGATGATGATGATGATGATGATGAT 1103
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 DB 1224 ACTGCAAAAGATGTGGAGCCCTTGTGAGAACTGTGCTTCCAGAGATTAAGGAGAGATA 1283
 QY 1324 AAGGGGAAATCTCTGAGAAAGCCAACTGAGAAATCTGACACAGAGCTGGAAGAGGCTTTG 1383
 DB 1284 AAGTGAATATCTCGAAAGAGCCAACTGAGAAATCTGAGCTGAGGAGAGAGAGGCTTTG 1343
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 QY 1441 AAAATGATGATTAATTAACAAAGCTTCAATCAAGAAAGTGAAGATTAATTCAGC 1500
 DB 1404 ACAGAGAGAGAAAGCCGAAACAGAGCCCTGTGCTCCAGAGAGATGAGATTAATTCAGC 1463
 QY 1501 CATCACTTCTAGTATGATATTTATATGACCCAAAGAGATGTAAGAGATTTGAAGG 1560
 DB 1464 CATGACTTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
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 QY 1621 CTGTGTGATTTGTCAAGGTGACCTTAATAATGATGATGATGATGATGATGATGATGAT 1680
 DB 1581 CATGTGTATCTGACAGGGGGGCTTAATAATGATGATGATGATGATGATGATGATGATGAT 1640
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 DB 1641 ACCCTCATGTCAATGTTTCAAGGTGCAAGAGCTTAAGAAAGAGATTAAGCTTGTCCAG 1700
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 DB 1701 TGTGCAAGACCCCAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1760
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 QY 1858 ATTCATATATTAAGTGAAGAAATTTGCTCAATTCATGATGATGATGATGATGATGAT 1916
 DB 1819 ATTTTATTAATTAAGTGAAGAAATTTGCTCAATTAATTAATTAATTAATTAATTA 1878
 QY 1917 TAATTTGA 1923
 DB 1879 TCTGTGA 1885

RESULT 6
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 taurus cDNA, mRNA sequence.
 ACCESSION DV775435
 VERSION DV775435.1 GI:82628295
 KEYWORDS EST.
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 REFERENCE Yoon,D.H., Lee,S.H., Park,J.H., Cho,Y.M., Lee,J.H., Kim,H.,
 Kim,H.Y., Park,J.H. and Oh,S.J.
 Gene Expression Profiling of the Bovine Liver, adipose, and
 skeletal muscle
 TITLE JOURNAL
 COMMENT Unpublished (2005)
 Contact: Dr. Du-Hak Yoon
 National Livestock Research Institute, RDA
 564 Omockhun-dong, Suwon, 441-350, Korea
 Tel: 82 31 290 1593

Fax: 82 31 290 1792
Email: dhyoon@da.go.kr.
Location/Qualifiers

FEATURES
source

1. 1180
/organism="Bos taurus"
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/db_xref="taxon:9913"
/sex="Four males mixed"
/cell_type="adipocyte"
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/lab_host="XLI-BlueMR" strain"
/clone_lib="Bos taurus CF-24-HW fat cDNA library"
/note="Organ: adipose tissue; Vector: Uni-ZAPXR; Site_1:
Scor1; Site_2: Xho I"

ORIGIN

Query Match 35.7%; Score 846.6; DB 10; Length 1180;
Best Local Similarity 87.3%; Pred. No. 3.2e-142;
Matches 987; Conservative 0; Mismatches 134; Indels 10; Gaps 5;

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25 GTAAAGGTTATATTTATCTGGCCAGATATCACTACACGATTAATGATGAGAAA 84
521 GCACACATATTTATATTTGTTCAATGATCTTCTAGAGATTGTTGGCGCAAG 580
85 ACAACACATATTTGTTGTTATGTTTCAATGATCTTCTAGAGGATTTGTTGAGTCCAG 144
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325 AGATATGTTCTTACCATCTACCTCATCTGAAAGAGAGAGAGTGTAGTGAACAGAGA 384
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385 AATTCAATGATATATCTGTGAAGACAGAAAGAGCCCAAAATCTGATGATTTTC 444
881 CTTTCTTGTGAAGAGCTGTGTGTATTAAGGAGATGTTGTGAAGAAG 940
445 CTTTCTTGTGAAGAGCTGTGTGTATTAAGGAGATGTTGTGAAGAAG 504
941 CAGTACAGTGAATCTACAGGAGCCCATCGAATCCGATCTTGTGCTGTGATGATGCA 1000
505 CAGTACAGTGAATCTACAGGAGCCCATCGAATCCGATCTGATGCTGTGATGATGCA 564
1001 ACATTCAAGTATGTTGTGATCAGAGTTCAGTTCAAGTCAAGTCAAGTTGATGATGCA 1060
565 ACATTCAAGTATGTTGTGATCAGAGTTCAGTTCAAGTCAAGTCAAGTTGATGATGCA 624
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625 AGTTAATCTCTCGAAGTGAAGATTAAGCTTGTGAAGAAGAAAGAACTTCTGCA 684
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Db 865 TCTTGAAGATTAAGGAAAGATTAAGGGAATGTTCTGAGAAAGCC-ACCTGAGAGATTC 923
Qy 1361 AACACAGCTGAAGAGGCTTGTGATGTTCTGATTTGTAAGAAACATATGATGATGATTC 1420
Db 924 GATGACAGAAAGACGAGGCTTGTGATGTTCTGATGTTCTGATGTTCTGATGTTCTG 982
Qy 1421 CAGAGAGTATGTTGTTGAGAAATGATGATTAATTAATTAACAGCTTCAATTCACAGA 1480
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Qy 1534 AAGAGATGTTGAAGATTTGAAGGAAAGAAACCAAGACAAAGAGA 1584
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RESULT 7
AK150530
LOCUS
DEFINITION
AK150530
Mus musculus bone marrow macrophage cDNA, RIKEN full-length
enriched library, clone:1830011G16 product:transformed mouse 373
cell double minute 2, full insert sequence.
AK150530
AK150530.1 GI:74151685
VERSION
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M.,
Sunt, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Obara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,
Aizawa, K., Iwata, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nakai, F., Pesole, G.,
Quackenbush, J., Schriml, L. M., Steubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barh, G., Blake, J., Boffelli, D., Bojunga, N.,

CONSRMT	Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, K., Hume, D.A., Kamliya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Saeki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohseki, S. and Hayashizaki, Y.
JOURNAL	RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
PUBMED	Functional annotation of a full-length mouse cDNA collection
REFERENCE	Nature 409 (6821), 685-690 (2001)
AUTHORS	11217851
CONSRMT	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nakai, I., Osato, N., Saito, R., Suzuki, H., Yamamata, T., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grilmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongsava, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Munata, K., Okido, T., Pavan, W.J., Petre, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, J., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, T., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komori, H., Nakamura, K., Sakazume, N., Sato, K., Shiraki, T., Maki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imochi, K., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata, K., Shigaawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
JOURNAL	PANTOM Consortium
PUBMED	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
REFERENCE	Nature 420 (6915), 563-573 (2002)
AUTHORS	12466851
CONSRMT	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Auraliya, R.N., Bailey, T.L., Banasi, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffel, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Keisel, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liu, S., McWilliam, S., Madan, B., Mader, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, P., Ohara, O., Okazaki, Y., Ohtsuka, V., Pang, K.C., Pavan, W.J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J.C., Reid, J.F., Ring, B.Z., Ringwald, M., Ros, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempke, C.A., Seno, S., Sees, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugier, K., Sultana, R., Takenaka, Y., Taki, K., Tamura, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamamichi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, N., Niimura, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Maki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
JOURNAL	FANTOM Consortium
PUBMED	The transcriptome landscape of the mammalian genome
REFERENCE	Science 309 (5740), 1559-1563 (2005)
AUTHORS	16141072
CONSRMT	Katayama, S., Tomaru, Y., Kasukawa, T., Maki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yagi, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
JOURNAL	RIKEN Genome Exploration Research Group
PUBMED	Antisense transcription in the mammalian transcriptome
REFERENCE	Science 309 (5740), 1564-1566 (2005)
AUTHORS	16141073
CONSRMT	8 (bases 1 to 2770)
JOURNAL	Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imochi, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Niimura, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Maki, K., Watanabe, A., Watanabe, M. and Hayashizaki, Y.
PUBMED	Direct Submission
REFERENCE	Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Shohjo-cho, Tsunumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9216)
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by David A. Hume (Dept. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.
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	/tissue_type="bone marrow"
	/clone_lib="RIKEN full-length enriched mouse cDNA library"
	1..2770
	/note="putative transformed mouse 3T3 cell double minute 2 (MGD MGI:96952 GB RC050902, evidence: BLASTN, 100%, match=2291)"
ORIGIN	Query Match
	34.7%; Score 824.2; DB 6; Length 2770;

Best Local Similarity 74.5%; Pred. No. 3.1e-138;
Matches 1223; Conservative 0; Mismatches 273; Indels 145; Gaps 9;

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Oy 305 CAGGGAATATGTCATACCAACATGCTGTACTACTGATGTGCTGTATACCACTCACA 364
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Oy 365 GATTCAGCTTCGGAACAAGAGACCTGGTTAGACCAAGCCATGCTTTGAAGTTAT 424
Db 136 GATTCAGCTTCGGAACAAGAGACCTGGTTAGACCAAGCCATGCTTTGAAGTTAT 195
Oy 425 AAAAGTCTGTGTGACAAAAGAACCTTATACTATGAAGAGGTCTTTTATCTTGG 484
Db 196 AAAAGTCTGTGTGACAAAAGAACCTTATACTATGAAGAGGTCTTTTATCTTGG 255
Oy 485 CCAAGTATATATGATCTAAACGATTTATATATGAGAACCAACATATTTATATTTG 544
Db 256 CCAAGTATATATGATCTAAACGATTTATATGAGAACCAACATATTTATATTTG 315
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Db 978 TAAAGGGAAGATTAAGTGAATCTCTGAAAAAGCCAAACTGGAATACTCAGCTCAGGC 1037
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Db 1038 AGAAGAAGCTTGTATGTTCTCGATTTGAAAAAGCTATAGTATGATTCAGAGATTC 1097
Oy 1430 ATGTTT---GAGGAAAAATGATTAATTTACAGAGTCTCAATCAACAGAAAGTGA 1486
Db 1098 ATGTTCTAGAGAGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1157
Oy 1487 AGACTATTTCTAGCCATCACTTCTAGTATGATTTATATATGACAGCAAGAGATGTA 1546
Db 1158 CGACTATTTCTAGCCATCACTTCTAGTATGATTTATATATGACAGCAAGAGATGTA 1217
Oy 1547 AGAGTTTGAAGGGAAGAAACCAAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1606
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Oy 1903 TCTTCTCTTATGATTAATTTGA 1923
Db 1573 TCACCTTAATTAATTTATCTCGA 1593

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RESULT 8
AK152685
LOCUS
DEFINITION
Mus musculus bone marrow macrophage cDNA, RIKEN full-length
enriched library, clone:1830082J21 product:transformed mouse 3T3
cell double minute 2, full insert sequence.
ACCESSION
AK152685
VERSION
AK152685.1 GI:74220382
KEYWORDS
HTC, CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitamura, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaehiwa, K., Fujiwaka, S., Inoue, K., Ozawa, Y., Izawa, M., Ohara, E., Matsui, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, T., Pezole, G., Quackenbush, J., Schriml, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzei, J., Mombaur, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyszewski, B., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S., and Hayashizaki, Y.

RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

11217851

5

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brasic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Goez, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Munata, K., Okido, T., Pavan, W.J., Perce, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semp, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wilming, L.G., Wyszewski, B., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyszewski, B., Wang, Y., Watanabe, Y., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayashi, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E., and Hayashizaki, Y.

FANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

12466851

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Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzi, R., Shumokawa, K., Bajic, V.B., Bremner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aldous, V., Allen, J.E., Amesni, I., Ambrosio, A., Apweiler, R., Attal, R., Auralic, R., Bailey, T.L., Bansal, M., Baxter, L., Belsel, K.W., Bersano, T., Bono, H., Chalk, A.M.,

Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemant, P., Ginget, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Huh, J., Iacono, M., Ikeo, K., Iwano, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kels, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Lunni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morita, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavoni, G., Pezole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semp, C.A., Seng, S., Seese, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Slinclair, B., Sperling, S., Stupka, E., Sugiyama, K., Sultana, R., Takenaka, Y., Taki, K., Tammo, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hume, D.A., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, K., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Pleasy, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J., and Hayashizaki, Y.

RIKEN Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome

Science 309 (5740), 1559-1563 (2005)

16141072

7

Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakashima, M., Nakamura, M., Nishida, H., Yagi, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J.S., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghini, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Yang, Z., Lenhard, B., and Wahlestedt, C.

RIKEN Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome

Science 309 (5740), 1564-1566 (2005)

16141073

8 (bases 1 to 2772)

Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume (Dep't. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES

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QY 1903 TCTTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
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DB 1573 TCACCTTATATTTATCTGAG 1593
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RESULT 9
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ACCESSION BU150642.1 GI:22664174
VERSION BU150642.1
KEYWORDS EST.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 892)
NH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgsbrs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LNCM2378 row: m column: 06
High quality sequence stop: 648.
Location/Qualifiers

FEATURES
source

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Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match      32.0%; Score 758.6; DB 3; Length 892;
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Matches 847; Conservative 0; Mismatches 34; Indels 8; Gaps 6;

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QY 2030 ATGAGAGTACTTGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2078
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RESULT 10
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LOCUS
DEFINITION   DKFZp4590965_r1.459 (synonym: pcor1) Pongo pygmaeus cDNA clone
DEFZp4590965_5', mRNA sequence.
CR789372
ACCESSION   CR789372.1 GI:53708254
VERSION
KEYWORDS
SOURCE
ORGANISM     Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pongo.
1 (bases 1 to 743)
Bahr,A., Lauber,J., Mewes,H.W., Well,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Bahr,A., Lauber,J., Mewes,H.W., et al.)
Unpublished (2004)
COMMENT
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
(Hilden/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp4590965) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp4590965
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
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FEATURES

source

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/tissue_type="cortex"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="459 (synonym: pcor1)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"
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ORIGIN

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Query Match      30.9%; Score 733.4; DB 8; Length 743;
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Best Local Similarity 99.2%; Pred. No. 8,5e-122;		Matches 737; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
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Db	1	GATGATATTCCTCTCTTATGAAAGCCGCTCTGTGTATTAAGGAGATATCT	60
Qy	930	TGTGAAGAAGCAGTAGCAGTGAATCTACAGGAGCCGATCCGATCTTGATGCT	989
Db	61	TGTGAAGAAGCAGTAGCAGTGAATCTACAGGAGCCGATCCGATCTTGATGCT	120
Qy	990	GCTGTAAGTGAACATTCAGGTGATGTTGATCAGAGATTCAGTTCAAGTTTACT	1049
Db	121	GCTGTAAGTGAACATTCAGGTGATGTTGATCAGAGATTCAGTTCAAGTTTACT	180
Qy	1050	GTGAAGATTTGAGTTGAATCTCTGACCTAGAAAGATTAGCTTATGTAAGAAGACAA	1109
Db	181	GTGAAGATTTGAGTTGAATCTCTGACCTAGAAAGATTAGCTTATGTAAGAAGACAA	240
Qy	1110	GAACCTCAGATGAGATGATGATGATATCAAGTTACTGTGTATCAGGAGGAGAGT	1169
Db	241	GAACCTCAGATGAGATGATGATGATATCAAGTTACTGTGTATCAGGAGGAGAGT	300
Qy	1170	GATACAGATTCATTTGAGAAGAGATCTGAAATTTCTTAGCTAGCTATTTGAATGCACT	1229
Db	301	GATACAGATTCATTTGAGAAGAGATCTGAAATTTCTTAGCTAGCTATTTGAATGCACT	360
Qy	1230	TCATGCAATGAAATGAATCCCCCTTCATCATCATTCGACACAGATGTTGGCCCTTCT	1289
Db	361	TCATGCAATGAAATGAATCCCCCTTCATCATCATTCGACACAGATGTTGGCCCTTCT	420
Qy	1290	GAGATTTGGCTCTCGAAGATTAAGGAAAGTAAAGGGGAAATCTCTGAGAAAGCCAA	1349
Db	421	GAGATTTGGCTCTCGAAGATTAAGGAAAGTAAAGGGGAAATCTCTGAGAAAGCCAA	480
Qy	1350	CTGAAAACTCAACCAAGCTGAGAGGGCTTTGATGTTCTGATTGTAAAAAACTATA	1409
Db	481	CTGAAAACTCAACCAAGCTGAGAGGGCTTTGATGTTCTGATTGTAAAAAACTATA	540
Qy	1410	GTGAATGATTCAGAGAGTCATGTGTGAGAAAAATGATGATTAATTAACACAGCTTCA	1469
Db	541	GTGAATGATTCAGAGAGTCATGTGTGAGAAAAATGATGATTAATTAACACAGCTTCA	600
Qy	1470	CAATCAAGAAAGAGAGAGCTATCTCAGCCATCACTTCTAGTATGATTTATATAC	1529
Db	601	CAATCAAGAAAGAGAGAGCTATCTCAGCCATCACTTCTAGTATGATTTATATAC	660
Qy	1530	AGCCAAGAGATGTGAAGAAGTTTGAAGGAAAGAAACCAAGACAAAGAGAGGTGTG	1589
Db	661	AGCCAAGAGATGTGAAGAAGTTTGAAGGAAAGAAACCAAGACAAAGAGAGGTGTG	720
Qy	1590	GAATCTAGTTGGCCCTTAATGC 1612	
Db	721	GAATCTAGTTGGCCCTTAATGC 743	

RESULT 11
 DR006283 759 bp mRNA linear EST 17-MAY-2005
 LOCUS TC118660 Human prostate, large insert, pCMV expression library Homo
 DEFINITION sapiens cDNA clone TC118660 5' similar to Homo sapiens Mdm2,
 transformed 3T3 cell double minute 2, p53 binding protein (mouse)
 (MDM2), transcript variant MDM2, mRNA sequence.
 ACCESSION DR006283.1 GI:66266156
 VERSION DR006283.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 759)
 AUTHORS Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,

TITLE		Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.	
JOURNAL		High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts	
COMMENT		Unpublished (2005) Contact: Kovacs, KF High Throughput cDNA Cloning Origene Technologies, Inc. (www.origene.com) 6 Taft Court, Suite 100, Rockville, MD 20850, USA Tel: 301 340 3188 Fax: 301 340 8606 Email: CDNA@origene.com This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc. Please contact Origene for access. Origene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850 Tel: (301) 340-3188 http://www.origene.com Seq primer: pCMV6 5prime forward vector primer, Origene Technologies Inc.	
FEATURES		Location/Qualifiers	
source		1..759 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="TC118660" /issue_type="Prostate" /clone_id="Human prostate, large insert, pCMV expression library" /note="Organ: Prostate; Vector: pCMV6-XL4; Site 1: EcoRI; Site 2: XhoI/SalI compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"	
ORIGIN		Query Match 30.3%; Score 718.4; DB 9; Length 759; Best Local Similarity 97.2%; Pred. No. 4.3e-119; Matches 742; Conservative 0; Mismatches 14; Indels 7; Gaps 1;	
Qy	134	CGTCCCTCCCGGATTAAGTCGTACGAGCGCCAGTGCCTCGCCCGGAGATGAAATGA	193
Db	4	CGAGCCTCCCGGATTAAGTCGTACGAGCGCCAGTGCCTCGCCCGGAGATGAAATGA	63
Qy	194	TCGCCGAGGCCGAGGCGTGTGCTTCCGAGTATGTCAGTCCCCGTGAAGAACTGGGG	253
Db	64	TCGCCGAGGCCGAGGCGTGTGCTTCCG-----CGGCCCCGTGAAGAACTGGGG	116
Qy	254	AGTCTTGAGGGACCCCGAGCTCCAAAGCGGAAACCCCGGATGTGAGAGAGCAAT	313
Db	117	AGTCTTGAGGGACCCCGAGCTCCAAAGCGGAAACCCCGGATGTGAGAGAGCAAT	176
Qy	314	GTGCAATACCAACATGTGTGTAACCTACTGATGTGTGTAAACCACTCAGATTCAGC	373
Db	177	GTGCAATACCAACATGTGTGTAACCTACTGATGTGTGTAAACCACTCAGATTCAGC	236
Qy	374	TTCCGAACCAAGACCTCTGTTAAGCAAGCCATTCCTTTTGAAGTTATTAAGTCTGT	433
Db	237	TTCCGAACCAAGACCTCTGTTAAGCAAGCCATTCCTTTTGAAGTTATTAAGTCTGT	296
Qy	434	TGTCGCAAAAAGACACTTATATCATGAAGAGGTTCTTTTTPACTTGGCAGATAT	493
Db	297	TGTCGCAAAAAGACACTTATATCATGAAGAGGTTCTTTTTPACTTGGCAGATAT	356
Qy	494	TATGATTAACGATTAATATGATGAGAGCAACATATTTGTATTTGTTCAATGATCT	553
Db	357	TATGATTAACGATTAATATGATGAGAGCAACATATTTGTATTTGTTCAATGATCT	416
Qy	554	TTTAGAGATTTTGTGGCGTGCCAGGCTTCTGTGAAAGAGCAGAGAAATATATAC	613

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Db 417 TCTAGAGATTGTTGGCCGTCAGAGCTTCTGTGTAAGACAGAGAAATATATATAC 476
Qy 614 CATGATCTACAGGAACCTTGTAAGTACATCAAGACAAATCATCGACTAGATAC 673
Db 477 CATGATCTACAGGAACCTTGTAAGTACATCAAGACAAATCATCGACTAGATAC 536
Qy 674 TGTGAGTGAAGAACGCTGTCACCTTGAAGTGGAGTATCAAAAGACCTTGTACAGA 733
Db 537 TGTGAGTGAAGAACGCTGTCACCTTGAAGTGGAGTATCAAAAGACCTTGTACAGA 596
Qy 734 GCTTCAGAGAGAAACCTTCATCTTCACATTTGGTTCTAGACCATCTACCTCATG 793
Db 597 GCTTCAGAGAGAAACCTTCATCTTCACATTTGGTTCTAGACCATCTACCTCATG 656
Qy 794 AAGAGAGCAATTTGTGAGACAGAAATTCAGATTAATCTGGTGAACGACAAAG 853
Db 657 AAGGAGAGCAATTTGTGAGACAGAAATTCAGATTAATCTGGTGAACGACAAAG 716
Qy 854 AAAAGCCACAAATCTGATGATTTCCCTTCTTGTATGAA 896
Db 717 AAAGCCACAAATCTGATGATTTCCCTTCTTGTATGAA 759
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RESULT 12
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LOCUS CH3#048_A05T7 Canine heart normalized cDNA library in pbluescript
DEFINITION Canis familiaris cDNA clone CH3#048_A05 5', mRNA sequence.
ACCESSION CF407361
VERSION CF407361.1 GI:34408184
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
```

```
REFERENCE 1 (bases 1 to 940)
AUTHORS Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A. L.
TITLE Expressed sequence tags from Canine heart.
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CH3#048_A05T3
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert Length: 1627 Std Error: 0.00
Seq primer: T7: TAAATACGACTGACCTATAGCG
High quality sequence start: 37
High quality sequence stop: 754.
Location/Qualifiers
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day fetal)"
/clone_lib="Canine heart normalized cDNA library in
pbluescript"
/notes="Organ: heart; Vector: pbluescript; Site 1: 5' of
vector NotI; Site 2: 3' of vector EcoRI; Tissue source:
dog heart (adult, 30 day - 40 day fetal), right and left
atria and ventricle. Dog breed - mixed (beagle, German
shepherd, pointer, Irish setter). Library construction:
oligo-dT primed"
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ORIGIN

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Query Match 30.0%; Score 712.2; DB 5; Length 940;
Best Local Similarity 89.0%; Pred. No. 5,4e-118;
Matches 804; Conservative 0; Mismatches 84; Indels 15; Gaps 3;
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Db 38 GCATGACGATGATCTTACAGGAGCGCATCGATCCGGATCTTGATGCTGGTGAATG 97
Qy 1000 AACATTCAGGATTTGGTGGATCAGATTCACTTTCAGATCAGTTTGTAGTAATTTG 1059
Db 98 AACATTCAGGATTTGGTGGATCAGATTCACTTTCAGATCAGTTTGTAGTAATTTG 157
Qy 1060 AAGTTGAATCTCTGACTCAGAGATTATACCTTTAGTGAAGACAGAACTTCAG 1119
Db 158 AAGTTGAATCTCTGACTCAGAGATTATACCTTTAGTGAAGACAGAACTTCAG 217
Qy 1120 ATGAAGATGATGAGTATATCAATTTCTGTGTTACAGGCGGGAGAGTACAGATT 1179
Db 218 ATGAAGATGATGAGTATATCAATTTCTGTGTTACAGGCGGGAGAGTATCAAGTT 277
Qy 1180 CATTGGAAGAGATCTGAAATTTCTTACGCTGACTATTGGAATTCATCATGCAATG 1239
Db 278 CATTGGAAGAGATCTGAAATTTCTTACGCTGACTATTGGAATTCATCATGCAATG 337
Qy 1240 AAATGAATCCCCCTTCATCAATTCAGATGTTGGCCCTTCGTGAGAAATGGC 1299
Db 338 AAATGAATCCCCCTTCATCAATTCAGATGTTGGCCCTTCGTGAGAAATGGC 397
Qy 1300 TTCCCTGAAGATTAAGGGAAGATTAAGGGAATCTCTGAGAAAGCCAAATGGAAT 1359
Db 398 TTCCCTGAAGATTAAGGGAAGATTAAGGGAATCTCTGAGAAAGCCAAATGGAAT 445
Qy 1360 CAACAGACTGAGAGAGGCTTTGATGTTCTGATTTGTAATAAATACTATATGATGAT 1419
Db 446 CAACAGACTGAGAGAGGCTTTGATGTTCTGATTTGTAATAAATACTATATGATGAT 505
Qy 1420 CCAGAGACTGAGTGTGTTGAGAGAAATGATGTAATAAATTCACAAAGCTTCACATCA 1479
Db 506 CCAGAGACTGAGTGTGTTGAGAGAAATGATGTAATAAATTCACAAAGCTTCACATCA 565
Qy 1480 AAATGAAGATTAATTCACAGCATCACTTCATGATTAATTTATGAGCCCAAGAG 1539
Db 566 AAATGAAGATTAATTCACAGCATCACTTCATGATTAATTTATGAGCCCAAGAG 625
Qy 1540 ATGTGAAGATTTGAAAGGAGAAACCAAGACAAAGAGAGTGTGATCTAGTT 1599
Db 626 ATGTGAAGATTTGAAAGGAGAAACCAAGACAAAGAGAGTGTGATCTAGTT 685
Qy 1600 TGCCCTTAATGCAATTTGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1659
Db 686 TGCCCTTAATGCAATTTGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 745
Qy 1660 TTGTTCATGCGAAACAGAGACATCTTATGCTGCTGTTTACATGTGCCAAAGAGCTTA 1719
Db 746 TTGTTCATGCGAAACAGAGACATCTTATGAGATGCTTACATGTGCCAAAGAGCTTA 805
Qy 1720 AAAGGATTAAGCCCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1779
Db 806 AAAGGATTAAGCCCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 864
Qy 1780 TCCCTTAATGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1837
Db 865 TCCCTTAATGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 924
Qy 1838 ATT 1840
Db 925 ATT 927
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RESULT 13
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LOCUS A1927905/c
DEFINITION wp03c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463758 3'
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similar to gb:M92424 MDM2 PROTEIN (HUMAN); mRNA sequence.
 AI927905 GI:5663869
 VERSION AI927905.1
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 743)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
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 Seq primer: -40UP from Gibco
 High quality sequence stop: 459.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /lab_host="DH10B"
 /clone_1ib="NCI CGAP Kid11"
 /note="Organ: Kidney; Vector: pT73D-Pac1; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and 88 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Patricia Bonaldo."

ORIGIN
 Query Match 29.6%; Score 701.2; DB 1; Length 743;
 Best Local Similarity 97.3%; Pred. No. 5.4e-116;
 Matches 723; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

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 DB 743 GTGACATTGGCTTCTGAGATAAAGGAAAGATPAAGGGGATTAATCTCTGAGAAAGCCA 684
 QY 1348 AACTGGAAGAACTCAACAAGCTGAAGAGGCTTGTGATTTCTGATTTGTAAGAACTA 1407
 DB 663 AACTGGAAGAACTCAACAAGCTGAAGAGGCTTGTGATTTCTGATTTGTAAGAACTA 624
 QY 1408 TAGTAATGATTCAGAGAGTCATGTGTGAGAAATGATGATTAATTAACAAGCTT 1467
 DB 623 TAGTAATGATTCAGAGAGTCATGTGTGAGAAATGATGATTAATTAACAAGCTT 564
 QY 1468 CACATCAACAAGAAAGTGAAGCTAATTTCTAGCCATCAACTTCTAGTACATTATTATA 1527
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 QY 1528 GCAGCAGAAGATGTAAGAGTTTGAAGGGAAGAAACCAACAAGAAAGAGAGCTT 1587
 DB 503 GCAGCAGAAGATGTAAGAGTTTGAAGGGAAGAAACCAACAAGAAAGAGAGCTT 444
 QY 1588 TGGAACTAGATTGGCCCTTAATGCCATTGAACCTTGTGTGATTTGTCAAGGTGACCTTA 1647
 DB 443 TGGAACTAGATTGGCCCTTAATGCCATTGAACCTTGTGTGATTTGTCAAGGTGACCTTA 384

QY 1648 AAAATGGTTCATGTCATGCAAGCAAAAGACATCTTATGGCCGTCTTACATGTCGAA 1707
 DB 383 AAAATGGTTCATGTCATGCAAGCAAAAGACATCTTATGGCCGTCTTACATGTCGAA 324
 QY 1708 AGAAGCTAAGAAAGAAAGATAAGCCCTGCCAGTATGTAGACAAACATTTCAATGATG 1767
 DB 323 AGAAGCTAAGAAAGAAAGATAAGCCCTGCCAGTATGTAGACAAACATTTCAATGATG 264
 QY 1768 TGTCTACTTATTTCCCTTAGTGTGACCTGTCTATTAAGAGATTATATTTCTACTATAT 1827
 DB 263 TGTCTACTTATTTCCCTTAGTGTGACCTGTCTATTAAGAGATTATATTTCTACTATAT 205
 QY 1828 AACCTAGAAATTTAGACAACTGAAATTTATTCATATCAAGTAAGTAAGTAAGTCCCT 1887
 DB 204 AACCTAGAAATTTAGACAACTGAAATTTATTCATATCAAGTAAGTAAGTAAGTCCCT 145
 QY 1888 CAATTCACATGATTTCTCTCTTATGATTAATTAATGACCTAGTGTAGTGAATATGTA 1947
 DB 144 CAATTCACATGATTTCTCTCTTATGATTAATTAATGACCTAGTGTAGTGAATATGTA 85
 QY 1948 ATACTTACTATTAATTTGACCTGAATATGAGCTCATTCCTTACACCAACTCTTAATTTTA 2007
 DB 84 ATACTTACTATTAATTTGACCTGAATATGAGCTCATTCCTTACACCAACTCTTAATTTTA 25
 QY 2008 AATATTTCTACTCTGTCTTAA 2030
 DB 24 AATATTTCTACTCTGTCTTAA 2

RESULT 14
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 DEFINITION 7k46c07.x1 NCI CGAP Ovi8 Homo sapiens cDNA clone IMAGE:3478285 3'
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 BP057574
 accession BP057574.1 GI:10811470
 keywords EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 709)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 481.
 Location/Qualifiers
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 /tissue_type="fibroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NCI CGAP Ovi8"
 /note="Organ: Ovary; Vector: pT73D-Pac1; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGAAGCGCGCGGACATTTTTTTTTTTTTT 3'];

ORIGIN
 Query Match 29.6%; Score 701.2; DB 1; Length 743;
 Best Local Similarity 97.3%; Pred. No. 5.4e-116;
 Matches 723; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1288 GTGAGATTGGCTTCTGAGATAAAGGAAAGATPAAGGGGAAATCTCTGAGAAAGCCA 1347
 DB 743 GTGACATTGGCTTCTGAGATAAAGGAAAGATPAAGGGGATTAATCTCTGAGAAAGCCA 684
 QY 1348 AACTGGAAGAACTCAACAAGCTGAAGAGGCTTGTGATTTCTGATTTGTAAGAACTA 1407
 DB 663 AACTGGAAGAACTCAACAAGCTGAAGAGGCTTGTGATTTCTGATTTGTAAGAACTA 624
 QY 1408 TAGTAATGATTCAGAGAGTCATGTGTGAGAAATGATGATTAATTAACAAGCTT 1467
 DB 623 TAGTAATGATTCAGAGAGTCATGTGTGAGAAATGATGATTAATTAACAAGCTT 564
 QY 1468 CACATCAACAAGAAAGTGAAGCTAATTTCTAGCCATCAACTTCTAGTACATTATTATA 1527
 DB 563 CACATCAACAAGAAAGTGAAGCTAATTTCTAGCCATCAACTTCTAGTACATTATTATA 504
 QY 1528 GCAGCAGAAGATGTAAGAGTTTGAAGGGAAGAAACCAACAAGAAAGAGAGCTT 1587
 DB 503 GCAGCAGAAGATGTAAGAGTTTGAAGGGAAGAAACCAACAAGAAAGAGAGCTT 444
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 DB 443 TGGAACTAGATTGGCCCTTAATGCCATTGAACCTTGTGTGATTTGTCAAGGTGACCTTA 384


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Oy 905 TCTGTGTATATAGGAGATATGTGTGAAGAAGCAGTACAGTGAATCTACAGGAC 964
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Db 668 TCTGTGTATATAGGAGATATGTGTGAAGAAGCAGTACAGTGAATCTACAGGAC 727
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Oy 965 GCCATCGAATCCCGAT-CTTGATGCTGTG-GTAACTGAACATTCAAGTATTGTTG 1020
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Db 728 GCCATCGAATCCCGATCTTGATGCTGTGTAGTGAACATTCAAGGATTGTTG 785
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Job time : 11274 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 13:41:36 / Search time 13538 Seconds
(without alignments)
11204.261 Million cell updates/sec

Title: US-09-966-724B-2
Perfect score: 2372
Sequence: 1 GCACCGCGCGAGCTTGCTG.....ATTACAGCAGTACGACCG 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 636136 seqs, 31973710525 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6531138

Minimum DB seq length: 5
Maximum DB seq length: 500

Post-processing: Listing first 1000 summaries

Database: GenEmbl:
1: gb_env:*
2: gb_pac:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hcg:*
13: gb_in:*
14: gb_cm:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	401	16.9	456	5	HS8278976 Homo sapi
2	359	15.1	388	5	AF092843 Homo sapi
3	313	13.2	399	2	BD005478 Cellular
4	313	13.2	399	2	AR202601 Sequence
5	313	13.2	399	5	HSU33202 Human mdm2-
6	250	10.5	480	5	AF385327 Homo sapi
7	245	10.3	393	5	HS8278977 Homo sapi
8	240	10.1	318	5	HS8491700 Homo sapi
9	225	9.5	309	2	BD005479 Cellular
10	225	9.5	309	2	AR202602 Sequence
11	225	9.4	297	5	HSU33203 Human mdm2-
12	222	9.4	297	5	HS8278978 Homo sapi
13	222	9.4	297	5	HS850516 Homo sapi
14	209	8.8	209	7	G66929 csmptdm2-pc
15	183	7.7	210	5	HS850518 Homo sapi
16	175	7.4	213	5	HS850519 Homo sapi
17	172	7.3	224	5	AF385324 Homo sapi
18	168	7.1	288	5	AF385326 Homo sapi

19	167	7.0	319	2	AX587650 Sequence
20	157	6.6	364	5	HS827688 Homo sapi
21	153	6.5	198	5	HS850517 Homo sapi
22	148	6.2	199	2	AR229721 Sequence
23	144	6.1	153	5	HS8491701 Homo sapi
24	142	6.0	201	7	BV206635 sqm12145
25	138	5.8	199	2	AR229722 Sequence
26	120	5.1	165	5	HS850520 Homo sapi
27	88	3.7	401	7	BV193037 sqm17651
28	78	3.3	397	2	AX981948 Sequence
29	78	3.3	397	2	BD116807 EST and e
30	78	3.3	397	2	AR421254 Sequence
31	77	3.2	427	7	AB140799 Homo sapi
32	77	3.2	440	7	AB152167 Homo sapi
33	76	3.2	291	5	HS2ALU385
34	73	3.1	73	2	BD074010 Antisense
35	73	3.1	73	2	AR721415 Sequence
36	73	3.1	401	7	BV195288 sqm18401
37	71	3.0	315	5	AY270309 Homo sapi
38	69	2.9	353	2	AX245117 Sequence
39	69	2.9	426	2	CQ469958 Sequence
40	69	2.9	426	2	CQ479126 Sequence
41	69	2.9	446	2	CQ503928 Sequence
42	69	2.9	449	2	CQ473654 Sequence
43	69	2.9	469	2	CQ482823 Sequence
44	69	2.9	475	2	CQ500302 Sequence
45	69	2.9	475	2	CQ509237 Sequence
46	69	2.9	475	2	CQ509244 Sequence
47	69	2.9	475	2	CQ512729 Sequence
48	69	2.9	499	7	BV012530 HSC226 (n
49	68	2.9	68	2	CQ876224 Sequence
50	68	2.9	68	2	CQ975386 Sequence
51	68	2.9	281	5	S70707 (repetitive
52	68	2.9	297	8	AF458110 Synthetic
53	68	2.9	309	8	AY341576 Synthetic
54	68	2.9	325	8	AY341577 Synthetic
55	68	2.9	355	8	AF458109 Synthetic
56	68	2.9	386	8	AF458108 Synthetic
57	68	2.9	419	8	AF458114 Synthetic
58	68	2.9	422	8	AY341575 Synthetic
59	68	2.9	433	8	AF458107 Synthetic
60	68	2.9	437	8	AF458113 Synthetic
61	68	2.9	440	8	AF458112 Synthetic
62	68	2.9	450	8	AY341573 Synthetic
63	68	2.9	453	8	AF458115 Synthetic
64	68	2.9	463	2	CQ407177 Sequence
65	68	2.9	480	5	AF015155 Homo sapi
66	67	2.8	241	2	CQ699533 Sequence
67	67	2.8	480	2	AX977481 Sequence
68	67	2.8	480	2	BD112340 EST and e
69	67	2.8	480	2	AR416787 Sequence
70	67	2.8	412	7	AB131382 Homo sapi
71	65	2.7	365	7	AB147854 Homo sapi
72	65	2.7	399	7	AB137509 Homo sapi
73	64	2.7	157	5	DQ193118 Homo sapi
74	64	2.7	212	2	CQ408208 Sequence
75	64	2.7	448	7	AF192029 Homo sapi
76	64	2.7	482	7	BV198158 sqm19671
77	60	2.5	60	2	CQ542955 Sequence
78	60	2.5	362	2	AX984612 Sequence
79	60	2.5	362	2	BD119471 EST and e
80	60	2.5	362	2	AR423918 Sequence
81	60	2.5	416	2	CQ464560 Sequence
82	60	2.5	441	2	AX986356 Sequence
83	60	2.5	441	2	BD121215 EST and e
84	60	2.5	441	2	AR425662 Sequence
85	59	2.5	121	2	CQ686451 Sequence
86	59	2.5	343	2	CQ432650 Sequence
87	59	2.5	348	2	CQ423842 Sequence
88	59	2.5	374	2	CQ407892 Sequence
89	59	2.5	421	2	CQ407826 Sequence
90	59	2.5	453	2	CQ395168 Sequence
91	59	2.5	453	2	CQ401508 Sequence

C 92	59	2.5	469	5	AY190793	C 165	55	2.3	288	8	HSU14568	U14568 **ALU WARN
C 93	58	2.4	170	2	CQ706690	C 166	55	2.3	299	5	HSALUCOL	U75335 H.sapiens A
C 94	58	2.4	185	2	CQ499343	C 167	55	2.3	317	5	HSU67827	U67827 Human prima
C 95	58	2.4	185	2	CQ508313	C 168	55	2.3	322	2	AX978974	AX978974 Sequence
C 96	58	2.4	191	2	BD038032	C 169	55	2.3	322	2	BD113833	BD113833 EST and e
C 97	58	2.4	191	2	AR738293	C 170	55	2.3	322	2	AR418280	AR418280 Sequence
C 98	58	2.4	191	2	AX902499	C 171	55	2.3	328	2	AX918265	AX918265 Sequence
C 99	58	2.4	251	7	BV187788	C 172	55	2.3	328	2	BD053798	BD053798 Sequence
C 100	58	2.4	281	2	CQ472768	C 173	55	2.3	328	2	AR754059	AR754059 Sequence
C 101	58	2.4	305	5	AY680020	C 174	55	2.3	343	5	AF344192	AF344192 Homo sapi
C 102	58	2.4	326	2	CQ518112	C 175	55	2.3	346	5	HSTU4LUI	X13240 Human Tu-al
C 103	58	2.4	354	2	CQ468351	C 176	55	2.3	347	5	AY270560	AY270560 Homo sapi
C 104	58	2.4	384	2	CQ487985	C 177	55	2.3	378	2	CQ481614	CQ481614 Sequence
C 105	58	2.4	388	2	CQ478711	C 178	55	2.3	382	2	AX983066	AX983066 Sequence
C 106	58	2.4	399	2	AX071526	C 179	55	2.3	382	2	BD117925	BD117925 EST and e
C 107	58	2.4	407	2	CQ478016	C 180	55	2.3	382	2	AR422372	AR422372 Sequence
C 108	58	2.4	407	2	CQ481729	C 181	55	2.3	385	2	CQ482993	CQ482993 Sequence
C 109	58	2.4	412	2	CQ394434	C 182	55	2.3	401	7	BV190239	BV190239 sqgm16652
C 110	58	2.4	412	2	CQ400793	C 183	55	2.3	401	7	BV198686	BV198686 sqgm19850
C 111	58	2.4	422	2	CQ486627	C 184	55	2.3	401	7	BV199101	BV199101 sqgm20000
C 112	58	2.4	425	2	CQ502870	C 185	55	2.3	404	2	AX335679	AX335679 Sequence
C 113	58	2.4	427	2	CQ499908	C 186	55	2.3	408	2	CQ502756	CQ502756 Sequence
C 114	58	2.4	430	2	CQ478745	C 187	55	2.3	408	7	AB152125	AB152125 Homo sapi
C 115	58	2.4	430	7	AB147097	C 188	55	2.3	413	2	CQ692899	CQ692899 Sequence
C 116	58	2.4	431	2	CQ469574	C 189	55	2.3	417	2	BD152511	BD152511 Primer fo
C 117	58	2.4	446	2	CQ499217	C 190	55	2.3	417	2	AX872449	AX872449 Sequence
C 118	58	2.4	450	2	CQ478143	C 191	55	2.3	423	5	AY318838	AY318838 Homo sapi
C 119	58	2.4	460	2	CQ469577	C 192	55	2.3	429	2	CQ395489	CQ395489 Sequence
C 120	58	2.4	460	2	CQ499942	C 193	55	2.3	429	2	CQ401824	CQ401824 Sequence
C 121	58	2.4	460	2	CQ508021	C 194	55	2.3	431	7	AB152216	AB152216 Homo sapi
C 122	58	2.4	463	2	AX983617	C 195	55	2.3	432	2	CQ692898	CQ692898 Sequence
C 123	58	2.4	463	2	BD118476	C 196	55	2.3	441	2	CQ473824	CQ473824 Sequence
C 124	58	2.4	463	2	AR422923	C 197	55	2.3	447	2	AX366896	AX366896 Sequence
C 125	58	2.4	467	2	CQ498722	C 198	55	2.3	449	2	CQ507108	CQ507108 Sequence
C 126	58	2.4	468	2	CQ516438	C 199	55	2.3	449	2	CQ521888	CQ521888 Sequence
C 127	57	2.4	481	2	CQ503076	C 200	55	2.3	451	2	CQ405886	CQ405886 Sequence
C 128	57	2.4	281	5	S70706	C 201	55	2.3	456	5	AY879679	AY879679 Pygathrix
C 129	57	2.4	405	7	G35449	C 202	55	2.3	459	7	AB145960	AB145960 Homo sapi
C 130	57	2.4	415	2	CQ396717	C 203	55	2.3	460	5	AY879664	AY879664 Pygathrix
C 131	57	2.4	415	2	CQ403026	C 204	55	2.3	460	5	AY879749	AY879749 Nasalis l
C 132	57	2.4	424	7	AB142946	C 205	55	2.3	467	5	AY879740	AY879740 Macaca mu
C 133	57	2.4	429	2	CQ478526	C 206	55	2.3	475	2	CQ699315	CQ699315 Sequence
C 134	57	2.4	456	7	BV198615	C 207	55	2.3	478	5	AF077058	AF077058 Pan trogl
C 135	57	2.4	463	2	CQ409410	C 208	55	2.3	479	7	AB136012	AB136012 Homo sapi
C 136	57	2.4	466	2	CQ499724	C 209	55	2.3	480	2	CQ413810	CQ413810 Sequence
C 137	57	2.4	486	2	CQ481937	C 210	55	2.3	482	5	AY879739	AY879739 Papio cyn
C 138	57	2.4	489	2	CQ520554	C 211	55	2.3	486	2	CQ518143	CQ518143 Sequence
C 139	57	2.4	494	2	BD152315	C 212	55	2.3	490	5	AY190785	AY190785 Homo sapi
C 140	56	2.4	494	2	AX872253	C 213	55	2.3	500	5	AY520144	AY520144 Homo sapi
C 141	56	2.4	397	2	AX389181	C 214	54	2.3	201	7	BV203717	BV203717 sqgm21286
C 142	56	2.4	401	2	CQ463660	C 215	54	2.3	251	7	BV187974	BV187974 sqgm15621
C 143	56	2.4	490	5	AY620557	C 216	54	2.3	317	2	CQ676042	CQ676042 Sequence
C 144	55	2.3	149	2	AX916718	C 217	54	2.3	326	2	CQ477715	CQ477715 Sequence
C 145	55	2.3	149	2	BD052251	C 218	54	2.3	340	7	AB140916	AB140916 Homo sapi
C 146	55	2.3	149	2	AR752512	C 219	54	2.3	341	2	CQ686043	CQ686043 Sequence
C 147	55	2.3	170	2	AX911162	C 220	54	2.3	375	2	CQ498918	CQ498918 Sequence
C 148	55	2.3	170	2	BD046695	C 221	54	2.3	375	2	CQ507887	CQ507887 Sequence
C 149	55	2.3	170	2	AR746956	C 222	54	2.3	398	2	CQ673791	CQ673791 Sequence
C 150	55	2.3	191	2	AX906934	C 223	54	2.3	407	2	CQ480930	CQ480930 Sequence
C 151	55	2.3	191	2	BD042467	C 224	54	2.3	411	2	AX333968	AX333968 Sequence
C 152	55	2.3	191	2	AR742728	C 225	54	2.3	411	2	AX407798	AX407798 Sequence
C 153	55	2.3	192	2	AX906260	C 226	54	2.3	436	5	HSALURT	X74556 H. sapiens (
C 154	55	2.3	192	2	BD041793	C 227	54	2.3	447	2	CQ471762	CQ471762 Sequence
C 155	55	2.3	192	2	AR742054	C 228	54	2.3	458	2	CQ502086	CQ502086 Sequence
C 156	55	2.3	201	2	CQ930498	C 229	54	2.3	458	2	CQ510960	CQ510960 Sequence
C 157	55	2.3	222	2	AX396130	C 230	54	2.3	463	2	AX385336	AX385336 Sequence
C 158	55	2.3	238	5	HSU02066	C 231	54	2.3	487	5	AY879767	AY879767 Pygathrix
C 159	55	2.3	241	5	HOMALNE51	C 232	54	2.3	495	2	CQ663735	CQ663735 Sequence
C 160	55	2.3	251	7	BV193228	C 233	53	2.2	311	2	AX982288	AX982288 Sequence
C 161	55	2.3	261	5	HS063XC5	C 234	53	2.2	311	2	BD117147	BD117147 EST and e
C 162	55	2.3	266	5	AX982981	C 235	53	2.2	311	2	AR421594	AR421594 Sequence
C 163	55	2.3	266	2	BD117840	C 236	53	2.2	339	2	CQ506919	CQ506919 Sequence
C 164	55	2.3	266	2	AR422287	C 237	53	2.2	394	2	CQ516315	CQ516315 Sequence

C 238	53	2.2	412	5	AY288777	C 311	50	2.1	364	2	AX245180	AX245180 Sequence
C 239	53	2.2	415	5	AY246543	C 312	50	2.1	366	2	C0662742	C0662742 Sequence
C 240	53	2.2	416	2	C0486501	C 313	50	2.1	377	2	C0478505	C0478505 Sequence
C 241	53	2.2	439	2	C0477001	C 314	50	2.1	378	2	C0478006	C0478006 Sequence
C 242	53	2.2	446	7	AB146903	C 315	50	2.1	378	2	C0487353	C0487353 Sequence
C 243	53	2.2	494	5	AF533323	C 316	50	2.1	380	2	C0477851	C0477851 Sequence
C 244	53	2.2	500	2	AX389152	C 317	50	2.1	380	2	C0499052	C0499052 Sequence
C 245	52	2.2	395	2	AX070585	C 318	50	2.1	393	2	C0477856	C0477856 Sequence
C 246	52	2.2	407	2	C0464107	C 319	50	2.1	396	2	AX986523	AX986523 Sequence
C 247	52	2.2	451	7	AB141369	C 320	50	2.1	396	2	BD121382	BD121382 Sequence
C 248	52	2.2	461	2	C0526512	C 321	50	2.1	396	2	AR425829	AR425829 Sequence
C 249	52	2.2	471	7	AB146055	C 322	50	2.1	399	5	AY271002	AY271002 Sequence
C 250	52	2.2	474	7	AB136916	C 323	50	2.1	400	2	C0507164	C0507164 Sequence
C 251	52	2.2	486	7	HS934617A	C 324	50	2.1	401	5	HSR290442	HSR290442 Sequence
C 252	52	2.2	487	2	C0516425	C 325	50	2.1	416	2	C0499057	C0499057 Sequence
C 253	51	2.2	192	5	AY733782	C 326	50	2.1	416	2	C0499207	C0499207 Sequence
C 254	51	2.2	201	2	C0928538	C 327	50	2.1	416	2	C0499703	C0499703 Sequence
C 255	51	2.2	231	2	AX916194	C 328	50	2.1	429	2	C0464658	C0464658 Sequence
C 256	51	2.2	231	2	BD051727	C 329	50	2.1	431	2	C0468683	C0468683 Sequence
C 257	51	2.2	231	2	AR751988	C 330	50	2.1	437	7	AB136990	AB136990 Sequence
C 258	51	2.2	300	2	BD213266	C 331	50	2.1	443	2	C0477396	C0477396 Sequence
C 259	51	2.2	300	2	AR766860	C 332	50	2.1	451	7	HS572K18S	HS572K18S Sequence
C 260	51	2.2	301	5	AF505387	C 333	50	2.1	452	7	AB146744	AB146744 Sequence
C 261	51	2.2	310	2	C0684514	C 334	50	2.1	454	2	C0525406	C0525406 Sequence
C 262	51	2.2	315	2	AX983321	C 335	50	2.1	465	2	AX396073	AX396073 Sequence
C 263	51	2.2	315	2	BD118180	C 336	50	2.1	471	2	AX385774	AX385774 Sequence
C 264	51	2.2	315	2	AR422627	C 337	50	2.1	471	7	AB144548	AB144548 Sequence
C 265	51	2.2	319	5	HS164WD10	C 338	50	2.1	488	2	C0516143	C0516143 Sequence
C 266	51	2.2	342	2	C0465499	C 339	50	2.1	488	2	C0694064	C0694064 Sequence
C 267	51	2.2	342	2	CS185923	C 340	50	2.1	499	2	BD036650	BD036650 Sequence
C 268	51	2.2	392	2	C0508809	C 341	49	2.1	249	2	AR736911	AR736911 Sequence
C 269	51	2.2	392	2	C0512217	C 342	49	2.1	249	2	AX901117	AX901117 Sequence
C 270	51	2.2	400	2	C0663878	C 343	49	2.1	275	2	C0465871	C0465871 Sequence
C 271	51	2.2	401	2	AX269790	C 344	49	2.1	275	2	C0465504	C0465504 Sequence
C 272	51	2.2	401	2	AX271321	C 345	49	2.1	275	2	C0466119	C0466119 Sequence
C 273	51	2.2	401	7	BV189547	C 346	49	2.1	301	2	C0468975	C0468975 Sequence
C 274	51	2.2	401	7	BV193556	C 347	49	2.1	317	2	BD229434	BD229434 Sequence
C 275	51	2.2	401	7	BV195408	C 348	49	2.1	334	2	C0467158	C0467158 Sequence
C 276	51	2.2	413	5	AY190767	C 349	49	2.1	364	2	CQ465504	CQ465504 Sequence
C 277	51	2.2	424	2	C0527394	C 350	49	2.1	374	2	CQ468838	CQ468838 Sequence
C 278	51	2.2	432	2	AX977510	C 351	49	2.1	378	2	CQ468688	CQ468688 Sequence
C 279	51	2.2	432	2	BD112369	C 352	49	2.1	449	5	BD193418	BD193418 Sequence
C 280	51	2.2	432	2	AR416816	C 353	49	2.1	455	7	AB142480	AB142480 Sequence
C 281	51	2.2	461	2	CQ465724	C 354	49	2.1	474	5	AY879764	AY879764 Sequence
C 282	51	2.2	471	5	BD193060	C 355	49	2.1	477	5	AY879765	AY879765 Sequence
C 283	51	2.2	479	7	AB143860	C 356	49	2.1	497	5	HTMC3AB	HTMC3AB Sequence
C 284	51	2.2	484	7	CQ525825	C 357	48	2.0	111	2	BD037862	BD037862 Sequence
C 285	51	2.2	500	7	BV198295	C 358	48	2.0	111	2	AR738123	AR738123 Sequence
C 286	50	2.1	286	2	AR685320	C 359	48	2.0	111	2	AX902329	AX902329 Sequence
C 287	50	2.1	95	2	AX916923	C 360	48	2.0	137	2	AX911794	AX911794 Sequence
C 288	50	2.1	95	2	BD052456	C 361	48	2.0	137	2	BD047327	BD047327 Sequence
C 289	50	2.1	95	2	AR752717	C 362	48	2.0	137	2	AR747588	AR747588 Sequence
C 290	50	2.1	101	7	BV188442	C 363	48	2.0	201	2	CS242644	CS242644 Sequence
C 291	50	2.1	101	7	BV185611	C 364	48	2.0	206	2	CQ460699	CQ460699 Sequence
C 292	50	2.1	133	2	AX907387	C 365	48	2.0	251	7	BY188182	BY188182 Sequence
C 293	50	2.1	133	2	BD042920	C 366	48	2.0	289	5	HTMALND167	HTMALND167 Sequence
C 294	50	2.1	133	2	AR743181	C 367	48	2.0	333	2	CQ429251	CQ429251 Sequence
C 295	50	2.1	115	2	AX906290	C 368	48	2.0	376	7	AB146586	AB146586 Sequence
C 296	50	2.1	215	2	BD041823	C 369	48	2.0	389	7	AB141482	AB141482 Sequence
C 297	50	2.1	215	2	AR742084	C 370	48	2.0	401	7	BY198657	BY198657 Sequence
C 298	50	2.1	239	7	AB150286	C 371	48	2.0	405	2	CS011490	CS011490 Sequence
C 299	50	2.1	252	2	AX912210	C 372	48	2.0	494	7	BY188630	BY188630 Sequence
C 300	50	2.1	252	2	AX912231	C 373	48	2.0	496	2	AX390281	AX390281 Sequence
C 301	50	2.1	252	2	BD047743	C 374	48	2.0	90	5	HTMALDLRFL	HTMALDLRFL Sequence
C 302	50	2.1	252	2	BD047764	C 375	47	2.0	164	2	AX981060	AX981060 Sequence
C 303	50	2.1	252	2	AR748004	C 376	47	2.0	164	2	BD115919	BD115919 Sequence
C 304	50	2.1	252	2	AR748004	C 377	47	2.0	164	2	AR420366	AR420366 Sequence
C 305	50	2.1	253	5	AY516812	C 378	47	2.0	204	2	AX915336	AX915336 Sequence
C 306	50	2.1	262	2	CQ486569	C 379	47	2.0	204	2	BD050869	BD050869 Sequence
C 307	50	2.1	273	2	CQ710831	C 380	47	2.0	204	2	AR751130	AR751130 Sequence
C 308	50	2.1	288	2	AR702541	C 381	47	2.0	281	2	AX971141	AX971141 Sequence
C 309	50	2.1	337	2	C0516381	C 382	47	2.0	281	2	BD109860	BD109860 Sequence
C 310	50	2.1	361	2	AX245185	C 383	47	2.0	281	2	AR414307	AR414307 Sequence

C 384	47	2.0	294	2	AX971136	457	46	1.9	420	2	CQ499871	CQ499871 Sequence
C 385	47	2.0	294	2	AX971137	458	46	1.9	420	2	CQ508673	CQ508673 Sequence
C 386	47	2.0	294	2	BD109855	459	46	1.9	426	7	AB137385	Homo sapi
C 387	47	2.0	294	2	BD109856	460	46	1.9	437	2	CQ469543	Sequence
C 388	47	2.0	294	2	AR414302	461	46	1.9	438	5	AY270850	Homo sapi
C 389	47	2.0	294	2	AR414303	462	46	1.9	438	7	AB138057	Homo sapi
C 390	47	2.0	298	2	AX980723	463	46	1.9	440	7	AB142046	Sequence
C 391	47	2.0	298	2	AX982524	464	46	1.9	440	7	AB142046	Sequence
C 392	47	2.0	298	2	BD115582	465	46	1.9	441	5	AY271109	Homo sapi
C 393	47	2.0	298	2	BD117383	466	46	1.9	471	7	AB130670	Homo sapi
C 394	47	2.0	298	2	AR420029	467	46	1.9	481	5	AY620633	Atelae ge
C 395	47	2.0	298	2	AR421830	468	46	1.9	493	2	CQ472923	Sequence
C 396	47	2.0	302	2	AX971134	469	45	1.9	155	2	CQ673077	Sequence
C 397	47	2.0	302	2	AX971139	470	45	1.9	191	2	AX962456	Sequence
C 398	47	2.0	302	2	BD109853	471	45	1.9	201	2	CQ931438	Sequence
C 399	47	2.0	302	2	BD109858	472	45	1.9	237	2	AX911740	Sequence
C 400	47	2.0	302	2	AR414300	473	45	1.9	237	2	BD047273	Sequence
C 401	47	2.0	302	2	AR414305	474	45	1.9	237	2	AR747534	Sequence
C 402	47	2.0	310	2	AX971140	475	45	1.9	250	2	CQ712391	Sequence
C 403	47	2.0	310	2	BD109859	476	45	1.9	251	7	BV198137	sgm19663
C 404	47	2.0	310	2	AR414306	477	45	1.9	265	2	CQ431981	Sequence
C 405	47	2.0	312	2	AX981366	478	45	1.9	279	2	BD032164	Sequence
C 406	47	2.0	312	2	BD116225	479	45	1.9	279	2	AR732425	Sequence
C 407	47	2.0	312	2	AR420672	480	45	1.9	279	2	AX896631	Sequence
C 408	47	2.0	314	2	AX981132	481	45	1.9	303	2	AX912649	Sequence
C 409	47	2.0	314	2	AX981166	482	45	1.9	303	2	BD048182	Sequence
C 410	47	2.0	314	2	BD115991	483	45	1.9	303	2	AR748443	Sequence
C 411	47	2.0	314	2	BD116025	484	45	1.9	310	2	CQ673169	Sequence
C 412	47	2.0	314	2	AR420438	485	45	1.9	315	2	CQ464953	Sequence
C 413	47	2.0	314	2	AR420472	486	45	1.9	317	5	AY271182	Homo sapi
C 414	47	2.0	316	2	CQ468848	487	45	1.9	336	2	CQ431109	Sequence
C 415	47	2.0	333	2	CQ423689	488	45	1.9	353	2	CQ422242	Sequence
C 416	47	2.0	347	2	CQ465180	489	45	1.9	353	2	CQ423132	Sequence
C 417	47	2.0	347	2	CQ472560	490	45	1.9	356	2	CQ469506	Sequence
C 418	47	2.0	386	2	CQ393568	491	45	1.9	371	2	CQ688497	Sequence
C 419	47	2.0	386	2	CQ399945	492	45	1.9	372	2	CQ481974	Sequence
C 420	47	2.0	391	2	AX247380	493	45	1.9	379	2	CQ503113	Sequence
C 421	47	2.0	400	7	G17369	494	45	1.9	379	2	AX972103	Sequence
C 422	47	2.0	400	7	G31584	495	45	1.9	387	2	BD110822	Sequence
C 423	47	2.0	400	7	G34163	496	45	1.9	387	2	BD110822	Sequence
C 424	47	2.0	401	7	BY190474	497	45	1.9	387	5	AR415269	Sequence
C 425	47	2.0	408	8	AT341574	498	45	1.9	393	5	AT270482	Homo sapi
C 426	47	2.0	421	2	AX984327	499	45	1.9	401	7	CQ472805	Sequence
C 427	47	2.0	421	2	BD119186	500	45	1.9	401	7	BD194535	Sequence
C 428	47	2.0	421	2	AR423633	501	45	1.9	402	2	CQ480468	Sequence
C 429	47	2.0	422	2	CQ406330	502	45	1.9	402	2	AX071389	Sequence
C 430	47	2.0	426	2	CQ479134	503	45	1.9	403	2	CQ431056	Sequence
C 431	47	2.0	430	2	CQ457455	504	45	1.9	417	2	CQ471300	Sequence
C 432	47	2.0	447	2	CQ489272	505	45	1.9	421	2	CQ427114	Sequence
C 433	47	2.0	447	2	CQ491621	506	45	1.9	429	7	AB147762	Homo sapi
C 434	47	2.0	465	7	HSJ08H2	507	45	1.9	434	2	CQ518466	Sequence
C 435	47	2.0	473	2	CQ500310	508	45	1.9	439	2	AX979747	Sequence
C 436	47	2.0	473	2	HMUT7746	509	45	1.9	439	2	BD114606	Sequence
C 437	47	2.0	480	7	AX386789	510	45	1.9	439	2	AR414606	Sequence
C 438	47	2.0	498	7	BY198115	511	45	1.9	440	2	AX985809	Sequence
C 439	47	2.0	500	2	CQ432616	512	45	1.9	440	2	BD120668	Sequence
C 440	46	1.9	208	2	CQ701657	513	45	1.9	440	2	AR425115	Sequence
C 441	46	1.9	226	5	HMALNE652	514	45	1.9	440	2	AX390737	Sequence
C 442	46	1.9	227	2	BD038133	515	45	1.9	443	2	CQ501639	Sequence
C 443	46	1.9	227	2	AR738394	516	45	1.9	443	2	CQ510563	Sequence
C 444	46	1.9	227	2	AX902600	517	45	1.9	446	7	AB146085	Homo sapi
C 445	46	1.9	282	2	CQ682649	518	45	1.9	448	5	AY318849	Sequence
C 446	46	1.9	282	5	AY270301	519	45	1.9	449	5	CQ463716	Sequence
C 447	46	1.9	324	7	AB142194	520	45	1.9	453	2	CQ394602	Sequence
C 448	46	1.9	349	7	HMUT6929	521	45	1.9	453	2	CQ400957	Sequence
C 449	46	1.9	355	2	CQ469337	522	45	1.9	468	2	CQ417528	Sequence
C 450	46	1.9	364	2	CQ677114	523	45	1.9	474	5	AY879733	Sequence
C 451	46	1.9	394	2	CQ478674	524	45	1.9	479	5	AY879732	Sequence
C 452	46	1.9	396	2	CQ503227	525	45	1.9	480	2	CQ524506	Sequence
C 453	46	1.9	396	2	CQ512074	526	45	1.9	489	2	AX983277	Sequence
C 454	46	1.9	401	7	BY193624	527	45	1.9	489	2	BD118136	Sequence
C 455	46	1.9	410	2	CQ469358	528	45	1.9	489	2	AR422583	Sequence
C 456	46	1.9	414	7	BY196092	529	44	1.9	76	2	BD037434	Sequence

C 530	44	1.9	76	2	AR737695	Sequence	C 603	44	1.9	394	2	AX071538	Sequence	AX071538	Sequence
C 531	44	1.9	76	2	AX901901	Sequence	C 604	44	1.9	401	2	AX270548	Sequence	AX270548	Sequence
C 532	44	1.9	102	2	AR702610	Sequence	C 605	44	1.9	401	2	AX272079	Sequence	AX272079	Sequence
C 533	44	1.9	108	5	HSU67803	Human small	C 606	44	1.9	401	7	BV192886	Sequence	BV192886	Sequence
C 534	44	1.9	147	2	BD039919	Sequence	C 607	44	1.9	401	7	BV198666	Sequence	BV198666	Sequence
C 535	44	1.9	147	2	AR740180	Sequence	C 608	44	1.9	405	2	CQ428889	Sequence	CQ428889	Sequence
C 536	44	1.9	147	2	AX904386	Sequence	C 609	44	1.9	406	2	AX967239	Sequence	AX967239	Sequence
C 537	44	1.9	148	2	BD039768	Sequence	C 610	44	1.9	406	2	BD122098	Sequence	BD122098	Sequence
C 538	44	1.9	148	2	AR740029	Sequence	C 611	44	1.9	406	2	AR426545	Sequence	AR426545	Sequence
C 539	44	1.9	148	2	AX904235	Sequence	C 612	44	1.9	406	2	AR426545	Sequence	AR426545	Sequence
C 540	44	1.9	158	5	AY516549	Homo sapi	C 613	44	1.9	409	2	AX387120	Sequence	AX387120	Sequence
C 541	44	1.9	188	2	BD039971	Sequence	C 614	44	1.9	409	5	AY879647	Sequence	AY879647	Sequence
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C 543	44	1.9	188	2	AR740232	Sequence	C 616	44	1.9	432	2	CQ519628	Sequence	CQ519628	Sequence
C 544	44	1.9	188	2	AR740234	Sequence	C 617	44	1.9	432	2	CQ521947	Sequence	CQ521947	Sequence
C 545	44	1.9	188	2	AX904438	Sequence	C 618	44	1.9	434	2	BV196153	Sequence	BV196153	Sequence
C 546	44	1.9	188	2	AX904440	Sequence	C 619	44	1.9	432	5	AY879645	Sequence	AY879645	Sequence
C 547	44	1.9	197	2	AX322172	Sequence	C 620	44	1.9	441	7	AB147336	Sequence	AB147336	Sequence
C 548	44	1.9	201	2	CS242640	Sequence	C 621	44	1.9	443	2	AX386927	Sequence	AX386927	Sequence
C 549	44	1.9	201	2	CS242641	Sequence	C 622	44	1.9	445	2	CQ422656	Sequence	CQ422656	Sequence
C 550	44	1.9	201	2	CS242645	Sequence	C 623	44	1.9	447	2	CQ422201	Sequence	CQ422201	Sequence
C 551	44	1.9	234	2	CQ674644	Sequence	C 624	44	1.9	451	2	CQ473561	Sequence	CQ473561	Sequence
C 552	44	1.9	237	2	BD039066	Sequence	C 625	44	1.9	451	5	AY879728	Sequence	AY879728	Sequence
C 553	44	1.9	237	2	AR739327	Sequence	C 626	44	1.9	452	7	AB129621	Sequence	AB129621	Sequence
C 554	44	1.9	237	2	AX903533	Sequence	C 627	44	1.9	456	2	CQ527763	Sequence	CQ527763	Sequence
C 555	44	1.9	251	7	BV188018	sqm15643	C 628	44	1.9	458	2	CQ520151	Sequence	CQ520151	Sequence
C 556	44	1.9	251	5	GGU46689	U14669 Gorilla gor	C 629	44	1.9	458	2	CQ520635	Sequence	CQ520635	Sequence
C 557	44	1.9	258	2	BD029803	Sequence	C 630	44	1.9	462	2	AX987240	Sequence	AX987240	Sequence
C 558	44	1.9	258	2	AR730064	Sequence	C 631	44	1.9	462	2	BD122099	Sequence	BD122099	Sequence
C 559	44	1.9	258	2	AX894270	Sequence	C 632	44	1.9	462	2	CQ484519	Sequence	CQ484519	Sequence
C 560	44	1.9	265	2	AX917347	Sequence	C 633	44	1.9	464	2	AR426546	Sequence	AR426546	Sequence
C 561	44	1.9	265	2	BD052880	Sequence	C 634	44	1.9	464	7	AB130200	Homo sapi	AB130200	Homo sapi
C 562	44	1.9	265	2	AR753141	Sequence	C 635	44	1.9	464	7	AB137289	Homo sapi	AB137289	Homo sapi
C 563	44	1.9	272	2	BD038062	Sequence	C 636	44	1.9	465	7	HMMWT5324	Sequence	HMMWT5324	Sequence
C 564	44	1.9	272	2	AR738323	Sequence	C 637	44	1.9	471	2	CQ503835	Sequence	CQ503835	Sequence
C 565	44	1.9	272	2	AX902529	Sequence	C 638	44	1.9	471	2	CQ512641	Sequence	CQ512641	Sequence
C 566	44	1.9	274	2	CQ689711	Sequence	C 639	44	1.9	479	2	CQ529911	Sequence	CQ529911	Sequence
C 567	44	1.9	280	5	HS35A12F	Sequence	C 640	44	1.9	481	2	CQ513872	Sequence	CQ513872	Sequence
C 568	44	1.9	284	7	AB129787	Homo sapi	C 641	44	1.9	490	2	BD125854	Sequence	BD125854	Sequence
C 569	44	1.9	292	2	CQ710934	Sequence	C 642	44	1.9	490	2	CQ781145	Sequence	CQ781145	Sequence
C 570	44	1.9	292	2	BD039669	Sequence	C 643	44	1.9	490	2	AX389604	Sequence	AX389604	Sequence
C 571	44	1.9	298	2	AR739930	Sequence	C 644	44	1.9	491	2	CQ477178	Sequence	CQ477178	Sequence
C 572	44	1.9	298	2	AX904136	Sequence	C 645	44	1.9	492	2	CQ514631	Sequence	CQ514631	Sequence
C 573	44	1.9	300	5	ORALU	L47222 Pongo pygma	C 646	44	1.9	500	7	G34608	human STR	G34608	human STR
C 574	44	1.9	309	2	AX388368	Sequence	C 647	44	1.8	80	5	HMMBRKAC	Sequence	HMMBRKAC	Sequence
C 575	44	1.9	309	7	AB130846	Homo sapi	C 648	44	1.8	92	2	AX197472	Sequence	AX197472	Sequence
C 576	44	1.9	309	7	AB136862	Homo sapi	C 649	44	1.8	165	2	AX906331	Sequence	AX906331	Sequence
C 577	44	1.9	311	2	CQ487790	Sequence	C 650	44	1.8	165	2	BD041864	Sequence	BD041864	Sequence
C 578	44	1.9	316	2	AX980615	Sequence	C 651	44	1.8	165	2	AR742125	Sequence	AR742125	Sequence
C 579	44	1.9	316	2	BD115474	Sequence	C 652	44	1.8	201	2	CQ926933	Sequence	CQ926933	Sequence
C 580	44	1.9	316	2	AR415921	EST and e	C 653	44	1.8	201	2	CQ930352	Sequence	CQ930352	Sequence
C 581	44	1.9	318	2	AX981896	Sequence	C 654	44	1.8	201	2	CQ930591	Sequence	CQ930591	Sequence
C 582	44	1.9	318	2	BD116755	EST and e	C 655	44	1.8	201	7	BV200808	Sequence	BV200808	Sequence
C 583	44	1.9	318	2	AR421202	Sequence	C 656	44	1.8	204	5	AF205207	Homo sapi	AF205207	Homo sapi
C 584	44	1.9	326	5	HUMALURPTE	M37551 Human AFP g	C 657	44	1.8	215	2	AX916343	Sequence	AX916343	Sequence
C 585	44	1.9	348	7	G49311	std4510H16	C 658	44	1.8	215	2	BD051876	Sequence	BD051876	Sequence
C 586	44	1.9	350	7	BV198786	sqm19806	C 659	44	1.8	215	2	AR752137	Sequence	AR752137	Sequence
C 587	44	1.9	350	7	CQ820053	Sequence	C 660	44	1.8	221	2	BD039504	Sequence	BD039504	Sequence
C 588	44	1.9	351	2	AX246983	Sequence	C 661	44	1.8	221	2	AR739765	Sequence	AR739765	Sequence
C 589	44	1.9	360	2	CQ671170	Sequence	C 662	44	1.8	221	2	AX903971	Sequence	AX903971	Sequence
C 590	44	1.9	361	2	CQ691466	Sequence	C 663	44	1.8	226	2	AX911670	Sequence	AX911670	Sequence
C 591	44	1.9	367	2	CQ420011	Sequence	C 664	44	1.8	226	2	BD047203	Sequence	BD047203	Sequence
C 592	44	1.9	369	2	AX070634	Sequence	C 665	44	1.8	226	2	AR747464	Sequence	AR747464	Sequence
C 593	44	1.9	371	2	CQ419353	Sequence	C 666	44	1.8	234	5	HSU02054	Human clone	HSU02054	Human clone
C 594	44	1.9	371	7	CQ514345	Sequence	C 667	44	1.8	241	2	BD040243	Sequence	BD040243	Sequence
C 595	44	1.9	371	7	HSC32F9	AL158331 H. sapiens	C 668	44	1.8	241	2	AR740504	Sequence	AR740504	Sequence
C 596	44	1.9	375	5	HSISPOLYA	222650 Homo sapien	C 669	44	1.8	241	2	AX904710	Sequence	AX904710	Sequence
C 597	44	1.9	380	2	CQ428246	Sequence	C 670	44	1.8	246	2	AX934995	Sequence	AX934995	Sequence
C 598	44	1.9	383	2	CQ465681	Sequence	C 671	44	1.8	248	2	CQ672838	Sequence	CQ672838	Sequence
C 599	44	1.9	387	2	CQ669022	Sequence	C 672	44	1.8	250	2	CQ696789	Sequence	CQ696789	Sequence
C 600	44	1.9	387	7	AB143387	Homo sapi	C 673	44	1.8	251	7	BV193156	Sequence	BV193156	Sequence
C 601	44	1.9	392	2	CQ466291	Sequence	C 674	44	1.8	251	7	BV196694	Sequence	BV196694	Sequence
C 602	44	1.9	392	2	CS012297	Sequence	C 675	44	1.8	251	7	BV198601	Sequence	BV198601	Sequence

C 676	43	1.8	251	7	BV199046	749	43	1.8	392	2	CQ469305	CQ469305 Sequence
C 677	43	1.8	255	7	AB129384	C 750	43	1.8	393	5	AY246451	AY246451 Pan trogl
C 678	43	1.8	267	7	CQ692636	C 751	43	1.8	396	5	CS147500	CS147500 Sequence
C 679	43	1.8	272	2	CQ464514	C 752	43	1.8	397	2	AX981812	AX981812 Sequence
C 680	43	1.8	274	2	AX907397	C 753	43	1.8	397	2	BD116671	BD116671 EST and e
C 681	43	1.8	274	2	BD042930	C 754	43	1.8	397	2	AR421118	AR421118 Sequence
C 682	43	1.8	274	2	AX743191	C 755	43	1.8	399	2	CQ459750	CQ459750 Sequence
C 683	43	1.8	291	2	AX980631	C 756	43	1.8	399	5	AY246453	AY246453 Pongo pyg
C 684	43	1.8	291	2	BD115490	C 757	43	1.8	401	7	G17084	G17084 human STS S
C 685	43	1.8	291	2	AR419937	C 758	43	1.8	401	2	CQ496671	CQ496671 Sequence
C 686	43	1.8	292	2	AX980583	C 759	43	1.8	401	7	AX070077	AX070077 Sequence
C 687	43	1.8	292	2	AX981858	C 760	43	1.8	401	7	BV194455	BV194455 sqm18112
C 688	43	1.8	292	2	BD115442	C 761	43	1.8	401	7	BV195759	BV195759 sqm18576
C 689	43	1.8	292	2	BD116717	C 762	43	1.8	402	2	CQ393830	CQ393830 Sequence
C 690	43	1.8	292	2	AR419889	C 763	43	1.8	402	2	CQ400201	CQ400201 Sequence
C 691	43	1.8	292	2	AR421164	C 764	43	1.8	402	2	CQ698294	CQ698294 Sequence
C 692	43	1.8	293	5	AY270547	C 765	43	1.8	403	2	CQ519971	CQ519971 Sequence
C 693	43	1.8	293	5	AY461426	C 766	43	1.8	406	2	CQ520574	CQ520574 Sequence
C 694	43	1.8	294	7	AB145951	C 767	43	1.8	407	7	AB135990	AB135990 Homo sapi
C 695	43	1.8	298	2	AX977375	C 768	43	1.8	408	2	CQ406586	CQ406586 Sequence
C 696	43	1.8	298	2	BD112234	C 769	43	1.8	408	2	CQ505797	CQ505797 Sequence
C 697	43	1.8	298	2	AR416681	C 770	43	1.8	409	2	CQ693877	CQ693877 Sequence
C 698	43	1.8	300	2	BD212915	C 771	43	1.8	411	5	AY055358	AY055358 Cercopit
C 699	43	1.8	300	2	BD212921	C 772	43	1.8	416	2	CQ502358	CQ502358 Sequence
C 700	43	1.8	300	2	AR766509	C 773	43	1.8	416	2	CQ511220	CQ511220 Sequence
C 701	43	1.8	300	2	AR766515	C 774	43	1.8	417	2	BD032114	BD032114 Sequence
C 702	43	1.8	301	2	AX912891	C 775	43	1.8	417	2	AR732375	AR732375 Sequence
C 703	43	1.8	301	2	BD048424	C 776	43	1.8	417	2	AX270812	AX270812 Sequence
C 704	43	1.8	301	2	AR748685	C 777	43	1.8	417	2	AX272343	AX272343 Sequence
C 705	43	1.8	307	2	AX982189	C 778	43	1.8	417	2	AX896581	AX896581 Sequence
C 706	43	1.8	307	2	BD117048	C 779	43	1.8	425	2	CQ462132	CQ462132 Sequence
C 707	43	1.8	307	2	AR421495	C 780	43	1.8	425	2	AB139357	AB139357 Homo sapi
C 708	43	1.8	311	5	HUMGP1IBGT	C 781	43	1.8	426	2	CQ462141	CQ462141 Sequence
C 709	43	1.8	316	5	AF344193	C 782	43	1.8	430	2	CQ433377	CQ433377 Sequence
C 710	43	1.8	318	7	HS344VA9	C 783	43	1.8	432	2	CQ522025	CQ522025 Sequence
C 711	43	1.8	327	2	CQ485049	C 784	43	1.8	435	2	CQ465379	CQ465379 Sequence
C 712	43	1.8	329	2	AX981919	C 785	43	1.8	449	5	AY879695	AY879695 Macaca si
C 713	43	1.8	329	2	BD116778	C 786	43	1.8	452	7	AB137078	AB137078 Homo sapi
C 714	43	1.8	329	2	AR421225	C 787	43	1.8	452	7	AB142628	AB142628 Homo sapi
C 715	43	1.8	332	2	CQ463743	C 788	43	1.8	453	7	AX387694	AX387694 Sequence
C 716	43	1.8	333	2	AX245330	C 789	43	1.8	453	7	AB135762	AB135762 Homo sapi
C 717	43	1.8	334	2	AX980577	C 790	43	1.8	455	2	CQ411120	CQ411120 Sequence
C 718	43	1.8	334	2	BD115436	C 791	43	1.8	455	2	CQ478473	CQ478473 Sequence
C 719	43	1.8	334	2	CQ475840	C 792	43	1.8	456	7	AB136789	AB136789 Homo sapi
C 720	43	1.8	334	2	AR419883	C 793	43	1.8	458	7	AB138404	AB138404 Homo sapi
C 721	43	1.8	335	2	AB144035	C 794	43	1.8	458	7	AB140130	AB140130 Homo sapi
C 722	43	1.8	338	5	HSU18399	C 795	43	1.8	459	7	AB137093	AB137093 Homo sapi
C 723	43	1.8	339	2	CQ460253	C 796	43	1.8	461	5	AY879663	AY879663 Nasaalis l
C 724	43	1.8	339	2	CQ481210	C 797	43	1.8	461	5	AY879696	AY879696 Macaca ne
C 725	43	1.8	347	2	AX981808	C 798	43	1.8	462	5	AY849288	AY849288 Pongo pyg
C 726	43	1.8	347	2	BD116667	C 799	43	1.8	463	2	CQ427872	CQ427872 Sequence
C 727	43	1.8	347	2	AR421114	C 800	43	1.8	463	5	AY879726	AY879726 Trachypit
C 728	43	1.8	349	2	CQ472445	C 801	43	1.8	465	5	AB138001	AB138001 Homo sapi
C 729	43	1.8	349	7	AB142481	C 802	43	1.8	466	5	HUM2C34B10	AB086194 Homo sapi
C 730	43	1.8	354	2	AX245515	C 803	43	1.8	466	7	AB137191	AB137191 Homo sapi
C 731	43	1.8	358	2	AX978258	C 804	43	1.8	469	2	CQ680952	CQ680952 Sequence
C 732	43	1.8	358	2	BD113117	C 805	43	1.8	476	2	BD152556	BD152556 Primer fo
C 733	43	1.8	358	2	AR417564	C 806	43	1.8	476	2	AX872494	AX872494 Sequence
C 734	43	1.8	360	2	AX977566	C 807	43	1.8	477	7	HUMUT7213B	L29762 Human STS U
C 735	43	1.8	360	2	BD114225	C 808	43	1.8	479	2	CQ488197	CQ488197 Sequence
C 736	43	1.8	360	2	AR416872	C 809	43	1.8	480	2	AX908520	AX908520 Sequence
C 737	43	1.8	369	2	CQ694519	C 810	43	1.8	480	2	BD044053	BD044053 Sequence
C 738	43	1.8	369	2	CQ695076	C 811	43	1.8	480	2	AR744314	AR744314 Sequence
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C 740	43	1.8	372	2	AX245202	C 813	43	1.8	481	2	BD110132	BD110132 EST and e
C 741	43	1.8	375	2	CQ458020	C 814	43	1.8	481	2	CQ471707	CQ471707 Sequence
C 742	43	1.8	376	2	CQ461990	C 815	43	1.8	481	2	AR414579	AR414579 Sequence
C 743	43	1.8	380	2	CQ415618	C 816	43	1.8	483	2	CQ426538	CQ426538 Sequence
C 744	43	1.8	380	2	CQ525220	C 817	43	1.8	484	5	AY879719	AY879719 Colobus g
C 745	43	1.8	387	2	CQ698367	C 818	43	1.8	485	5	G34139	G34139 human STS S
C 746	43	1.8	388	7	AB148206	C 819	43	1.8	487	5	AY791283	AY791283 Pongo pyg
C 747	43	1.8	390	5	AY246452	C 820	43	1.8	488	7	HS658E22T	AY117247 H. sapiens
C 748	43	1.8	391	2	CQ472042	C 821	43	1.8	492	2	AX971399	AX971399 Sequence

C 968	42	1.8	488	2	BD118164	BD118164 EST and e
969	42	1.8	488	2	BD152085	BD152085 Primer fo
C 970	42	1.8	488	2	AR422611	Sequence
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973	42	1.8	496	2	BD154130	BD154130 Primer fo
974	42	1.8	496	2	AX874068	AX874068 Sequence
C 975	41	1.7	86	2	BD038739	BD038739 Sequence
C 976	41	1.7	86	2	AR739000	AR739000 Sequence
C 977	41	1.7	86	2	AX903206	AX903206 Sequence
978	41	1.7	152	2	AX911297	AX911297 Sequence
979	41	1.7	152	2	BD046830	BD046830 Sequence
980	41	1.7	152	2	AR747091	AR747091 Sequence
C 981	41	1.7	161	7	HUMC5206	L28253 Human chrom
C 982	41	1.7	165	5	AY270680	AY270680 Homo sapi
C 983	41	1.7	201	7	BY207464	BY207464 eqm22355
C 984	41	1.7	201	7	BY207465	BY207465 eqm22355
C 985	41	1.7	233	2	CQ463179	CQ463179 Sequence
C 986	41	1.7	234	2	CQ694480	CQ694480 Sequence
C 987	41	1.7	236	2	CQ657181	CQ657181 Sequence
C 988	41	1.7	244	2	BD024112	BD024112 Sequence
C 989	41	1.7	244	2	AR724373	AR724373 Sequence
C 990	41	1.7	244	2	AX884502	AX884502 Sequence
C 991	41	1.7	264	5	HSU90299	U90299 Human chrom
992	41	1.7	265	2	AX979106	AX979106 Sequence
993	41	1.7	265	2	BD113965	BD113965 EST and e
994	41	1.7	265	2	AR418412	AR418412 Sequence
C 995	41	1.7	269	2	CQ467663	CQ467663 Sequence
C 996	41	1.7	274	2	CQ682637	CQ682637 Sequence
C 997	41	1.7	274	2	CQ696893	CQ696893 Sequence
C 998	41	1.7	278	2	CQ518279	CQ518279 Sequence
C 999	41	1.7	279	2	CQ485391	CQ485391 Sequence
C1000	41	1.7	280	5	HS3ALU27S	Z30996 H. sapiens D

ALIGNMENTS

RESULT 1	456 bp	mRNA	linear	PRI 30-MAY-2001
LOCUS	HS278976	456 bp	mRNA	linear
DEFINITION	Homo sapiens mRNA for p53-binding protein (MDM2 gene), alternatively spliced variant ISI.			
ACCESSION	AJ278976			
VERSION	AJ278976.1	GI:10045128		
KEYWORDS	alternative splicing; mdm2 gene; p53-binding protein.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1			
AUTHORS	Bartel,F., Meye,A., Wurl,P., Kappler,M., Bache,M., Lautenschlager,C., Grunbaum,U., Schmidt,H. and Taubert,H.			
TITLE	Amplification of the MDM2 gene, but not expression of splice variants of MDM2 mRNA, is associated with prognosis in soft tissue sarcoma			
JOURNAL	Int. J. Cancer 95 (3), 168-175 (2001)			
PUBMED	11307150			
REFERENCE	2 (bases 1 to 456)			
AUTHORS	Bartel,F.			
TITLE	Direct Submision			
JOURNAL	Submitted (06-SEP-2000) Bartel F., Institute for Pathology, University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097 Halle, GERMANY			
COMMENT	Related sequences: AJ278975-AJ278978, AJ276888.			
FEATURES	Location/Qualifiers			
SOURCE	1..456			
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mRNA

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/note="alternatively spliced variant ISI"

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/experiment="experimental evidence, no additional details recorded"

/note="alternatively spliced variant ISI"

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/translation="MCTMNSVPLDQAVTTSQIPDKTIVNSRESCVENDKINO ASQSESDYSQSTSSITLYSSQEDYKFERBERTQKESVSSFLNAIEPCVICO GRPKNGIVGKTHLMACFTCAKRLKRRKPCVCKPIQMIIVLYFP"

ORIGIN

Query Match 16.9%; Score 401; DB 5; Length 456;

Best Local Similarity 100.0%; Pred. No. 1.8e-215; Indels 0; Gaps 0;

Matches 401; Conservative 0; Mismatches 0;

Cy	1387	TTCCCTGATTGAAAAAACTATAGTGAATTCACAGAGTCATGTTGAGGAAATG	1446
Db	56	TTCCCTGATTGAAAAAACTATAGTGAATTCACAGAGTCATGTTGAGGAAATG	115
Cy	1447	ATGATTAATTTACACAGCTTCACATCAAGAAAGTGAAGCTATTTCTCAGCATCA	1506
Db	116	ATGATTAATTTACACAGCTTCACATCAAGAAAGTGAAGCTATTTCTCAGCATCA	175
Cy	1507	CTTCTAGTACATATTTATAGCAGCCAGAGATGGAAGATTTGAAAGGAGAA	1566
Db	176	CTTCTAGTACATATTTATAGCAGCCAGAGATGGAAGATTTGAAAGGAGAA	235
Cy	1567	CCCAAGACAAAGAGAGTGTGAATCTAGTTGCCCTTAATGCAATGAACTTTGTG	1626
Db	236	CCCAAGACAAAGAGAGTGTGAATCTAGTTGCCCTTAATGCAATGAACTTTGTG	295
Cy	1627	TGATTTGTCAAGGTGCACTTAAATGTGTCATTTGTCATGCAAAACGAGATCTTA	1686
Db	296	TGATTTGTCAAGGTGCACTTAAATGTGTCATTTGTCATGCAAAACGAGATCTTA	355
Cy	1687	TGGCCTGCTTACATGCGAAGAGCTAAAGAAATTAAGCCGCGCCAGTATGTA	1746
Db	356	TGGCCTGCTTACATGCGAAGAGCTAAAGAAATTAAGCCGCGCCAGTATGTA	415
Cy	1747	GACAACCAATTCAAATGATGCTAATTTCCCTAG	1787
Db	416	GACAACCAATTCAAATGATGCTAATTTCCCTAG	456
RESULT 2			
LOCUS	AF092843	388 bp	mRNA linear PRI 11-DEC-2001
DEFINITION	Homo sapiens MDM2 protein (MDM2) mRNA, alternatively spliced, partial cds.		
ACCESSION	AF092843		
VERSION	AF092843.1	GI:17483719	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 388)		
AUTHORS	Tamborini,E., Della Torre,G., Lavarino,C., Azzarelli,A., Carlinelli,P., Pierotti,M.A. and Piloti,S.		
TITLE	Analysis of the molecular species generated by MDM2 gene amplification in liposarcomas		
JOURNAL	Int. J. Cancer 92 (6), 790-796 (2001)		

PUBMED 11351297
REFERENCE 2 (bases 1 to 388)
AUTHORS Tamborini, E., Pierotti, M.A., Della Torre, G., Lavarino, C., Buto', S.,
Dejia, D. and Pilotti, S.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1998) Dipartimento di Anatomia Patologica,
Istituto Nazionale per lo Studio e la Cura dei Tumori, Via Venezian
1, Milan, MI 20133, Italy

FEATURES
source
1..388
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/chromosome="12"
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1..>388
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IYRLDVLPVLDLSIR"

ORIGIN
Query Match 15.1%; Score 359; DB 5; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.4e-191;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 CGCGAAAACCCCGATGCTGAGAGACAGCAAAATGTGCAATACCAATGCTGTACTTA 339
Db 1 CGCGAAAACCCCGATGCTGAGAGACAGCAAAATGTGCAATACCAATGCTGTACTTA 60
QY 340 CTGATGCTGCTGTACCACTTCACGATTCAGAGCTTGGAAACAAGACCTCGTTAAAC 399
Db 61 CTGATGCTGCTGTACCACTTCACGATTCAGAGCTTGGAAACAAGACCTCGTTAAAC 120
QY 400 CAAAGCCATTGCTTGAAGTTAATTAAGTCTGTTGGTGCACAAAAGACCTTAATACTA 459
Db 121 CAAAGCCATTGCTTGAAGTTAATTAAGTCTGTTGGTGCACAAAAGACCTTAATACTA 180
QY 460 TGAAGAAGTCTTTTATCTTGGCCAGTATATTATGACTAAACGATTATATGATGAGA 519
Db 181 TGAAGAAGTCTTTTATCTTGGCCAGTATATTATGACTAAACGATTATATGATGAGA 240
QY 520 AGCAACAACATATTGATATTGTTCAAAATGATCTTCAAGAGATTGTTGGCGTCCAA 579
Db 241 AGCAACAACATATTGATATTGTTCAAAATGATCTTCAAGAGATTGTTGGCGTCCAA 300
QY 580 GCTTCTCTGTGAAGACACAGAAAATATATACATGATCTACAGAACTTGTGAGTAA 638
Db 301 GCTTCTCTGTGAAGACACAGAAAATATATACATGATCTACAGAACTTGTGAGTAA 359

RESULT 3
BD005478 399 bp DNA linear PAT 31-JAN-2002
LOCUS Cellular immunogens useful cancer vaccines.
ACCESSION BD005478.1 GI:18631849
VERSION JP 2001501909-A/8.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 399)
AUTHORS Halpern, M.S. and England, J.M.
TITLE Cellular immunogens useful cancer vaccines
JOURNAL Patent: JP 2001501909-A 8 13-FEB-2001;
ALLEGHENY UNIVERSITY OF THE HEALTH SCIENCES

COMMENT OS Unidentified
PN JP 2001501909-A/8
PD 13-FEB-2001
PF 13-JAN-1997 JP 1997526124
PR 19-JAN-1996 US 60/010262
PI MICHAEL S HALPERN, JAMES M ENGLAND
PC A01K63/00, A61K39/00, A61K39/38, A61K48/00, C12N5/00, C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH key
FT source 1..399
Location/Qualifiers
FEATURES 1..399
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ORIGIN
Query Match 13.2%; Score 313; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.1e-165;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1475 ACAAGAAAGTGAAGACTATCTCAGCCATCACTTCTGTAGCATTTATTTATAGACGCA 1534
Db 87 ACAAGAAAGTGAAGACTATCTCAGCCATCACTTCTGTAGCATTTATTTATAGACGCA 146
QY 1535 AGAAGATGTGAAGAGTTTGAAGAGGAAAGAAACCAAGACAAAGAGAGTGTGAATC 1594
Db 147 AGAAGATGTGAAGAGTTTGAAGAGGAAAGAAACCAAGACAAAGAGAGTGTGAATC 206
QY 1595 TAGTTGGCCCTTAATGCGATTGAACCTTGTGTGATTTGTCAAGTGCACCTAAATAATG 1654
Db 207 TAGTTGGCCCTTAATGCGATTGAACCTTGTGTGATTTGTCAAGTGCACCTAAATAATG 266
QY 1655 TTGATTTGCCATGAGCAAAACAGACATCTTAATGCGCTTTACATGTGCAAGAAAGCT 1714
Db 267 TTGATTTGCCATGAGCAAAACAGACATCTTAATGCGCTTTACATGTGCAAGAAAGCT 326
QY 1715 AAAAGAAAGAAATAGCCCTGCCAGTATGTAGCAACCAATTTGAATGATGTGCTAAC 1774
Db 327 AAAAGAAAGAAATAGCCCTGCCAGTATGTAGCAACCAATTTGAATGATGTGCTAAC 386
QY 1775 TTATTTCCCTTAG 1787
Db 387 TTATTTCCCTTAG 399

RESULT 4
AR202601 399 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 8 from patent US 6365151.
ACCESSION AR202601
VERSION AR202601.1 GI:21498773
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 399)
AUTHORS Halpern, M.S. and England, J.M.
TITLE Cellular immunogens comprising cognate proto-oncogenes
JOURNAL Patent: US 6365151-A 8 02-APR-2002;
FEATURES location/Qualifiers
source 1..399
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ORIGIN
Query Match 13.2%; Score 313; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.1e-165;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1475 ACAAGAAAGTGAAGACTATCTCAGCCATCACTTCTGTAGCATTTATTTATAGACGCA 1534

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Db ACAAGAAAGTGAAGACTATCTCTCAGCCATCACTCTGTAGTACATTATTATTAGACGCCA 146
QY 1535 AGAAGATGTGAAAGAGTTTGAAGAGGAAGAAACCCAGACAAAGAGAGTGTGAAATC 1594
Db 147 AGAAGATGTGAAAGAGTTTGAAGAGGAAGAAACCCAGACAAAGAGAGTGTGAAATC 206
QY 1595 TAGTTGGCCCTTAATGCAATTTGAACCTTGTGTATTTGTCAAGGTGCACTTAAATATG 1654
Db 207 TAGTTGGCCCTTAATGCAATTTGAACCTTGTGTATTTGTCAAGGTGCACTTAAATATG 266
QY 1655 TTGCATTGTCCATGCGCAAAACAGACATCTTATGCGCTGCTTTACATGTGCAAAAGACT 1714
Db 267 TTGCATTGTCCATGCGCAAAACAGACATCTTATGCGCTGCTTTACATGTGCAAAAGACT 326
QY 1715 AAAAGAAAGAAATAGAGCCCTGCCAGTATGTAGCAACCAATTCAAATGATTTGCTTAC 1774
Db 327 AAAAGAAAGAAATAGAGCCCTGCCAGTATGTAGCAACCAATTCAAATGATTTGCTTAC 386
QY 1775 TTATTTCCCTTAG 1787
Db 387 TTATTTCCCTTAG 399

RESULT 5
HSU33202 399 bp mRNA linear PRI 13-DEC-2001
LOCUS Human mdm2-D (mdm2) mRNA, complete cds.
DEFINITION U33202.1 GI:992682
ACCESSION U33202.1 GI:992682
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (sites)
REFERENCE
AUTHORS Sigalas I., Calvert A.H., Anderson J.J., Neal D.B. and Lunec J.
TITLE Alternatively spliced mdm2 transcripts with loss of p53 binding
domain sequences: transforming ability and frequent detection in
human cancer
JOURNAL Nat. Med. 2 (8), 912-917 (1996)
REFERENCE
PUBMED 8705862
AUTHORS Lunec J.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-1995) John Lunec, Cancer Research Unit,
University of Newcastle Upon Tyne - Medical School, Framlington
Place, Newcastle upon Tyne, NE2 4HH, U.K.
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ORIGIN

Query Match 13.2%; Score 313; DB 5; Length 399;
Best Local Similarity 100.0%; Pred. No. 2,1e-165;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1475 ACAAGAAAGTGAAGACTATCTCTCAGCCATCACTCTGTAGTACATTATTATTAGACGCCA 1514
Db 87 ACAAGAAAGTGAAGACTATCTCTCAGCCATCACTCTGTAGTACATTATTATTAGACGCCA 146
QY 1535 AGAAGATGTGAAAGAGTTTGAAGAGGAAGAAACCCAGACAAAGAGAGTGTGAAATC 1594
Db 147 AGAAGATGTGAAAGAGTTTGAAGAGGAAGAAACCCAGACAAAGAGAGTGTGAAATC 206
QY 1595 TAGTTGGCCCTTAATGCAATTTGAACCTTGTGTATTTGTCAAGGTGCACTTAAATATG 1654
Db 207 TAGTTGGCCCTTAATGCAATTTGAACCTTGTGTATTTGTCAAGGTGCACTTAAATATG 266
QY 1655 TTGCATTGTCCATGCGCAAAACAGACATCTTATGCGCTGCTTTACATGTGCAAAAGACT 1714
Db 267 TTGCATTGTCCATGCGCAAAACAGACATCTTATGCGCTGCTTTACATGTGCAAAAGACT 326
QY 1715 AAAAGAAAGAAATAGAGCCCTGCCAGTATGTAGCAACCAATTCAAATGATTTGCTTAC 1774
Db 327 AAAAGAAAGAAATAGAGCCCTGCCAGTATGTAGCAACCAATTCAAATGATTTGCTTAC 386
QY 1775 TTATTTCCCTTAG 1787
Db 387 TTATTTCCCTTAG 399

RESULT 6
AF385327 480 bp mRNA linear PRI 11-OCT-2001
LOCUS Homo sapiens MDM2 variant FB55 (MDM2) mRNA, complete cds.
DEFINITION AF385327
ACCESSION AF385327
VERSION AF385327.1 GI:16033453
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 480)
REFERENCE
AUTHORS Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.
TITLE Novel mdm2 splice variants identified in pediatric rhabdomyosarcoma
tumors and cell lines
JOURNAL Unpublished
REFERENCE
PUBMED 120480
AUTHORS Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2001) Molecular Pharmacology, St. Jude Children's
Research Hospital, 332 N. Lauderdale, Memphis, TN 38105, USA
FEATURES
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ORIGIN

Query Match 10.5%; Score 250; DB 5; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 977 GGATTTGATGCTGCTGTAAGGAACATTCAGGTGATTGTTGATCAGGATTCGTTTC 1036
DB 156 GGATTTGATGCTGCTGTAAGGAACATTCAGGTGATTGTTGATCAGGATTCGTTTC 215

QY 1037 AGATCAGTTAGTGTAGATTTGAATTTGAATCTCTCCAGTCAGGAAGATTATAGCCTTAG 1096
DB 216 AGATCAGTTAGTGTAGATTTGAATTTGAATCTCTCCAGTCAGGAAGATTATAGCCTTAG 275

QY 1097 TGAAGAACAGACAAGAACTCTCAGATGAGATGATGATATCAAGTTACTGTGTATCA 1156
DB 276 TGAAGAACAGACAAGAACTCTCAGATGAGATGATGATATCAAGTTACTGTGTATCA 335

QY 1157 GCGACGGGAGAGTGTACAGATTCATTTGAGAGAGATCCTGAATTTCTTACGCTGACTA 1216
DB 336 GCGACGGGAGAGTGTACAGATTCATTTGAGAGAGATCCTGAATTTCTTACGCTGACTA 395

QY 1217 TTGGAATGC 1226
DB 396 TTGGAATGC 405

RESULT 7
HSA278977 393 bp mRNA linear PRI 15-APR-2005
LOCUS Homo sapiens mRNA for p53-binding protein (MDM2 gene),
DEFINITION alternatively spliced variant PM2.
ACCESSION AJ278977
VERSION AJ278977.1 GI:10045130
KEYWORDS alternative splicing; mdm2 gene; p53-binding protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Bartel,F., Meye,A., Wurl,P., Kappler,M., Bache,M.,
Tautenschlaeger,C., Grunbaum,U., Schmidt,H. and Taubert,H.
TITLE Amplification of the MDM2 gene, but not expression of splice
variants of MDM2 mRNA, is associated with prognosis in soft tissue
sarcoma
JOURNAL Int. J. Cancer 95 (3), 168-175 (2001)
PUBMED 11307150
REFERENCE 2 (bases 1 to 393)
AUTHORS Bartel,F.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Bartel F., Institute for Pathology,
Halle, GERMANY
COMMENT Related sequences: AJ278975-AJ278978, AJ276888.
FEATURES
SOURCE location/Qualifiers
1..393
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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<1..>393
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/product="p53 binding protein"
/note="alternatively spliced variant PM2"
1..393
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/experiment="experimental evidence, no additional details
recorded"
/note="alternatively spliced variant PM2"
/codon_start=1
/product="p53 binding protein"

ORIGIN
Query Match 10.3%; Score 245; DB 5; Length 393;
Best Local Similarity 100.0%; Pred. No. 1e-126;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1543 TGAAGAGTTTGAAGAGGAAGAAACCCAGCAAGAGAGAGTGTGAATCTACTTGC 1602
DB 149 TGAAGAGTTTGAAGAGGAAGAAACCCAGCAAGAGAGTGTGAATCTACTTGC 208

QY 1603 CCCTTAATGCCATTGAACCTTGTGTGATTTGTCAAGTGCACCTAAATGGTGCATTG 1662
DB 209 CCCTTAATGCCATTGAACCTTGTGTGATTTGTCAAGTGCACCTAAATGGTGCATTG 268

QY 1663 TCATGCGAAGAACAGACATCTTATGCGCTGCTTACATGTGCAAGAGCTAAAGAAAA 1722
DB 269 TCATGCGAAGAACAGACATCTTATGCGCTGCTTACATGTGCAAGAGCTAAAGAAAA 328

QY 1723 GGAATAGCCCTGCCAGATGATGACCAACCAATTCAAATGATGTGCTAATTTC 1782
DB 329 GGAATAGCCCTGCCAGATGATGACCAACCAATTCAAATGATGTGCTAATTTC 388

QY 1783 CCTAG 1787
DB 389 CCTAG 393

RESULT 8
HSA491700 318 bp mRNA linear PRI 15-APR-2005
LOCUS Homo sapiens mRNA for p53-binding protein alternatively spliced
isoform l1_15 (MDM2 gene).
DEFINITION
ACCESSION AJ491700
VERSION AJ491700.1 GI:21628670
KEYWORDS alternative splicing; MDM2 gene; p53-binding protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Bartel,F., Pinkert,D., Kappler,M., Bache,M., Schmidt,H. and
Taubert,H.
TITLE Alternatively and aberrantly spliced transcripts of the MDM2 mRNA
occur frequently in human soft tissue sarcoma and in multiple
normal tissues
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 318)
AUTHORS Bartel,F.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2002) Bartel F., Institute for Pathology,
University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097
Halle, GERMANY
COMMENT
FEATURES
SOURCE location/Qualifiers
1..318
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="lung"
1..318
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1..318
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/note="alternatively spliced isoform l1_15
stop codon at bp 260-262 lost due to aberrant splicing"

JOURNAL Nat. Med. 2 (8), 912-917 (1996)
PUBMED 8705862
REFERENCE 2 (bases 1 to 309)
AUTHORS Lunec, J.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-1995) John Lunec, Cancer Research Unit,
University of Newcastle upon Tyne - Medical School, Framlington
Place, Newcastle upon Tyne, NE2 4HH, U.K.

FEATURES
SOURCE Location/Qualifiers
1..309
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
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/sex="female"
/tissue_type="primary ovarian tumor"
1..309
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1..309
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/db_xref="GI:992685"
/translation="MCNTNMSVPTDGAVTTSQIPASBOETLVRPKLLKLSVGAK
KDYTKMEVLFYLGQYIMTKRLYDEKQOHVNDGANLPPLVDLSIRELYISNYITLGI"

CDS
gene
1..309
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1..309
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/db_xref="GI:992685"
/translation="MCNTNMSVPTDGAVTTSQIPASBOETLVRPKLLKLSVGAK
KDYTKMEVLFYLGQYIMTKRLYDEKQOHVNDGANLPPLVDLSIRELYISNYITLGI"

ORIGIN
Query Match 9.5%; Score 225; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.5e-115;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 ATGTGCAATACCACTGTCTGTACTCTATGATGCTGTGACCACTCAAGATTCCA 371
Db 1 ATGTGCAATACCACTGTCTGTACTCTATGATGCTGTGACCACTCAAGATTCCA 60

Qy 372 GCTTCGAAACAAGAGACCCCTGGTTAGACCAAGCATTTGTAAGTTTAAAGTCT 431
Db 61 GCTTCGAAACAAGAGACCCCTGGTTAGACCAAGCATTTGTAAGTTTAAAGTCT 120

Qy 432 GTTGTGCACAAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGCCAGAT 491
Db 121 GTTGTGCACAAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGCCAGAT 180

Qy 492 ATTATGACTAAACGATTATATGATGAGAGCAACAACATATTGTA 536
Db 181 ATTATGACTAAACGATTATATGATGAGAGCAACAACATATTGTA 225

RESULT 12
HSA278978 297 bp mRNA linear PRI 30-MAY-2001
LOCUS HSA278978
DEFINITION Homo sapiens mRNA for p53-binding protein (MDM2 gene),
alternatively spliced variant EU2.
ACCESSION AJ278978
VERSION AJ278978.1 GI:10045132
KEYWORDS alternative splicing; mdm2 gene; p53-binding protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Bartel, F., Meye, A., Wurl, P., Kappler, M., Bachle, M.,
Lauteschläger, C., Grunbaum, U., Schmidt, H. and Taubert, H.
TITLE Amplification of the MDM2 gene, but not expression of splice
variants of MDM2 mRNA, is associated with prognosis in soft tissue
sarcoma

JOURNAL Int. J. Cancer 95 (3), 168-175 (2001)
PUBMED 11307150
REFERENCE 2 (bases 1 to 297)
AUTHORS Bartel, F.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Bartel, F., Institute for Pathology,
University of Halle, Faculty of Medicine, Magdeburger Str. 14, 06097
Halle, GERMANY

COMMENT Related sequences: AJ278975-AJ278978, AJ276888.

FEATURES
SOURCE Location/Qualifiers
1..297
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="thadomyosarcoma"
1..297
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1..297
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/product="p53 binding protein"
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1..297
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/experiment="experimental evidence, no additional details recorded"
/note="alternatively spliced variant EU2"
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/protein_id="CAC07812.1"
/db_xref="GI:10045133"
/db_xref="UniProtKB/TREMBL:Q9H4C2"
/translation="MCNTNMSVPTDGAVTTSQIPASBOETLVRPKLLKLSVGAK
KDYTKMEVLFYLGQYIMTKRLYDEKQOHVNDGANLPPLVDLSIRELYISNYITLGI"

CDS
mRNA
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1..297
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/product="p53 binding protein"
/note="alternatively spliced variant EU2"
1..297
/gene="MDM2"
/strand name="human homolog of mouse double minute 2"
/experiment="experimental evidence, no additional details recorded"
/note="alternatively spliced variant EU2"
/codon_start=1
/product="p53 binding protein"
/protein_id="CAC07812.1"
/db_xref="GI:10045133"
/db_xref="UniProtKB/TREMBL:Q9H4C2"
/translation="MCNTNMSVPTDGAVTTSQIPASBOETLVRPKLLKLSVGAK
KDYTKMEVLFYLGQYIMTKRLYDEKQOHVNDGANLPPLVDLSIRELYISNYITLGI"

ORIGIN
Query Match 9.4%; Score 222; DB 5; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1566 ACCCAAGCAAGAAGAGAGTGAATCTAGTTGCCCCCTTAATGCAATGAACCTTGT 1625
Db 76 ACCCAAGCAAGAAGAGAGTGAATCTAGTTGCCCCCTTAATGCAATGAACCTTGT 135

Qy 1626 GTGATTGTCAAGTGCACCTTAATAATGTTGCATTGTCATGCAAAACAGACATCTT 1685
Db 136 GTGATTGTCAAGTGCACCTTAATAATGTTGCATTGTCATGCAAAACAGACATCTT 195

Qy 1686 ATGGCTGCTTTACATGTGCAAGAGCTTAAGAAAGAAAGAAAGCCCTGCCAGTATGT 1745
Db 196 ATGGCTGCTTTACATGTGCAAGAGCTTAAGAAAGAAAGAAAGCCCTGCCAGTATGT 255

Qy 1746 AGACAACCAATTCGAATGTTGCTACTATTTCCCTTGG 1787
Db 256 AGACAACCAATTCGAATGTTGCTACTATTTCCCTTGG 297

RESULT 13
HSA550516 297 bp mRNA linear PRI 19-MAR-2003
LOCUS HSA550516
DEFINITION Homo sapiens mRNA for HDM2-HD1 protein (HDM2 gene).
ACCESSION AJ550516
VERSION AJ550516.1 GI:29125740
KEYWORDS alternative splicing; HDM2 gene; HDM2-HD1 protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Sturzenhecker, B., Schlotz, T., Quentlin, T., Kube, D., Jung, W. and
Trumper, L.
TITLE Abundant expression of spliced HDM2 in Hodgkin Lymphoma cells does

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

not interfere with p14ARF and p53 binding
Unpublished
2 (bases 1 to 297)
Sturzenhocker B.
Direct Submission
Submitted (18-MAR-2003) Sturzenhocker B., Hematology/Oncology,
University of Goettingen, Robert-Koch-Str. 40, Goettingen, 37075,
GERMANY

FEATURES
source

location/Qualifiers
1..297
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="12"
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/cell_line="KM-H2"
/note="Hodgkin-derived human cell line"
1..297
/gene="HDM2"
1..297
/function="oncogene"
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/protein_id="CAD79455.1"
/db_xref="GI:29125741"
/translation="MCNTNMSVPTDGAVTTSQIPASPOETDKESEVSSLPUNAIP
CVICGRPKNGCI VHKTGHLMACFTCAKLKKKKPCVPRQPIQIMIVLTFPP"

ORIGIN

Query Match 9.4%; Score 222; DB 5; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAAGCAAGAGAGAGAGTGAATCTAGTTGCCCTTATGCAATGAACTTGT 1625
Db 76 ACCCAAGCAAGAGAGAGTGAATCTAGTTGCCCTTATGCAATGAACTTGT 135
QY 1626 GTGATTGTCAAGGTGCAAGCTTAATAATGTTGCAATGCGCAAAACAGACATCTT 1685
Db 136 GTGATTGTCAAGGTGCAAGCTTAATAATGTTGCAATGCGCAAAACAGACATCTT 195
QY 1686 ATGGCTGCTTACATGTGCAAGAGCTTAAGAAAGAAAGAAATAGCCCTGCCAGTATGT 1745
Db 196 ATGGCTGCTTACATGTGCAAGAGCTTAAGAAAGAAAGAAATAGCCCTGCCAGTATGT 255
QY 1746 AGAACAACCAATTCAGATGTTGCTAATCTATTTCCTTAG 1787
Db 256 AGAACAACCAATTCAGATGTTGCTAATCTATTTCCTTAG 297

RESULT 14

LOCUS G66929 209 bp DNA linear STS 24-AUG-2000
DEFINITION csmipm2-pcr7-1 Human Homo sapiens STS genomic, sequence tagged
ACCESSION G66929
VERSION G66929.1 GI:9909460
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 209)
Wong, G.K.S., Yu, J., Yang, Z., Passey, D., Kibukawa, M., Paddock, M. and
Olson, M.
Gene based polymorphism discovery
Unpublished (2000)
TITLE JOURNAL
AUTHORS
COMMENT Contact: Gene Ka-Shu Wong
Genome Center
University of Washington

Fluke Hall, Box 352145, Seattle, WA 98195, USA
Tel: 206/685-7348
Fax: 206/685-7344
Email: gks@u.washington.edu
Primer A: ATGGCTGCTTACATGTGTC
Primer B: TGAAATGAGCAATTTCTTAC
STS size: 209
PCR Profile:
Presoak: 92 degrees C for 1.00 minute
Denaturation: 92 degrees C for 0.16 minute
Annealing: 60-65 degrees C for 0.50 minute
Polymerization: 72 degrees C for 1.00 minute
PCR Cycles: 35
Thermal Cycler: Perkin Elmer TC
Protocol:

Template: 7 ng
Primer: each 0.5 uM
dNTPs: each 100 uM
Taq Polymerase: 0.025 units/uL
Total Vol: 10 uL

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3.
Location/Qualifiers
1..209
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="12q14.3-q15"
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1..209
/gene="MDM2"
1..209
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1..20
complement(189..209)

ORIGIN
primer_bind
complement(189..209)

Query Match 8.8%; Score 209; DB 7; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.3e-106;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 ATGGCTGCTTACATGTGCAAGAGCTTAAGAAAGAAAGAAATAGCCCTGCCAGTATGT 1745
Db 1 ATGGCTGCTTACATGTGCAAGAGCTTAAGAAAGAAAGAAATAGCCCTGCCAGTATGT 60
QY 1746 AGAACAACCAATTCAGATGTTGCTAATCTATTTCCTTAGTGAACCTGCTATAAGAG 1805
Db 61 AGAACAACCAATTCAGATGTTGCTAATCTATTTCCTTAGTGAACCTGCTATAAGAG 120
QY 1806 AATTATATATTTCTAATCTATAATAACCTAGCAATTTGACAACTGAAATTTATTCACAT 1865
Db 121 AATTATATATTTCTAATCTATAATAACCTAGCAATTTGACAACTGAAATTTATTCACAT 180
QY 1866 ATATCAAGTGAGAAATAGCCTCAATCA 1894
Db 181 ATATCAAGTGAGAAATAGCCTCAATCA 209

RESULT 15

LOCUS HSAS50518 210 bp mRNA linear PRI 15-APR-2005
DEFINITION Homo sapiens mRNA for HDM2-HD3 protein (HDM2 gene).
ACCESSION AJ550518
VERSION AJ550518.1 GI:29125744
KEYWORDS alternative splicing; HDM2 gene; HDM2-HD3 protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1
AUTHORS Sturzenhocker, B., Schlotz, T., Quentin, T., Kube, D., Jung, W. and Trumper, L.
TITLE Abundant expression of spliced HDM2 in Hodgkin Lymphoma cells does not interfere with p14ARF and p53 binding
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 210)
AUTHORS Sturzenhocker, B.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) Sturzenhocker B., Hematology/Oncology, University of Goettingen, Robert-Koch-Str. 40, Goettingen, 37075, GERMANY

FEATURES
source
1..210
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
/map="12q14.3-q15"
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/note="Hodgkin-derived human cell line"
1..210
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1..210
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/db_xref="GOA:O86WA4"
/db_xref="InterPro:IPR003121"
/db_xref="UniProtKB/TrEMBL:O86WA4"
/translation="MCNTNMSVPTDGAATTSQIPASEQETLVRPKPLLLKLLKSVGAQ KDVTYMKREVLPLYGLGYISNYITLGI"

ORIGIN
Query Match 7.7%; Score 183; DB 5; Length 210;
Best Local Similarity 100.0%; Pred. No. 2.1e-91;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS HS4550519 213 bp mRNA linear PRI 15-APR-2005
DEFINITION Homo sapiens mRNA for HDM2-HD5 protein (HDM2 gene).
ACCESSION AJ550519
VERSION AJ550519.1 GI:29125746
KEYWORDS alternative splicing; HDM2 gene; HDM2-HD5 protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Sturzenhocker, B., Schlotz, T., Quentin, T., Kube, D., Jung, W. and

TITLE Trumper, L.
JOURNAL Abundant expression of spliced HDM2 in Hodgkin Lymphoma cells does not interfere with p14ARF and p53 binding
REFERENCE 2 (bases 1 to 213)
AUTHORS Sturzenhocker, B.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) Sturzenhocker B., Hematology/Oncology, University of Goettingen, Robert-Koch-Str. 40, Goettingen, 37075, GERMANY

FEATURES
source
1..213
/organism="Homo sapiens"
/mol_type="mRNA"
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/chromosome="12"
/map="12q14.3-q15"
/cell_line="LA236"
/note="Hodgkin-derived human cell line"
1..213
/gene="HDM2"
1..213
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/translation="MCNTNMSVPTDGAATTSQIPASEQETLVRPKPLLLKLLKSVGAQ KDVTYMKREVLPLYGLLYMCKEAKKE"

ORIGIN
Query Match 7.4%; Score 175; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 7.3e-87;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS AF385324 224 bp mRNA linear PRI 11-OCT-2001
DEFINITION Homo sapiens MDW2 variant FB28 (MDW2) mRNA, complete cds, alternatively spliced.
ACCESSION AF385324
VERSION AF385324.1 GI:16033444
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 224)
AUTHORS Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.
TITLE Novel mdm2 splice variants identified in pediatric rhabdomyosarcoma tumors and cell lines
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 224)
AUTHORS Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.
TITLE Direct Submission

JOURNAL Submitted (24-MAY-2001) Molecular Pharmacology, St. Jude Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38105, USA

FEATURES

source

Location/Qualifiers

1..224

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="rhabdomyosarcoma tumor"

1..224

/gene="MDM2"

1..201

/note="MDM2"

/note="alternatively spliced"

/codon_start=1

/product="MDM2 variant FB28"

/protein_id="AA13244.1"

/db_xref="GI:16033445"

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KDYTMKEVLFYLAQYVDNPK"

ORIGIN

Query Match 7.3%; Score 172; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.7e-85; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 0;

QY 312 ATGTGCAATACCAACATGTCTGTACCTAAGTGTGCTGTACCACTCAAGATTCCA 371
DB 1 ATGTGCAATACCAACATGTCTGTACCTAAGTGTGCTGTACCACTCAAGATTCCA 60
QY 372 GCTTGGACAAGACAGCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 431
DB 61 GCTTCGGAACAAGACAGCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 120
QY 432 GTTGTGCAACAAAGACACTTATCTATGAAGAGTCTTTTATCTTG 483
DB 121 GTTGTGCAACAAAGACACTTATCTATGAAGAGTCTTTTATCTTG 172

RESULT 18

AF385326

LOCUS Homo sapiens MDM2 variant FB30 (MDM2) mRNA, complete cds, 288 bp mRNA linear PRI 11-OCT-2001

DEFINITION AF385326

ACCESSION AF385326

VERSION AF385326.1 GI:16033450

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 288)

Bartel,F., Taylor,A.C., Taubert,H. and Harris,L.C.

Novel mdm2 splice variants identified in pediatric rhabdomyosarcoma

tumors and cell lines

Unpublished

2 (bases 1 to 288)

Bartel,F., Taylor,A.C., Taubert,H. and Harris,L.C.

Direct Submission

Submitted (24-MAY-2001) Molecular Pharmacology, St. Jude Children's

Research Hospital, 332 N. Lauderdale, Memphis, TN 38105, USA

JOURNAL

AUTHORS

TITLE

FEATURES

source

1..288

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="rhabdomyosarcoma tumor"

/note="Same sequence isolated from rhabdomyosarcoma cell

line"

1..288

/gene="MDM2"

1..288

/gene="MDM2"

/note="alternatively spliced"
/codon_start=1
/product="MDM2 variant FB30"
/protein_id="AA13244.1"
/db_xref="GI:16033445"
/translation="MCTNINMSVPTDGAVTTSQIPASQETLVRRPKLLIKLKSVAQ
KDYTMKEVLFYKTGHLMACTCAKKLKRKNRCPVCRPIQIVITLTPP"

ORIGIN

Query Match 7.1%; Score 168; DB 5; Length 288;
Best Local Similarity 100.0%; Pred. No. 6.6e-83; Indels 0; Gaps 0;
Matches 168; Conservative 0; Mismatches 0;

QY 312 ATGTGCAATACCAACATGTCTGTACCTAAGTGTGCTGTACCACTCAAGATTCCA 371
DB 1 ATGTGCAATACCAACATGTCTGTACCTAAGTGTGCTGTACCACTCAAGATTCCA 60
QY 372 GCTTGGACAAGACAGCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 431
DB 61 GCTTCGGAACAAGACAGCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 120
QY 432 GTTGTGCAACAAAGACACTTATCTATGAAGAGTCTTTTATCTTG 479
DB 121 GTTGTGCAACAAAGACACTTATCTATGAAGAGTCTTTTATCTTG 168

RESULT 19

AX587650

LOCUS AX587650 319 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 120 from Patent WO0246467.

ACCESSION AX587650

VERSION AX587650.1 GI:27656423

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE

1 Bertucci,F., Houlgate,R., Birnbaum,D., Nguyen,C., Viens,P. and

Pert,V.

Gene expression profiling of primary breast carcinomas using arrays

of candidate genes

Patent: WO 0246467-A 120 13-JUN-2002;

Ipsogen (FR)

JOURNAL

FEATURES

source

1..319

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="primer"

1..319

/note="5' terminal sequence. mouse double minute 2, human

homolog of; p53-binding protein (MDM2) gene."

misc_feature

ORIGIN

Query Match 7.0%; Score 167; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 2.4e-82; Indels 0; Gaps 0;
Matches 167; Conservative 0; Mismatches 0;

QY 1773 ACTTATTTCCCTGTTGACCTGCTATAGAGAAATATATATTTCTTACATTAACCC 1832
DB 2 ACTTATTTCCCTGTTGACCTGCTATAGAGAAATATATATTTCTTACATTAACCC 61
QY 1833 TAGGAATTTGACAAAGCTGAATTTATTCATATATCAAGTGAAGAAATGCTCAATT 1892
DB 62 TAGGAATTTGACAAAGCTGAATTTATTCATATATCAAGTGAAGAAATGCTCAATT 121
QY 1893 CACATAGATTTCTTCTTTAGTAATTAATGACCTACTTGGTAGTG 1939
DB 122 CACATAGATTTCTTCTTTAGTAATTAATGACCTACTTGGTAGTG 168

RESULT 20

HSA276888

LOCUS HSA276888 364 bp mRNA linear PRI 30-MAY-2001
 DEFINITION Homo sapiens non-productive mRNA for p53-binding protein,
 alternatively spliced variant DS2 (MDM2 gene).
 ACCESSION AJ276888
 VERSION AJ276888.1 GI:7327962
 KEYWORDS alternative splicing; DS2; mdm2 gene; p53-binding.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE
 AUTHORS Bartel,F., Meyer,A., Wurl,P., Kappler,M., Bache,M.,
 Latenschlaeger,C., Grunbaum,U., Schmidt,H. and Taubert,H.
 TITLE Amplification of the MDM2 gene, but not expression of splice
 variants of MDM2 mRNA, is associated with prognosis in soft tissue
 sarcoma
 JOURNAL Int. J. Cancer 95 (3), 168-175 (2001)
 PUBMED 11307150
 REFERENCE 2 (bases 1 to 364)
 AUTHORS Bartel,F.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAR-2000) Bartel F., Institute for Pathology,
 University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097
 Halle, GERMANY

FEATURES
 source
 1..364
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 1..364
 /gene="MDM2"
 /pseudo
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 /gene="MDM2"
 /note="alternatively spliced isoform DS2"
 /pseudo
 1..364
 /gene="MDM2"
 /standard_name="human homolog of mouse double minute 2"
 /note="alternatively spliced isoform DS2"
 /pseudo
 /codon_start=1
 /product="p53-binding protein"

ORIGIN
 Query Match 6.6%; Score 157; DB 5; Length 364;
 Best Local Similarity 100.0%; Pred. No. 1.1e-76;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTCTGTACTCTAGTGTGCTGTACACCACTCAGATTCCA 371
 Db 1 ATGTGCAATACCAACATGTCTGTACTCTAGTGTGCTGTACACCACTCAGATTCCA 60

QY 372 GCTTCGGAACAAGAGACCTGCTTAGACCAAGCCATTGCTTTGAAGTTAAGTCT 431
 Db 61 GCTTCGGAACAAGAGACCTGCTTAGACCAAGCCATTGCTTTGAAGTTAAGTCT 120

QY 432 GTTGGTGCACAAAAAGACCTTATCTATCTAAGAAGAG 468
 Db 121 GTTGGTGCACAAAAAGACCTTATCTATCTAAGAAGAG 157

RESULT 21
 LOCUS HSA50517 198 bp mRNA linear PRI 15-APR-2005
 DEFINITION Homo sapiens mRNA for HDM2-HD2 protein (HDM2 gene).
 ACCESSION AJ505017
 VERSION AJ505017.1 GI:29125742
 KEYWORDS alternative splicing; HDM2 gene; HDM2-HD2 protein.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE
 AUTHORS Sturzenhockeier,B., Schlott,T., Quentin,T., Kube,D., Jung,W. and
 Trumper,L.
 TITLE Abundant expression of spliced HDM2 in Hodgkin Lymphoma cells does
 not interfere with p14ARF and p53 binding
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 198)
 AUTHORS Sturzenhockeier,B.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAR-2003) Sturzenhockeier B., Hematology/Oncology,
 University of Goettingen, Robert-Koch-Str. 40, Goettingen, 37075,
 GERMANY

FEATURES
 source
 1..198
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="12"
 /map="12q14.3-q15"
 /cell_line="KM-H2"
 /note="Hodgkin-derived human cell line"
 1..198
 /gene="HDM2"
 1..198
 /gene="HDM2"
 /function="oncogene"
 /codon_start=1
 /product="HDM2-HD2 protein"
 /protein_id="CAD79456.1"
 /db_xref="GI:29125743"
 /db_xref="UniProtKB/TrEMBL:O86N45"
 /translation="MCNTNMSVPTDGAATTSQIPASEQETLVRPKLLIKLKSVAQ
 KDTYTKRHHIYQSEKMPQFT"

ORIGIN
 Query Match 6.5%; Score 153; DB 5; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.4e-74;
 Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTCTGTACTCTAGTGTGCTGTACACCACTCAGATTCCA 371
 Db 1 ATGTGCAATACCAACATGTCTGTACTCTAGTGTGCTGTACACCACTCAGATTCCA 60

QY 372 GCTTCGGAACAAGAGACCTGCTTAGACCAAGCCATTGCTTTGAAGTTAAGTCT 431
 Db 61 GCTTCGGAACAAGAGACCTGCTTAGACCAAGCCATTGCTTTGAAGTTAAGTCT 120

QY 432 GTTGGTGCACAAAAAGACCTTATCTATCTAAGAAG 464
 Db 121 GTTGGTGCACAAAAAGACCTTATCTATCTAAGAAG 153

RESULT 22
 LOCUS AR229721 199 bp RNA linear PAT 20-DEC-2002
 DEFINITION Sequence 1 from patent US 6451524.
 ACCESSION AR229721
 VERSION AR229721.1 GI:27269545
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 199)
 AUTHORS Ecker,D.J.
 TITLE Identification of disease predictive nucleic acids
 JOURNAL Patent: US 6451524-A 1 17-SEP-2002;
 ISIS Pharmaceuticals, Inc.; Carlsbad, CA
 FEATURES
 source
 1..199
 /organism="unknown"
 /mol_type="unassigned RNA"

ORIGIN

Query Match 6.2%; Score 148; DB 2; Length 199;
Best Local Similarity 99.5%; Pred. No. 1.7e-71;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 244 GAAACTGGGAGCTTTGAGGAGACCCCGACTCCAGCCGAAAAACCCCGATGGTGAAGA 303
Db 1 GAAACTGGGAGCTTTGAGGAGACCCCGACTCCAGCCGAAAAACCCCGATGGTGAAGA 60

QY 304 GCAGGCAAAATGTGCAATTCACAATGTGTGTACCTACTGATGGTGTCTTAACCACTTAC 363
Db 61 GCAGGCAAAATGTGCAATTCACAATGTGTGTACCTACTGATGGTGTCTTAACCACTTAC 120

QY 364 AGATTCCAGCTTCGGAACAAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAT 423
Db 121 AGATTCCAGCTTCGGAACAAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAT 180

QY 424 TAAAGTCTGTTGTGCACA 442
Db 181 TAAAGTCTGTTGTGCACA 199

RESULT 23
HSA491701 153 bp mRNA linear PRI 27-JUN-2002
LOCUS Homo sapiens mRNA for p53-binding protein alternatively spliced
DEFINITION isoform SP56 (MDM2 gene).
ACCESSION AJ491701
VERSION AJ491701.1 GI:21628672
KEYWORDS alternative splicing; MDM2 gene; p53-binding protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Bartel,F., Pinkert,D., Kappler,M., Bache,M., Schmidt,H. and
Tauber,H.
Alternatively and aberrantly spliced transcripts of the MDM2 mRNA
occur frequently in human soft tissue sarcoma and in multiple
normal tissues
Unpublished
2 (bases 1 to 153)
Bartel,F.
Direct Submission
Submitted (25-JUN-2002) Bartel F., Institute for Pathology,
University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097
Halle, GERMANY
FEATURES
source Location/Qualifiers
1..153
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="lymphocyte"
1..153
/gene="MDM2"
1..153
/gene="MDM2"
/note="alternatively spliced isoform SP56"
/codon_start=1
/product="p53-binding protein"
/protein_id="CAD36962.1"
/db_xref="GI:21628672"
/db_xref="UniProtKB/TrEMBL:O8NDV9"
/translation="MCNTNMGVPTDGAVTTSQIPASEQETLVRPKPLIKLKSVAQ
KDTYFP"

ORIGIN

Query Match 6.1%; Score 144; DB 5; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.3e-69;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTCTGTACTACTGATGTGTCTGTAAACCACTCAAGATTCCA 371
Db 1 ATGTGCAATACCAACATGTCTGTACTACTGATGTGTCTGTAAACCACTCAAGATTCCA 60

QY 372 GCTTCGGACAAGAGACCCCTGTTAGACCAAAAGCCATTGCTTTGAAGTTATTAAGTCT 431
Db 61 GCTTCGGACAAGAGACCCCTGTTAGACCAAAAGCCATTGCTTTGAAGTTATTAAGTCT 120

QY 432 GTTGATGACAAAAGACACTTAT 455
Db 121 GTTGATGACAAAAGACACTTAT 144

RESULT 24
BV206635/c 201 bp DNA linear STS 10-JUN-2004
LOCUS sqgm221450 Human DNA (Sequenc) Homo sapiens STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV206635
VERSION BV206635.1 GI:48176880
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 201)
Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
Genome Res. (2004) In press
JOURNAL COMMENT
AUTHORS
REFERENCE
TITLE
CONTACT: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 201.
FEATURES
source Location/Qualifiers
1..201
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_id="Human DNA (Sequenc)"
<1..>201

ORIGIN

Query Match 6.0%; Score 142; DB 7; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.3e-68;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 234 CCCCGTGAAGAACTGGGGAGTCTTGAAGGACCCCGGACTCCAGCGCGAAACCCCGG 293
Db 193 CCCCGTGAAGAACTGGGGAGTCTTGAAGGACCCCGGACTCCAGCGCGAAACCCCGG 134

QY 294 ATGGTGAAGAGCAGAGCAAAATGTGCAATACCAACATGTCTGTACTACTGATGTGTCTGA 353
Db 133 ATGGTGAAGAGCAGAGCAAAATGTGCAATACCAACATGTCTGTACTACTGATGTGTCTGA 74

QY 354 ACCACCTCAGATTCAGAGCTTCGGAAACAAGAGACCTGTGTTAGACCAAGCCATTGCTT 413
Db 73 ACCACCTCAGATTCAGAGCTTCGGAAACAAGAGACCTGTGTTAGACCAAGCCATTGCTT 14

QY 414 TTGAAGTTATTA 426
Db 13 TTGAAGTTATTA 1

RESULT 25
AR229722 199 bp RNA linear PAT 20-DEC-2002
LOCUS AR229722
DEFINITION Sequence 2 from patent US 6451524.
ACCESSION AR229722
VERSION AR229722.1 GI:27269546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Ecker, D.J.
TITLE Identification of disease predictive nucleic acids
JOURNAL Patent: US 6451524-A 2 17-SEP-2002;
ISTIS Pharmaceuticals, Inc.; Calisbad, CA
FEATURES
SOURCE
1. .199
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN
Query Match 5.8%; Score 138; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 8.2e-66;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 305 CAGGAATGTCATACCAATGCTGTACTGTGTGCTGTACCACTCACA 364
DB 62 CAGGCAATGTCATACCAATGCTGTACTGTGTGCTGTACCACTCACA 121
QY 365 GATTCACGCTTGGAAACAAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATT 424
DB 122 GATTCACGCTTGGAAACAAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATT 181
QY 425 AAAGTCGTGGTGACCA 442
DB 182 AAAGTCGTGGTGACCA 199
RESULT 26
HSAS50520 165 bp mRNA linear PRI 19-MAR-2003
LOCUS HSAS50520
DEFINITION Homo sapiens mRNA for HDM2-HD4 protein (HDM2 gene).
ACCESSION AJ550520
VERSION AJ550520.1 GI:29125748
KEYWORDS alternative splicing; HDM2 gene; HDM2-HD4 protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Stutzenhofer, B., Schlott, T., Quentin, T., Kube, D., Jung, W. and
Trummer, L.
TITLE Abundant expression of spliced HDM2 in Hodgkin Lymphoma cells does
not interfere with p14ARF and p53 binding
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165)
AUTHORS Stutzenhofer, B.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) Stutzenhofer, B., Hematology/Oncology,
University of Goettingen, Robert-Koch-Str. 40, Goettingen, 37075,
GERMANY
FEATURES
SOURCE
1. .165
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
/map="12q14.3-q15"
/cell_line="HDM2"
/note="Hodgkin-derived human cell line"
1. .165
/gene="HDM2"
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CDS
1. .165
/gene="HDM2"
/function="oncogene"
/codon_start=1
/product="HDM2-HD4 protein"
/protein_id="CAD79459.1"
/db_xref="GI:29125749"
/translation="MCNTNMSVPPDGAATTSQIPASBOETLVPRPLKLKLSIREL
YISNTITLGI"
ORIGIN
Query Match 5.1%; Score 120; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-55;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 312 ATGTGCAATACCAATGCTGTACTGTATGATGCTGTAAACCACTCAGATTCCA 371
DB 1 ATGTGCAATACCAATGCTGTACTGTATGATGCTGTAAACCACTCAGATTCCA 60
QY 372 GCTTGGAAACAAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTAAGTCT 431
DB 61 GCTTGGAAACAAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTAAGTCT 120
RESULT 27
BV193037 401 bp DNA linear STS 10-JUN-2004
LOCUS BV193037
DEFINITION sqm176519 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
tagged site.
ACCESSION BV193037
VERSION BV193037.1 GI:48035762
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Nelson, R.M., Marnellios, G., Kammerer, S., Hoyaj, C.R., Shi, M.M.,
Cantor, C.R. and Braun, A.
TITLE Large-scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL Genome Res. (2004) In press
COMMENT
Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 401.
Location/Qualifiers
1. .401
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human DNA (Sequenom)"
<1. .>401
ORIGIN
Query Match 3.7%; Score 88; DB 7; Length 401;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTACCGTGTGTAGCAGATGCTGCATCTCTGACCTGTCGATCGCCACCTC 2333
DB 289 GGGTTTACCGTGTGTAGCAGATGCTGCATCTCTGACCTGTCGATCGCCACCTC 348
QY 2334 GGGCTCCCAAGTGTGGATTACAGCC 2361
|||||

Db 349 GGCCCTCCCAAGTCTGGATTACAGGC 376

RESULT 28

AX981948/c 397 bp DNA linear PAT 15-JAN-2004

LOCUS Sequence 12751 from Patent EP1104808.

ACCESSION AX981948

VERSION AX981948.1 GI:40988088

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.

TITLE ESts and encoded human proteins

JOURNAL Patent: EP 1104808-A 12751 06-JUN-2001; Genset (FR)

FEATURES

source Location/Qualifiers

1..397

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 3.3%; Score 78; DB 2; Length 397;

Best Local Similarity 100.0%; Pred. No. 9.7e-32;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2284 GTGTTAGCCAGAGTGTCTGATCTCCTGACCTGTCGATCCGCCACCTGGCCTCCCA 2343

Db 210 GTGTTAGCCAGAGTGTCTGATCTCCTGACCTGTCGATCCGCCACCTGGCCTCCCA 151

Qy 2344 AGTCTGGGATTACAGGC 2361

Db 150 AGTCTGGGATTACAGGC 133

RESULT 29

BD116807/c 397 bp DNA linear PAT 18-SEP-2002

LOCUS ESt and encoded human protein.

DEFINITION BD116807

ACCESSION BD116807.1 GI:23211711

VERSION JP 2002010789-A/8884.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 397)

AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

TITLE ESt and encoded human protein

JOURNAL Patent: JP 2002010789-A 8884 15-JAN-2002; Genset CORP

COMMENT

OS Homo sapiens (human)

PN JP 2002010789-A/8884

PD 15-JAN-2002

PF 07-AUG-2000 JP 2000280989

PI 05-AUG-1999 US 60/147499

PI JEAN BABUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI GIORDANO

PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC C12N1/21,

PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC C12N15/00

CC n=a, g, c or t Location/Qualifiers

PH key misc_feature 250.

FT misc_feature 250.

FEATURES

source Location/Qualifiers

1..397

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 3.3%; Score 78; DB 2; Length 397;

Best Local Similarity 100.0%; Pred. No. 9.7e-32;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2284 GTGTTAGCCAGAGTGTCTGATCTCCTGACCTGTCGATCCGCCACCTGGCCTCCCA 2343

Db 210 GTGTTAGCCAGAGTGTCTGATCTCCTGACCTGTCGATCCGCCACCTGGCCTCCCA 151

Qy 2344 AGTCTGGGATTACAGGC 2361

Db 150 AGTCTGGGATTACAGGC 133

RESULT 30

AR421254/c 397 bp DNA linear PAT 18-DEC-2003

LOCUS Sequence 12751 from patent US 6639063.

ACCESSION AR421254

VERSION AR421254.1 GI:40176364

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 397)

AUTHORS Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.

TITLE ESt's and encoded human proteins

JOURNAL Patent: US 6639063-A 12751 28-OCT-2003; Genset S.A.;; WOX;

FEATURES

source Location/Qualifiers

1..397

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 3.3%; Score 78; DB 2; Length 397;

Best Local Similarity 100.0%; Pred. No. 9.7e-32;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2284 GTGTTAGCCAGAGTGTCTGATCTCCTGACCTGTCGATCCGCCACCTGGCCTCCCA 2343

Db 210 GTGTTAGCCAGAGTGTCTGATCTCCTGACCTGTCGATCCGCCACCTGGCCTCCCA 151

Qy 2344 AGTCTGGGATTACAGGC 2361

Db 150 AGTCTGGGATTACAGGC 133

RESULT 31

AB140799/c 427 bp DNA linear STS 27-OCT-2005

LOCUS Homo sapiens DNA, STS on chromosome 11, D11S04061, sequence tagged site.

DEFINITION AB140799

ACCESSION AB140799

VERSION AB140799.1 GI:62161617

KEYWORDS STS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Taniya, G., Shinya, M., Imanishi, T., Ikuta, T., Makino, S., Okamoto, K., Furugaki, K., Matsunoto, T., Mano, S., Ando, S., Nozaki, Y., Yukawa, W., Nakashige, R., Yamaguchi, D., Ishibashi, H., Yonekura, M., Nakami, Y., Takayama, S., Endo, T., Saruwatari, T., Tsgura, M., Yoshikawa, Y., Fujimoto, K., Oka, A., Chiku, S., Iinsen, S.E., Giphart, M.J., Kulski, J.K., Fukazawa, T., Hashimoto, H., Kimura, M., Hoshina, Y.,

Suzuki, Y., Hotta, T., Mochida, J., Minezaki, T., Komai, K., Shiozawa, S., Taniguchi, A., Yamanaka, H., Kametani, N., Gojobori, T., Bahram, S. and Inoko, H.
Whole genome association study of rheumatoid arthritis using 27 039 microsatellites
Hum. Mol. Genet. 14 (16), 2305-2321 (2005)

JOURNAL PUBMED 16000323
REFERENCE 2 (bases 1 to 427)
AUTHORS Tamaya, G., Makino, S., Fujimoto, K., Oka, A., Hayashi, H., Denda, A., Linsen, S.E., Ikuta, T., Shinya, M., Endo, T., Tomizawa, M., Tokubo, E., Sato, R., Takaki, A., Nagatsuka, Y., Watanabe, H., Adachi, S., Makino, Y., Nakano, S., Yamamoto, A., Yoshida, K., Okamoto, K., Yamaguchi, D., Ishibashi, H., Yonekura, M., Takayama, S., Nakami, Y., Saruwatari, T., Brand, A., van Hiltten, J.A., van de Watering, L.M., Giphart, M.J., Bahram, S., Kulski, Y.J. and Inoko, H.
Direct Submission
Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of Medicine, Department of Genetic Information, Bohseidai, Isehara, Kanagawa, 259-1193, Japan (E-mail:hinoko@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)
Polymorphisms were confirmed by comparing with the pooled DNA typing data of 88 Dutch population or 100 Australian. When there was no significant difference between the Japanese and these Caucasians, individual typing was performed to confirm polymorphisms.

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="11"
/map="11q13.2"
/note="pooled DNA of 100 Japanese unrelated individuals sequence tagged site D11S04061"
1..22
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/PCR_conditions="denaturation 96degC 5 min, 57degC 1 min, 72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec, 72degC 1 min"
360..406
/note="sequence tagged site D11S04061"
/rpt_type=tandem
/rpt_unit_seg="aat"
complement(403..427)
/note="3' primer: CACACTCAGCTAATGTTTAACTTAT"

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Best Local Similarity 100.0%; Pred. No. 3.5e-31;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAA 2344
|||||
DB 173 TGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAA 114
|||||

QY 2345 GTGCTGGATTACAGGC 2361
|||||
DB 113 GTGCTGGATTACAGGC 97
|||||

RESULT 32
ABI52167
LOCUS Homo sapiens DNA, STS on chromosome 10, D10S09061, sequence tagged site.
ACCESSION ABI52167
VERSION ABI52167.1 GI:62172985
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Tamaya, G., Shinya, M., Imanishi, T., Ikuta, T., Makino, S., Okamoto, K., Furugaki, K., Matsumoto, T., Mano, S., Ando, S., Nozaki, Y., Yukawa, W., Nakashige, R., Yamaguchi, D., Ishibashi, H., Yonekura, M., Nakami, Y., Takayama, S., Endo, T., Saruwatari, T., Yaegira, M., Yoshikawa, Y., Fujimoto, K., Oka, A., Chiku, S., Linsen, S.E., Giphart, M.J., Kulski, J.K., Fukazawa, T., Hashimoto, H., Kimura, M., Hoshina, Y., Suzuki, Y., Hotta, T., Mochida, J., Minezaki, T., Komai, K., Shiozawa, S., Taniguchi, A., Yamanaka, H., Kametani, N., Gojobori, T., Bahram, S. and Inoko, H.
Whole genome association study of rheumatoid arthritis using 27 039 microsatellites
Hum. Mol. Genet. 14 (16), 2305-2321 (2005)

JOURNAL PUBMED 16000323
REFERENCE 2 (bases 1 to 440)
AUTHORS Tamaya, G., Makino, S., Fujimoto, K., Oka, A., Hayashi, H., Denda, A., Linsen, S.E., Ikuta, T., Shinya, M., Endo, T., Tomizawa, M., Tokubo, E., Sato, R., Takaki, A., Nagatsuka, Y., Watanabe, H., Adachi, S., Makino, Y., Nakano, S., Yamamoto, A., Yoshida, K., Okamoto, K., Yamaguchi, D., Ishibashi, H., Yonekura, M., Takayama, S., Nakami, Y., Saruwatari, T., Brand, A., van Hiltten, J.A., van de Watering, L.M., Giphart, M.J., Bahram, S., Kulski, Y.J. and Inoko, H.
Direct Submission
Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of Medicine, Department of Genetic Information, Bohseidai, Isehara, Kanagawa, 259-1193, Japan (E-mail:hinoko@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)
Polymorphisms were confirmed by comparing with the pooled DNA typing data of 88 Dutch population or 100 Australian. When there was no significant difference between the Japanese and these Caucasians, individual typing was performed to confirm polymorphisms.

FEATURES
source location/Qualifiers
1..440
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q21.1"
/note="pooled DNA of 100 Japanese unrelated individuals sequence tagged site D10S09061"
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/PCR_conditions="denaturation 96degC 5 min, 57degC 1 min, 72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec, 72degC 1 min"
88..126
/note="sequence tagged site D10S09061"
/rpt_type=tandem
/rpt_unit_seg="tttg"
complement(420..440)
/note="3' primer: CTCACGCTCTGTAAGTAG"

ORIGIN
primer_bind
Query Match 3.2%; Score 77; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.5e-31;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAA 2344
|||||
DB 314 TGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAA 373
|||||

QY 2345 GTGCTGGATTACAGGC 2361
|||||
DB 374 GTGCTGGATTACAGGC 390
|||||

RESULT 33
HS2ALU385/c
LOCUS HS2ALU385
DEFINITION H.sapiens DNA for Mhc Alu elements.
ACCESSION Z30959
VERSION Z30959.1 GI:461305

KEYWORDS All element; major histocompatibility complex.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 291)
AUTHORS Mulkova-Pajdelova, M., Satla, Y., O'Huigin, C., Mayer, W.E.,
Figuerola, F. and Klein, J.
TITLE All elements of the primate major histocompatibility complex
JOURNAL Mamm. Genome (1994) In press
REFERENCE 2 (bases 1 to 291)
AUTHORS O'Huigin, C.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1994) O'Huigin C., Max-Planck-Institut fuer
Biologie, Abteilung Immunogenetik, Corrensstr. 42, 72076 Tuebingen,
Germany
FEATURES Location/Qualifiers
source 1..291
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN repeat_region 1..291
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Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2286 GTTAGCCAGATGCTCTGATCTCTGACCTTGATCCGCCACCTGGCCTCCCAAG 2345
Db 96 GTTAGCCAGATGCTCTGATCTCTGACCTTGATCCGCCACCTGGCCTCCCAAG 37
Oy 2346 TGCTGGAGTTACAGGC 2361
Db 36 TGCTGGAGTTACAGGC 21
RESULT 34
BD074010/c 73 bp DNA linear PAT 27-AUG-2002
LOCUS BD074010
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074010
VERSION BD074010.1 GI:22619613
KEYWORDS JP 2001513996-A/49.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 73)
AUTHORS Chen, J., Agrawal, S. and Zhang, R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 49 11-SEP-2001;
COMMENT HYBRIDON INC.
OS Unidentified
PN JP 2001513996-A/49
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384 06-MAY-1998 US 09/073567 PI
JIANPONG CHEN, SUDHIR AGRAWAL, RUTEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH key Location/Qualifiers
FT source 1..73
/organism="Unidentified".
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source 1..73
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ORIGIN

Query Match 3.1%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 9.1e-29;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 665 AGGTACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAGACCT 724
Db 73 AGGTACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAGACCT 14
Oy 725 TGTACAGAGCTT 737
Db 13 TGTACAGAGCTT 1
RESULT 35
AR721415/c 73 bp DNA linear PAT 07-OCT-2005
LOCUS AR721415
DEFINITION Sequence 49 from patent US 6946447.
ACCESSION AR721415
VERSION AR721415.1 GI:77372938
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 73)
AUTHORS Chen, J., Agrawal, S. and Zhang, R.
TITLE MDM2-specific antisense oligonucleotides
JOURNAL Patent: US 6946447-A 49 20-SEP-2005;
HYBRIDON, Inc.; Cambridge, MA;
WOX;
FEATURES Location/Qualifiers
source 1..73
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 3.1%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 9.1e-29;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 665 AGGTACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAGACCT 724
Db 73 AGGTACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAGACCT 14
Oy 725 TGTACAGAGCTT 737
Db 13 TGTACAGAGCTT 1
RESULT 36
BV195288/c 401 bp DNA linear STS 10-JUN-2004
LOCUS BV195288
DEFINITION sqm194015 Human DNA (Sequencem) Homo sapiens STS genomic, sequence
tagged site.
ACCESSION BV195288
VERSION BV195288.1 GI:48039039
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 401)
AUTHORS Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M.,
Cantor, C.R. and Braun, A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA

Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 401.

FEATURES
source

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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ORIGIN
STS

Query Match 3.1%; Score 73; DB 7; Length 401;
Best Local Similarity 100.0%; Pred. No. 6.8e-29;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGCTCGATCTCTGACCTCGTATCGCCGCACTCGGCTCCCAA 2344
|||||
DB 159 TGTAGCCAGATGCTCGATCTCTGACCTCGTATCGCCGCACTCGGCTCCCAA 100
|||||

QY 2345 GTGCTGGATTAC 2357
|||||
DB 99 GTGCTGGATTAC 87
|||||

RESULT 37
AY270309 315 bp DNA linear PRI 08-JUL-2003
LOCUS Homo sapiens clone SKT02-C5 putative promoter sequence.
DEFINITION
ACCESSION AY270309
VERSION AY270309.1 GI:30720522
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 315)
Khabbata-Ford,S., Liu,Y., Gleason,C., Dickson,M., Altman,R.B.,
Batoglou,S. and Myers,R.M.
Identification of promoter regions in the human genome by using a
retroviral plasmid library-based functional reporter gene assay
Genome Res. 13 (7), 1765-1774 (2003)

REFERENCE
AUTHORS
JOURNAL
PUBMED
2 (bases 1 to 315)
Khabbata Ford,S., Liu,Y. and Myers,R.M.
Direct Submission
Submitted (07-APR-2003) Genetics, Stanford University School of
Medicine, 300 Pasteur Drive, Stanford, CA 94305-5120, USA
JOURNAL
Location/Qualifiers
1..315
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/clone="SKT02-C5"
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retroviral plasmid library-based functional reporter
assay"

FEATURES
source

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1..315
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/mol_type="genomic DNA"
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/clone="SKT02-C5"
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retroviral plasmid library-based functional reporter
assay"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.7e-28;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCGGCCCACTC 2333
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DB 116 GGGTTTACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCGGCCCACTC 57
|||||
QY 2334 GGCTTCCCAA 2344
|||||

DB 56 GGCTTCCCAA 46
|||||

RESULT 38
AX245117 353 bp DNA linear PAT 28-SEP-2001
LOCUS
DEFINITION Sequence 47 from Patent WO0166753.
ACCESSION AX245117
VERSION AX245117.1 GI:15859791
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Ckvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Crain,B.
Human genes and gene expression products
Patent: WO 0166753-A 47 13-SEP-2001;
Chiron Corporation (US) ; Hysq Inc. (US)
Location/Qualifiers
1..353
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

REFERENCE
AUTHORS

JOURNAL
TITLE
Human genes and gene expression products
Patent: WO 0166753-A 47 13-SEP-2001;
Chiron Corporation (US) ; Hysq Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.9%; Score 69; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACACGCGTTTACCGTGTAGCCAGATGCTCGATCTCTGACCTGCT 2319
|||||
DB 70 TTTTAGTAGACACGCGTTTACCGTGTAGCCAGATGCTCGATCTCTGACCTGCT 129
|||||

QY 2320 GATCGGCC 2328
|||||
DB 130 GATCGGCC 138
|||||

RESULT 39
CQ469958 426 bp DNA linear PAT 31-JAN-2004
LOCUS
DEFINITION Sequence 1824 from Patent WO0160860.
ACCESSION CQ469958
VERSION CQ469958.1 GI:41435577
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
Schlegel,R., Endege,W.O. and Monahan,J.E.
Genes differentially expressed in human prostate cancer and their
use
Patent: WO 0160860-A 1824 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
1..426
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

REFERENCE
AUTHORS

JOURNAL
TITLE
Genes differentially expressed in human prostate cancer and their
use
Patent: WO 0160860-A 1824 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
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FEATURES
source

ORIGIN

Query Match 2.9%; Score 69; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTACCGTGTGTAACCGAGATGGTCTGATCTCCTGACTCGT 2319
|||||
Db 91 TTTTAGTAGAGACAGGGTTTACCGTGTGTAACCGAGATGGTCTGATCTCCTGACTCGT 32
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QY 2320 GATCCGGCCC 2328
|||||
Db 31 GATCCGGCCC 23

RESULT 40

CQ479126/c CQ479126 426 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 10993 from Patent WO0160860.
DEFINITION CQ479126
ACCESSION CQ479126
VERSION CQ479126.1 GI:41444745

KEYWORDS

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS 1
TITLE Schlegel, R., Endege, W. O. and Monahan, J. E.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

JOURNAL
TITL Schlegel, R., Endege, W. O. and Monahan, J. E.
Genes differentially expressed in human prostate cancer and their
use

Patent: WO 0160860-A 10993 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)

FEATURES

source
1..426
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.9%; Score 69; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTACCGTGTGTAACCGAGATGGTCTGATCTCCTGACTCGT 2319
|||||
Db 91 TTTTAGTAGAGACAGGGTTTACCGTGTGTAACCGAGATGGTCTGATCTCCTGACTCGT 32
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QY 2320 GATCCGGCCC 2328
|||||
Db 31 GATCCGGCCC 23

Search completed: August 4, 2006, 17:52:38
Job time : 13578 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 13:45:22 ; Search time 449 Seconds
(without alignments)
9884.789 Million cell updates/sec

Title: US-09-966-724B-2

Perfect score: 2372
Sequence: 1 GCACCGCGCGAGCTTGCTG.....ATTACGAGCATGACGACCG 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 93554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 1952600

Minimum DB seq length: 5

Maximum DB seq length: 500

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA:*

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- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A/COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B/COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7/COMB.seq:*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP/COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE/COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	313	13.2	399	US-09-167-322-8	Sequence 8, Appl.
2	225	9.5	399	US-09-167-322-9	Sequence 9, Appl.
3	148	6.2	199	US-09-200-355-1	Sequence 1, Appl.
4	138	5.8	199	US-09-200-355-2	Sequence 2, Appl.
5	78	3.3	397	US-09-621-976-12751	Sequence 12751, A
6	73	3.1	73	US-09-073-567-49	Sequence 49, Appl.
7	73	3.1	73	US-09-541-848-49	Sequence 49, Appl.
8	67	2.8	480	US-09-621-976-8284	Sequence 8284, Ap
9	60	2.5	362	US-09-621-976-15415	Sequence 15415, A
10	60	2.5	441	US-09-621-976-17159	Sequence 17159, A
11	58	2.4	191	US-09-513-999C-18362	Sequence 18362, A
12	58	2.4	463	US-09-621-976-14420	Sequence 14420, A
13	55	2.3	149	US-09-513-999C-32581	Sequence 32581, A
14	55	2.3	170	US-09-513-999C-27025	Sequence 27025, A
15	55	2.3	191	US-09-513-999C-22797	Sequence 22797, A
16	55	2.3	192	US-09-513-999C-32123	Sequence 32123, A
17	55	2.3	258	US-09-984-429-629	Sequence 629, App
18	55	2.3	266	US-09-621-976-13784	Sequence 13784, A
19	55	2.3	294	US-09-984-429-627	Sequence 627, App
20	55	2.3	300	US-09-984-429-678	Sequence 678, App
21	55	2.3	301	US-09-984-429-638	Sequence 638, App
22	55	2.3	316	US-09-984-429-618	Sequence 618, App
23	55	2.3	322	US-09-621-976-9777	Sequence 9777, Ap

24	2.3	322	5	US-09-984-429-679	Sequence 679, App
25	2.3	328	5	US-09-513-999C-34128	Sequence 34128, A
26	2.3	370	5	US-09-984-429-521	Sequence 521, App
27	2.3	382	3	US-09-621-976-13869	Sequence 13869, A
28	2.3	466	3	US-09-949-016-80631	Sequence 80631, A
29	2.3	411	4	US-09-880-107-445	Sequence 445, App
30	2.2	301	5	US-09-984-429-643	Sequence 643, App
31	2.2	311	3	US-09-621-976-13091	Sequence 13091, A
32	2.2	231	3	US-09-513-999C-32057	Sequence 32057, A
33	2.2	300	4	US-09-297-648-1408	Sequence 1408, Ap
34	2.2	315	3	US-09-621-976-14124	Sequence 14124, A
35	2.2	432	3	US-09-621-976-8313	Sequence 8313, Ap
36	2.1	50	3	US-10-131-827-4749	Sequence 4749, Ap
37	2.1	50	5	US-10-131-831-4749	Sequence 4749, Ap
38	2.1	95	3	US-09-513-999C-32786	Sequence 32786, A
39	2.1	133	3	US-09-513-999C-23250	Sequence 23250, A
40	2.1	215	3	US-09-513-999C-22153	Sequence 22153, A
41	2.1	252	3	US-09-513-999C-28073	Sequence 28073, A
42	2.1	252	3	US-09-513-999C-28094	Sequence 28094, A
43	2.1	288	3	US-09-973-278-870	Sequence 870, App
44	2.1	301	5	US-09-984-429-644	Sequence 644, App
45	2.1	323	5	US-09-984-429-669	Sequence 669, App
46	2.1	396	3	US-09-621-976-17326	Sequence 17326, A
47	2.1	249	3	US-09-513-999C-16980	Sequence 16980, A
48	2.1	317	3	US-09-385-982-109	Sequence 109, App
49	2.0	111	3	US-09-513-999C-18192	Sequence 18192, A
50	2.0	137	3	US-09-513-999C-27657	Sequence 27657, A
51	2.0	242	5	US-09-984-429-614	Sequence 614, App
52	2.0	243	5	US-09-984-429-675	Sequence 675, App
53	2.0	164	3	US-09-621-976-11863	Sequence 11863, A
54	2.0	284	3	US-09-513-999C-31129	Sequence 31129, A
55	2.0	281	3	US-09-621-976-1944	Sequence 1944, App
56	2.0	281	5	US-09-984-429-668	Sequence 668, App
57	2.0	294	3	US-09-621-976-1939	Sequence 1939, App
58	2.0	294	3	US-09-621-976-1940	Sequence 1940, App
59	2.0	298	3	US-09-621-976-11526	Sequence 11526, A
60	2.0	298	3	US-09-621-976-13327	Sequence 13327, A
61	2.0	302	3	US-09-621-976-1937	Sequence 1937, App
62	2.0	302	3	US-09-621-976-1942	Sequence 1942, App
63	2.0	310	3	US-09-621-976-1943	Sequence 1943, App
64	2.0	314	3	US-09-621-976-12169	Sequence 12169, A
65	2.0	314	3	US-09-621-976-11935	Sequence 11935, A
66	2.0	314	3	US-09-621-976-11969	Sequence 11969, A
67	2.0	421	3	US-09-621-976-15130	Sequence 15130, A
68	1.9	442	3	US-09-949-016-128506	Sequence 128506, A
69	1.9	227	3	US-09-513-999C-18463	Sequence 18463, A
70	1.9	237	3	US-09-513-999C-27603	Sequence 27603, A
71	1.9	279	3	US-09-513-999C-12484	Sequence 12484, A
72	1.9	303	3	US-09-513-999C-28512	Sequence 28512, A
73	1.9	387	3	US-09-621-976-2306	Sequence 2306, App
74	1.9	417	3	US-09-495-050A-282	Sequence 282, App
75	1.9	439	3	US-09-621-976-10550	Sequence 10550, A
76	1.9	440	3	US-09-621-976-16612	Sequence 16612, A
77	1.9	480	3	US-09-621-976-14080	Sequence 14080, A
78	1.9	495	3	US-09-495-050A-17	Sequence 17, Appl
79	1.9	76	3	US-09-513-999C-17764	Sequence 17764, A
80	1.9	102	3	US-09-973-278-939	Sequence 939, App
81	1.9	147	3	US-09-513-999C-20249	Sequence 20249, A
82	1.9	148	3	US-09-513-999C-20098	Sequence 20098, A
83	1.9	188	3	US-09-513-999C-20303	Sequence 20303, A
84	1.9	188	3	US-09-513-999C-20303	Sequence 20303, A
85	1.9	237	3	US-09-513-999C-19336	Sequence 19336, A
86	1.9	258	3	US-09-513-999C-10113	Sequence 10113, A
87	1.9	261	5	US-09-984-429-661	Sequence 661, App
88	1.9	265	3	US-09-513-999C-33210	Sequence 33210, A
89	1.9	272	3	US-09-513-999C-18392	Sequence 18392, A
90	1.9	298	3	US-09-513-999C-19999	Sequence 19999, A
91	1.9	304	5	US-09-984-429-660	Sequence 660, App
92	1.9	307	5	US-09-984-429-685	Sequence 685, App
93	1.9	316	3	US-09-621-976-11418	Sequence 11418, A
94	1.9	318	3	US-09-621-976-12699	Sequence 12699, A
95	1.9	406	3	US-09-621-976-18042	Sequence 18042, A
96	1.9	462	3	US-09-621-976-18043	Sequence 18043, A

97	43	1.8	165	3	US-09-513-999C-22194	Sequence 22194, A	170	40	1.7	137	3	US-09-621-976-11180	Sequence 11180, A
98	43	1.8	215	3	US-09-513-999C-32206	Sequence 32206, A	171	40	1.7	107	3	US-09-513-999C-18620	Sequence 18620, A
99	43	1.8	221	3	US-09-513-999C-19834	Sequence 19834, A	172	40	1.7	166	3	US-09-513-999C-16892	Sequence 16892, A
100	43	1.8	226	3	US-09-513-999C-27533	Sequence 27533, A	173	40	1.7	237	3	US-09-513-999C-25994	Sequence 25994, A
101	43	1.8	241	3	US-09-513-999C-20573	Sequence 20573, A	174	40	1.7	227	3	US-09-513-999C-26027	Sequence 26027, A
102	43	1.8	274	3	US-09-513-999C-23260	Sequence 23260, A	175	40	1.7	250	3	US-09-513-999C-16022	Sequence 16022, A
103	43	1.8	291	3	US-09-621-976-11434	Sequence 11434, A	176	40	1.7	257	3	US-09-513-999C-32565	Sequence 32565, A
104	43	1.8	292	3	US-09-621-976-11386	Sequence 11386, A	177	40	1.7	222	3	US-09-513-999C-10209	Sequence 10209, A
105	43	1.8	292	3	US-09-621-976-12661	Sequence 12661, A	178	40	1.7	312	3	US-09-621-976-13853	Sequence 13853, A
106	43	1.8	298	3	US-09-621-976-8178	Sequence 8178, Ap	179	40	1.7	334	3	US-09-513-999C-25749	Sequence 25749, A
107	43	1.8	300	4	US-09-297-648-1057	Sequence 1057, Ap	180	40	1.7	325	3	US-09-513-999C-14409	Sequence 14409, A
108	43	1.8	300	4	US-09-297-648-1063	Sequence 1063, Ap	181	40	1.7	350	3	US-09-513-999C-17193	Sequence 17193, A
109	43	1.8	301	4	US-09-513-999C-28754	Sequence 28754, A	182	40	1.7	366	3	US-09-513-999C-36693	Sequence 36693, A
110	43	1.8	307	3	US-09-621-976-12992	Sequence 12992, A	183	40	1.7	387	3	US-09-621-976-11273	Sequence 12733, A
111	43	1.8	329	3	US-09-621-976-12722	Sequence 12722, A	184	40	1.7	416	3	US-09-621-976-8359	Sequence 8359, Ap
112	43	1.8	347	3	US-09-621-976-11380	Sequence 11380, A	185	40	1.7	458	3	US-09-621-976-8215	Sequence 8215, Ap
113	43	1.8	347	3	US-09-621-976-12611	Sequence 12611, A	186	40	1.7	467	3	US-09-621-976-10171	Sequence 10171, A
114	43	1.8	358	3	US-09-621-976-1061	Sequence 9061, Ap	187	40	1.7	468	3	US-09-621-976-13868	Sequence 13868, A
115	43	1.8	360	3	US-09-621-976-8369	Sequence 8369, Ap	188	40	1.7	481	3	US-09-621-976-12206	Sequence 2206, Ap
116	43	1.8	397	3	US-09-621-976-12615	Sequence 12615, A	189	39	1.6	85	2	US-08-454-557C-92	Sequence 92, Appl
117	43	1.8	417	3	US-09-513-999C-12444	Sequence 12444, A	190	39	1.6	85	2	US-08-340-426D-92	Sequence 92, Appl
118	43	1.8	480	3	US-09-513-999C-24383	Sequence 24383, A	191	39	1.6	85	2	US-08-450-673C-92	Sequence 92, Appl
119	43	1.8	481	3	US-09-621-976-2216	Sequence 2216, Ap	192	39	1.6	85	7	PCT-US95-1711A-92	Sequence 92, Appl
120	43	1.8	492	3	US-09-621-976-2202	Sequence 2202, Ap	193	39	1.6	99	3	US-09-513-999C-18805	Sequence 18805, A
121	43	1.8	500	3	US-09-621-976-13791	Sequence 13791, A	194	39	1.6	150	3	US-09-513-999C-17051	Sequence 17051, A
122	42	1.8	123	3	US-09-513-999C-30000	Sequence 30000, A	195	39	1.6	170	3	US-09-513-999C-27289	Sequence 27289, A
123	42	1.8	129	3	US-09-513-999C-19314	Sequence 19314, A	196	39	1.6	180	3	US-09-513-999C-17981	Sequence 17981, A
124	42	1.8	151	3	US-09-513-999C-21800	Sequence 21800, A	197	39	1.6	193	3	US-09-513-999C-20284	Sequence 20284, A
125	42	1.8	159	3	US-09-513-999C-35428	Sequence 35428, A	198	39	1.6	198	2	US-08-967-101-107	Sequence 107, App
126	42	1.8	207	3	US-09-513-999C-17255	Sequence 17255, A	199	39	1.6	198	2	US-08-952-541-107	Sequence 107, App
127	42	1.8	279	3	US-09-621-976-11877	Sequence 11877, A	200	39	1.6	198	3	US-09-124-698-107	Sequence 107, App
128	42	1.8	301	3	US-09-621-976-12190	Sequence 12190, A	201	39	1.6	198	3	US-09-127-480-107	Sequence 107, App
129	42	1.8	306	3	US-09-621-976-12017	Sequence 12017, A	202	39	1.6	198	3	US-08-496-841C-107	Sequence 107, App
130	42	1.8	311	3	US-09-621-976-2093	Sequence 2093, Ap	203	39	1.6	198	3	US-09-124-523-107	Sequence 107, App
131	42	1.8	312	3	US-09-621-976-12418	Sequence 12418, A	204	39	1.6	198	3	US-09-636-796A-107	Sequence 107, App
132	42	1.8	314	3	US-09-621-976-13604	Sequence 13604, A	205	39	1.6	198	3	US-08-431-048R-107	Sequence 107, App
133	42	1.8	314	3	US-09-621-976-12340	Sequence 12340, A	206	39	1.6	222	4	US-09-689-159A-107	Sequence 107, App
134	42	1.8	320	2	US-08-629-939-5	Sequence 5, Appli	207	39	1.6	222	3	US-09-513-999C-20719	Sequence 20719, A
135	42	1.8	320	2	US-08-759-873-5	Sequence 5, Appli	208	39	1.6	229	3	US-09-513-999C-33332	Sequence 33332, A
136	42	1.8	325	3	US-09-621-976-12097	Sequence 12097, A	209	39	1.6	273	5	US-09-984-429-673	Sequence 24738, A
137	42	1.8	326	3	US-09-621-976-12018	Sequence 12018, A	210	39	1.6	277	3	US-09-513-999C-9959	Sequence 9559, Ap
138	42	1.8	326	3	US-09-513-999C-26142	Sequence 26142, A	211	39	1.6	280	5	US-09-984-429-657	Sequence 657, App
139	42	1.8	327	3	US-09-621-976-12423	Sequence 12423, A	212	39	1.6	332	3	US-09-621-976-10344	Sequence 10344, A
140	42	1.8	332	3	US-09-513-999C-31177	Sequence 31177, A	213	39	1.6	282	3	US-09-513-999C-34474	Sequence 34474, A
141	42	1.8	412	3	US-09-621-976-15301	Sequence 15301, A	214	39	1.6	306	3	US-09-621-976-12837	Sequence 12837, A
142	42	1.8	438	3	US-09-621-976-15688	Sequence 15688, A	215	39	1.6	315	3	US-09-513-999C-33653	Sequence 33653, A
143	42	1.8	445	3	US-09-621-976-14297	Sequence 14297, A	216	39	1.6	328	3	US-09-621-976-14797	Sequence 14797, A
144	42	1.8	460	3	US-09-918-686-26	Sequence 26, Appl	217	39	1.6	330	3	US-09-621-976-1274	Sequence 2274, Ap
145	42	1.8	488	3	US-09-621-976-14108	Sequence 14108, A	218	39	1.6	332	3	US-09-621-976-10344	Sequence 10344, A
146	41	1.7	86	3	US-09-513-999C-19069	Sequence 19069, A	219	39	1.6	363	3	US-09-621-976-12877	Sequence 12877, A
147	41	1.7	152	3	US-09-513-999C-27160	Sequence 27160, A	220	39	1.6	379	3	US-09-513-999C-28773	Sequence 28773, A
148	41	1.7	244	3	US-09-513-999C-365	Sequence 365, App	221	39	1.6	381	3	US-09-621-976-13054	Sequence 13054, A
149	41	1.7	265	3	US-09-621-976-9909	Sequence 9909, Ap	222	39	1.6	386	2	US-08-967-101-103	Sequence 103, App
150	41	1.7	290	3	US-09-513-999C-30130	Sequence 30130, A	223	39	1.6	386	2	US-08-952-541-103	Sequence 103, App
151	41	1.7	294	3	US-09-621-976-11647	Sequence 11647, A	224	39	1.6	386	3	US-09-124-698-103	Sequence 103, App
152	41	1.7	296	3	US-09-621-976-11776	Sequence 11776, A	225	39	1.6	386	3	US-09-127-480-103	Sequence 103, App
153	41	1.7	306	3	US-09-621-976-11831	Sequence 11831, A	226	39	1.6	386	3	US-08-496-841C-103	Sequence 103, App
154	41	1.7	310	3	US-09-621-976-12288	Sequence 12288, A	227	39	1.6	386	3	US-09-124-523-103	Sequence 103, App
155	41	1.7	311	3	US-09-621-976-11982	Sequence 11982, A	228	39	1.6	386	3	US-09-636-796A-103	Sequence 103, App
156	41	1.7	313	3	US-09-621-976-12373	Sequence 12373, A	229	39	1.6	386	3	US-08-431-048R-103	Sequence 103, App
157	41	1.7	323	3	US-09-621-976-12178	Sequence 12178, A	230	39	1.6	386	3	US-09-689-159A-103	Sequence 14894, A
158	41	1.7	324	3	US-09-621-976-12122	Sequence 12122, A	231	39	1.6	386	4	US-09-621-976-14877	Sequence 14877, A
159	41	1.7	324	3	US-09-621-976-12124	Sequence 12124, A	232	39	1.6	393	3	US-09-513-999C-20260	Sequence 20260, A
160	41	1.7	324	3	US-09-621-976-13570	Sequence 13570, A	233	39	1.6	403	3	US-09-949-016-139450	Sequence 139450, A
161	41	1.7	383	3	US-09-513-999C-12045	Sequence 12045, A	234	39	1.6	403	3	US-09-621-976-234	Sequence 234, App
162	41	1.7	445	3	US-09-513-999C-23555	Sequence 23555, A	235	39	1.6	412	3	US-09-513-999C-30942	Sequence 30942, A
163	41	1.7	464	3	US-09-513-999C-3453	Sequence 23453, A	236	39	1.6	437	3	US-09-621-976-14877	Sequence 14877, A
164	41	1.7	500	3	US-09-280-805-2	Sequence 2, Appli	237	39	1.6	437	3	US-09-949-016-139451	Sequence 139451, A
165	41	1.7	500	3	US-09-048-810-2	Sequence 2, Appli	238	39	1.6	439	3	US-10-002-623-735	Sequence 735, App
166	40	1.7	106	3	US-09-973-278-888	Sequence 888, App	239	39	1.6	459	3	US-09-621-976-13990	Sequence 13990, A
167	40	1.7	124	3	US-09-513-999C-17263	Sequence 17263, A	240	39	1.6	474	3	US-09-621-976-80	Sequence 90, Appl
168	40	1.7	124	3	US-09-513-999C-18967	Sequence 18967, A	241	39	1.6	476	3	US-09-621-976-10092	Sequence 10092, A
169	40	1.7	127	3	US-09-513-999C-17828	Sequence 17828, A	242	39	1.6	480	3	US-09-621-976-12757	Sequence 12757, A

C 243	39	1.6	487	3	US-09-621-976-2302	Sequence 2302, App	316	37	1.6	338	3	US-09-513-999C-26831	Sequence 26831, A
C 244	38	1.6	79	3	US-09-513-999C-18764	Sequence 18764, A	317	37	1.6	338	3	US-09-513-999C-33396	Sequence 33396, A
C 245	38	1.6	79	3	US-09-513-999C-28108	Sequence 28108, A	318	37	1.6	339	3	US-09-621-976-8848	Sequence 9888, App
C 246	38	1.6	102	3	US-09-513-999C-33303	Sequence 23303, A	319	37	1.6	339	3	US-09-513-999C-10091	Sequence 10091, A
C 247	38	1.6	131	3	US-09-513-999C-17351	Sequence 17351, A	C 320	37	1.6	354	3	US-09-973-278-811	Sequence 811, App
C 248	38	1.6	134	3	US-09-513-999C-16210	Sequence 16210, A	321	37	1.6	355	3	US-09-702-705-749	Sequence 749, App
C 249	38	1.6	138	5	US-09-984-429-294	Sequence 294, App	322	37	1.6	355	3	US-09-736-457-749	Sequence 749, App
C 250	38	1.6	138	5	US-09-984-429-295	Sequence 295, App	323	37	1.6	355	3	US-09-614-1248-749	Sequence 749, App
C 251	38	1.6	152	3	US-09-513-999C-15980	Sequence 15980, A	324	37	1.6	355	3	US-09-671-325-749	Sequence 749, App
C 252	38	1.6	152	2	US-09-848-701-2	Sequence 2, App1	325	37	1.6	355	3	US-09-589-184-749	Sequence 749, App
C 253	38	1.6	158	3	US-09-513-999C-19663	Sequence 19663, A	326	37	1.6	355	3	US-09-658-824-749	Sequence 749, App
C 254	38	1.6	171	3	US-09-513-999C-18843	Sequence 18843, A	327	37	1.6	355	3	US-10-017-754-749	Sequence 749, App
C 255	38	1.6	178	3	US-09-513-999C-13563	Sequence 13563, A	328	37	1.6	355	3	US-09-651-563-749	Sequence 749, App
C 256	38	1.6	214	2	US-08-222-177A-37	Sequence 37, App1	329	37	1.6	355	3	US-09-519-642-749	Sequence 749, App
C 257	38	1.6	214	3	US-09-513-999C-18744	Sequence 18744, A	C 330	37	1.6	356	3	US-09-973-278-804	Sequence 804, App
C 258	38	1.6	226	3	US-09-513-999C-27507	Sequence 27507, A	331	37	1.6	358	3	US-09-513-999C-24918	Sequence 24918, A
C 259	38	1.6	239	3	US-09-513-999C-8875	Sequence 8875, App	C 332	37	1.6	360	3	US-09-621-976-10753	Sequence 10753, A
C 260	38	1.6	239	3	US-09-513-999C-34306	Sequence 34306, A	C 333	37	1.6	373	3	US-09-621-976-14515	Sequence 14515, A
C 261	38	1.6	295	3	US-09-621-976-13118	Sequence 13118, A	C 334	37	1.6	382	4	US-09-880-107-3013	Sequence 3013, App
C 262	38	1.6	313	3	US-09-621-976-13773	Sequence 13773, A	C 335	37	1.6	390	3	US-09-513-999C-29193	Sequence 29193, App
C 263	38	1.6	324	3	US-09-513-999C-30662	Sequence 30662, A	C 336	37	1.6	394	3	US-09-621-976-8541	Sequence 8541, App
C 264	38	1.6	324	3	US-09-513-999C-20002	Sequence 20002, A	C 337	37	1.6	394	3	US-09-621-976-11726	Sequence 11726, A
C 265	38	1.6	331	3	US-09-513-999C-36325	Sequence 36325, A	C 338	37	1.6	417	3	US-09-621-976-10384	Sequence 10384, A
C 266	38	1.6	336	3	US-09-621-976-9328	Sequence 9328, App	C 339	37	1.6	417	3	US-09-621-976-14784	Sequence 14784, A
C 267	38	1.6	347	3	US-09-513-999C-31729	Sequence 31729, A	C 340	37	1.6	420	3	US-09-621-976-12142	Sequence 12142, A
C 268	38	1.6	369	3	US-09-621-976-9151	Sequence 9151, App	C 341	37	1.6	439	3	US-09-513-999C-13441	Sequence 13441, A
C 269	38	1.6	407	3	US-09-621-976-19005	Sequence 19005, A	C 342	37	1.6	450	4	US-09-880-107-2675	Sequence 2675, App
C 270	38	1.6	425	3	US-09-949-016-160086	Sequence 160086, A	C 343	37	1.6	458	3	US-09-621-976-18682	Sequence 18682, A
C 271	38	1.6	430	3	US-09-513-999C-27366	Sequence 27366, A	C 344	37	1.6	463	3	US-09-621-976-2246	Sequence 2246, App
C 272	38	1.6	440	3	US-09-513-999C-32413	Sequence 32413, A	C 345	37	1.6	467	3	US-09-621-976-8269	Sequence 8269, App
C 273	38	1.6	447	3	US-09-621-976-14454	Sequence 14454, A	C 346	37	1.6	471	3	US-09-621-976-8039	Sequence 8039, App
C 274	38	1.6	457	3	US-09-949-016-160085	Sequence 160085, A	C 347	37	1.6	491	3	US-09-621-976-1986	Sequence 1986, App
C 275	38	1.6	473	3	US-09-621-976-17275	Sequence 17275, A	C 348	37	1.6	494	3	US-09-621-976-12737	Sequence 12737, A
C 276	38	1.6	486	3	US-09-621-976-1993	Sequence 1993, App	C 349	36	1.5	51	3	US-09-443-199C-683	Sequence 683, App
C 277	38	1.6	489	3	US-09-621-976-16466	Sequence 16466, A	C 350	36	1.5	101	3	US-09-621-976-12392	Sequence 12392, A
C 278	37	1.6	493	3	US-09-621-976-11551	Sequence 11551, A	C 351	36	1.5	103	3	US-09-621-976-12007	Sequence 12007, A
C 279	37	1.6	51	3	US-09-443-199C-911	Sequence 911, App	C 352	36	1.5	104	3	US-09-621-976-12251	Sequence 12251, A
C 280	37	1.6	84	3	US-09-513-999C-16592	Sequence 16592, A	C 353	36	1.5	109	3	US-09-621-976-11645	Sequence 11645, A
C 281	37	1.6	90	3	US-09-621-976-15041	Sequence 15041, A	C 354	36	1.5	111	3	US-09-621-976-13332	Sequence 13332, A
C 282	37	1.6	107	3	US-09-513-999C-23682	Sequence 23682, A	C 355	36	1.5	118	3	US-09-621-976-11692	Sequence 11692, A
C 283	37	1.6	107	3	US-09-513-999C-23684	Sequence 23684, A	C 356	36	1.5	118	3	US-09-621-976-11880	Sequence 11880, A
C 284	37	1.6	113	3	US-09-621-976-14993	Sequence 14993, A	C 357	36	1.5	118	3	US-09-621-976-11862	Sequence 11862, A
C 285	37	1.6	125	3	US-09-621-976-14992	Sequence 14992, A	C 358	36	1.5	118	3	US-09-621-976-12204	Sequence 12204, A
C 286	37	1.6	125	7	PCT-US95-09114-17	Sequence 17, App1	C 359	36	1.5	119	3	US-09-621-976-11955	Sequence 11955, A
C 287	37	1.6	135	3	US-09-621-976-14722	Sequence 14722, A	C 360	36	1.5	132	3	US-09-513-999C-18493	Sequence 18493, A
C 288	37	1.6	135	3	US-09-513-999C-16746	Sequence 16746, A	C 361	36	1.5	137	3	US-09-621-976-11950	Sequence 11950, A
C 289	37	1.6	135	3	US-09-513-999C-18385	Sequence 18385, A	C 362	36	1.5	140	3	US-09-621-976-12422	Sequence 12422, A
C 290	37	1.6	143	3	US-09-513-999C-20446	Sequence 20446, A	C 363	36	1.5	145	3	US-09-621-976-12053	Sequence 12053, A
C 291	37	1.6	149	3	US-09-513-999C-19423	Sequence 19423, A	C 364	36	1.5	152	3	US-09-621-976-11624	Sequence 11624, A
C 292	37	1.6	149	3	US-09-513-999C-30024	Sequence 30024, A	C 365	36	1.5	152	3	US-09-621-976-11957	Sequence 11957, A
C 293	37	1.6	162	3	US-09-621-976-14777	Sequence 14777, A	C 366	36	1.5	156	3	US-09-621-976-12157	Sequence 12157, A
C 294	37	1.6	162	3	US-09-621-976-14782	Sequence 14782, A	C 367	36	1.5	156	3	US-09-621-976-12406	Sequence 12406, A
C 295	37	1.6	162	3	US-09-621-976-15017	Sequence 15017, A	C 368	36	1.5	157	3	US-09-621-976-12187	Sequence 12187, A
C 296	37	1.6	162	3	US-09-621-976-15061	Sequence 15061, A	C 369	36	1.5	157	3	US-09-621-976-13607	Sequence 13607, A
C 297	37	1.6	162	3	US-09-621-976-15089	Sequence 15089, A	C 370	36	1.5	158	3	US-09-621-976-11870	Sequence 11870, A
C 298	37	1.6	163	3	US-09-513-999C-16993	Sequence 16993, A	C 371	36	1.5	158	3	US-09-621-976-12431	Sequence 12431, A
C 299	37	1.6	166	3	US-09-621-976-14999	Sequence 14999, A	C 372	36	1.5	158	3	US-09-621-976-12438	Sequence 12438, A
C 300	37	1.6	178	3	US-09-513-999C-16844	Sequence 16844, A	C 373	36	1.5	174	3	US-09-513-999C-18825	Sequence 18825, A
C 301	37	1.6	178	3	US-09-513-999C-17823	Sequence 17823, A	C 374	36	1.5	174	3	US-09-513-999C-19654	Sequence 19654, A
C 302	37	1.6	187	3	US-09-513-999C-24264	Sequence 24264, A	C 375	36	1.5	180	3	US-09-513-999C-21037	Sequence 21037, A
C 303	37	1.6	187	3	US-09-513-999C-18526	Sequence 18526, A	C 376	36	1.5	182	3	US-09-513-999C-17039	Sequence 17039, A
C 304	37	1.6	205	3	US-09-513-999C-16620	Sequence 16620, A	C 377	36	1.5	200	3	US-09-513-999C-27536	Sequence 27536, A
C 305	37	1.6	213	3	US-09-513-999C-16910	Sequence 16910, A	C 378	36	1.5	240	3	US-09-513-999C-17856	Sequence 17856, A
C 306	37	1.6	219	3	US-09-513-999C-9620	Sequence 9620, App	C 379	36	1.5	244	3	US-09-513-999C-15857	Sequence 15857, A
C 307	37	1.6	219	3	US-09-513-999C-33924	Sequence 33924, A	C 380	36	1.5	260	4	US-09-297-648-502	Sequence 502, App
C 308	37	1.6	273	3	US-09-513-999C-19801	Sequence 19801, A	C 381	36	1.5	281	3	US-09-513-999C-17062	Sequence 17062, App
C 309	37	1.6	285	3	US-09-513-999C-35879	Sequence 35879, A	C 382	36	1.5	293	3	US-09-513-999C-18980	Sequence 18980, A
C 310	37	1.6	288	3	US-09-513-999C-16626	Sequence 16626, A	C 383	36	1.5	293	3	US-09-621-976-12021	Sequence 12021, A
C 311	37	1.6	300	4	US-09-297-648-1446	Sequence 1446, App	C 384	36	1.5	296	3	US-09-621-976-14400	Sequence 14400, A
C 312	37	1.6	306	4	US-09-297-648-2341	Sequence 2341, App	C 385	36	1.5	300	4	US-09-297-648-196	Sequence 196, App
C 313	37	1.6	306	5	US-09-984-429-686	Sequence 686, App	C 386	36	1.5	300	4	US-09-297-648-205	Sequence 205, App
C 314	37	1.6	322	3	US-09-513-999C-16668	Sequence 16668, A	C 387	36	1.5	302	3	US-09-621-976-9427	Sequence 9427, App
C 315	37	1.6	338	3	US-09-513-999C-25503	Sequence 25503, A	C 388	36	1.5	302	3	US-09-621-976-12333	Sequence 12333, A

C 389	36	1.5	306	3	US-09-621-976-2196	Sequence 2196, Ap	C 462	35	1.5	369	3	US-09-621-976-14473	Sequence 14473, A
C 390	36	1.5	309	3	US-09-621-976-11582	Sequence 11582, A	C 463	35	1.5	382	3	US-09-621-976-8184	Sequence 8184, Ap
C 391	36	1.5	314	3	US-09-621-976-14078	Sequence 14078, A	C 464	35	1.5	394	4	US-09-880-107-2055	Sequence 2055, Ap
C 392	36	1.5	321	3	US-09-621-976-13503	Sequence 13503, A	C 465	35	1.5	400	3	US-09-621-976-10517	Sequence 10517, A
C 393	36	1.5	322	3	US-09-621-976-11620	Sequence 11620, A	C 466	35	1.5	414	3	US-09-621-976-2658	Sequence 2658, Ap
C 394	36	1.5	325	3	US-09-513-999C-36178	Sequence 36178, A	C 467	35	1.5	420	3	US-09-621-976-9373	Sequence 9373, Ap
C 395	36	1.5	329	3	US-09-513-999C-17380	Sequence 17380, A	C 468	35	1.5	424	3	US-09-513-999C-13801	Sequence 13801, Ap
C 396	36	1.5	344	3	US-09-513-999C-21486	Sequence 21486, A	C 469	35	1.5	426	3	US-09-621-976-16521	Sequence 16521, A
C 397	36	1.5	371	3	US-09-513-999C-23720	Sequence 23720, A	C 470	35	1.5	427	3	US-08-579-445-25	Sequence 25, Ap1
C 398	36	1.5	372	3	US-09-513-999C-17285	Sequence 17285, A	C 471	35	1.5	428	3	US-09-949-016-20585	Sequence 20585, A
C 399	36	1.5	377	3	US-09-513-999C-31189	Sequence 31189, A	C 472	35	1.5	447	3	US-09-621-976-14007	Sequence 14007, A
C 400	36	1.5	386	3	US-09-640-173-46	Sequence 46, Ap1	C 473	35	1.5	447	3	US-09-621-976-14459	Sequence 14459, A
C 401	36	1.5	396	3	US-09-713-550-46	Sequence 46, Ap1	C 474	35	1.5	438	3	US-09-621-976-12510	Sequence 12510, A
C 402	36	1.5	396	3	US-09-825-294-46	Sequence 46, Ap1	C 475	35	1.5	460	3	US-09-621-976-8148	Sequence 8148, Ap
C 403	36	1.5	396	3	US-09-970-966-46	Sequence 46, Ap1	C 476	35	1.5	463	3	US-09-621-976-3201	Sequence 3201, Ap
C 404	36	1.5	412	4	US-09-880-107-1164	Sequence 1164, Ap	C 477	35	1.5	476	3	US-09-621-976-17689	Sequence 17689, A
C 405	36	1.5	420	3	US-09-621-976-15374	Sequence 15374, A	C 478	35	1.5	477	3	US-09-621-976-12572	Sequence 12572, A
C 406	36	1.5	420	3	US-09-880-107-3663	Sequence 3663, Ap	C 479	35	1.5	480	3	US-09-621-976-10666	Sequence 10666, A
C 407	36	1.5	441	3	US-09-621-976-14089	Sequence 14089, A	C 480	35	1.5	481	3	US-09-621-976-10533	Sequence 10533, A
C 408	36	1.5	446	3	US-09-621-976-13229	Sequence 13229, A	C 481	35	1.5	494	3	US-09-621-976-18845	Sequence 18845, A
C 409	36	1.5	447	3	US-09-621-976-10595	Sequence 10595, A	C 482	35	1.5	497	3	US-09-621-976-140	Sequence 140, App
C 410	36	1.5	455	3	US-09-621-976-8240	Sequence 8240, Ap	C 483	34	1.4	65	3	US-09-513-999C-17000	Sequence 17000, A
C 411	36	1.5	456	3	US-09-621-976-12630	Sequence 12630, A	C 484	34	1.4	101	3	US-09-513-999C-17473	Sequence 17473, A
C 412	36	1.5	468	3	US-09-621-976-13744	Sequence 13744, A	C 485	34	1.4	101	3	US-09-513-999C-16632	Sequence 16632, A
C 413	36	1.5	500	3	US-09-621-976-10438	Sequence 10438, A	C 486	34	1.4	126	3	US-09-513-999C-15607	Sequence 15607, A
C 414	35	1.5	40	3	US-09-540-699-17	Sequence 17, Ap1	C 487	34	1.4	130	3	US-09-621-976-12768	Sequence 12768, A
C 415	35	1.5	115	3	US-09-513-999C-18063	Sequence 18063, A	C 488	34	1.4	135	3	US-09-513-999C-26889	Sequence 26889, A
C 416	35	1.5	115	3	US-09-513-999C-19038	Sequence 19038, A	C 489	34	1.4	138	3	US-09-513-999C-19218	Sequence 19218, A
C 417	35	1.5	124	3	US-09-513-999C-18097	Sequence 18097, A	C 490	34	1.4	139	3	US-09-513-999C-18431	Sequence 18431, A
C 418	35	1.5	124	3	US-09-513-999C-20484	Sequence 20484, A	C 491	34	1.4	140	5	US-09-984-429-261	Sequence 261, App
C 419	35	1.5	166	3	US-09-621-976-10847	Sequence 10847, A	C 492	34	1.4	141	3	US-09-513-999C-21387	Sequence 21387, A
C 420	35	1.5	170	3	US-09-621-976-14401	Sequence 14401, A	C 493	34	1.4	145	3	US-09-513-999C-25952	Sequence 25952, A
C 421	35	1.5	185	3	US-09-513-999C-34032	Sequence 34032, A	C 494	34	1.4	145	3	US-09-513-999C-26527	Sequence 26527, A
C 422	35	1.5	192	3	US-09-495-050A-763	Sequence 63, Ap1	C 495	34	1.4	175	3	US-09-513-999C-8715	Sequence 8715, Ap
C 423	35	1.5	206	3	US-09-513-999C-26612	Sequence 26612, A	C 496	34	1.4	181	3	US-09-513-999C-16835	Sequence 16835, A
C 424	35	1.5	208	3	US-09-513-999C-17111	Sequence 17111, A	C 497	34	1.4	181	3	US-09-513-999C-19355	Sequence 19355, A
C 425	35	1.5	215	3	US-09-513-999C-27302	Sequence 27302, A	C 498	34	1.4	184	2	US-08-340-673C-47	Sequence 47, Ap1
C 426	35	1.5	215	3	US-09-023-655-150	Sequence 150, App	C 499	34	1.4	184	2	US-08-450-673C-47	Sequence 47, Ap1
C 427	35	1.5	217	3	US-09-513-999C-16604	Sequence 16604, A	C 500	34	1.4	184	2	US-08-450-673C-47	Sequence 47, Ap1
C 428	35	1.5	218	3	US-09-513-999C-26923	Sequence 26923, A	C 501	34	1.4	187	7	PCT-US95-17111A-47	Sequence 47, Ap1
C 429	35	1.5	223	3	US-09-513-999C-21151	Sequence 21151, A	C 502	34	1.4	187	5	US-09-984-429-483	Sequence 483, App
C 430	35	1.5	231	3	US-09-513-999C-21343	Sequence 21343, A	C 503	34	1.4	208	3	US-09-513-999C-19987	Sequence 19987, A
C 431	35	1.5	237	3	US-09-513-999C-33731	Sequence 33731, A	C 504	34	1.4	210	3	US-09-513-999C-24401	Sequence 24401, A
C 432	35	1.5	237	3	US-09-513-999C-27187	Sequence 27187, A	C 505	34	1.4	224	3	US-09-513-999C-24365	Sequence 24365, A
C 433	35	1.5	247	3	US-09-513-999C-21296	Sequence 21296, A	C 506	34	1.4	236	3	US-09-621-976-13310	Sequence 13310, A
C 434	35	1.5	257	3	US-09-513-999C-3718	Sequence 3718, Ap	C 507	34	1.4	243	5	US-09-543-679A-2765	Sequence 2765, Ap
C 435	35	1.5	273	3	US-09-513-999C-16599	Sequence 16599, A	C 508	34	1.4	245	2	US-08-454-557C-86	Sequence 86, Ap1
C 436	35	1.5	275	3	US-09-513-999C-9068	Sequence 9068, Ap	C 509	34	1.4	245	2	US-08-340-626D-86	Sequence 86, Ap1
C 437	35	1.5	275	3	US-09-513-999C-28170	Sequence 28170, A	C 510	34	1.4	245	2	US-08-450-673C-86	Sequence 86, Ap1
C 438	35	1.5	282	2	US-08-133-629-8	Sequence 8, Ap1	C 511	34	1.4	245	7	PCT-US95-17111A-86	Sequence 86, Ap1
C 439	35	1.5	283	2	US-08-579-445-26	Sequence 26, Ap1	C 512	34	1.4	253	3	US-09-513-999C-30649	Sequence 30649, A
C 440	35	1.5	288	2	US-08-157-171-8	Sequence 8, Ap1	C 513	34	1.4	253	3	US-09-513-999C-14829	Sequence 14829, A
C 441	35	1.5	291	5	US-09-984-429-645	Sequence 645, App	C 514	34	1.4	253	3	US-09-621-976-11370	Sequence 11370, A
C 442	35	1.5	292	3	US-09-513-999C-18140	Sequence 18140, A	C 515	34	1.4	296	3	US-09-621-976-12310	Sequence 12310, A
C 443	35	1.5	293	3	US-09-513-999C-17411	Sequence 17411, A	C 516	34	1.4	297	3	US-09-621-976-11543	Sequence 11543, A
C 444	35	1.5	299	5	US-09-984-429-630	Sequence 630, App	C 517	34	1.4	298	3	US-09-513-999C-19899	Sequence 19899, A
C 445	35	1.5	300	5	US-09-984-429-621	Sequence 621, App	C 518	34	1.4	301	3	US-09-621-976-11951	Sequence 11951, A
C 446	35	1.5	304	3	US-09-513-999C-25565	Sequence 25565, A	C 519	34	1.4	302	3	US-09-621-976-11755	Sequence 11755, A
C 447	35	1.5	304	3	US-09-513-999C-8924	Sequence 8924, Ap	C 520	34	1.4	303	3	US-09-621-976-474	Sequence 474, App
C 448	35	1.5	304	3	US-09-513-999C-21629	Sequence 21629, A	C 521	34	1.4	312	3	US-09-621-976-11535	Sequence 11535, A
C 449	35	1.5	305	5	US-09-984-429-620	Sequence 620, App	C 522	34	1.4	312	3	US-09-621-976-11971	Sequence 11971, A
C 450	35	1.5	306	5	US-09-513-999C-27209	Sequence 27209, A	C 523	34	1.4	313	3	US-09-621-976-12055	Sequence 12055, A
C 451	35	1.5	306	5	US-09-984-429-626	Sequence 626, App	C 524	34	1.4	313	3	US-09-621-976-12266	Sequence 12266, A
C 452	35	1.5	310	5	US-09-984-429-671	Sequence 671, App	C 525	34	1.4	313	3	US-09-621-976-13588	Sequence 13588, A
C 453	35	1.5	316	5	US-09-984-429-622	Sequence 622, App	C 526	34	1.4	314	3	US-09-621-976-11517	Sequence 11517, A
C 454	35	1.5	316	5	US-09-984-429-631	Sequence 631, App	C 527	34	1.4	314	3	US-09-621-976-11886	Sequence 11886, A
C 455	35	1.5	323	3	US-09-513-999C-26295	Sequence 26295, A	C 528	34	1.4	315	3	US-09-621-976-11542	Sequence 11542, A
C 456	35	1.5	333	3	US-09-513-999C-25719	Sequence 25719, A	C 529	34	1.4	316	3	US-09-621-976-8130	Sequence 8130, App
C 457	35	1.5	345	3	US-09-621-976-9884	Sequence 9884, Ap	C 530	34	1.4	317	5	US-09-984-429-617	Sequence 617, App
C 458	35	1.5	348	3	US-09-513-999C-30771	Sequence 30771, A	C 531	34	1.4	319	5	US-09-513-999C-23107	Sequence 23107, A
C 459	35	1.5	349	3	US-09-513-999C-24062	Sequence 24062, A	C 532	34	1.4	327	3	US-09-513-999C-23664	Sequence 23664, A
C 460	35	1.5	355	3	US-09-513-999C-21525	Sequence 21525, A	C 533	34	1.4	334	3	US-09-621-976-18396	Sequence 18396, A
C 461	35	1.5	363	3	US-09-513-999C-22223	Sequence 22223, A	C 534	34	1.4	348	3		

C 545	34	1.4	352	3	US-09-621-976-17996	Sequence 17996, A	C 608	32	1.3	144	3	US-09-621-976-11625	Sequence 11625, A
C 536	34	1.4	379	3	US-09-621-976-13874	Sequence 13874, A	C 609	32	1.3	155	3	US-09-513-999C-22921	Sequence 22921, A
C 538	34	1.4	396	3	US-09-513-999C-13826	Sequence 13826, A	C 610	32	1.3	161	3	US-09-621-976-10059	Sequence 10059, A
C 539	34	1.4	414	3	US-09-621-976-10717	Sequence 10717, A	C 611	32	1.3	161	3	US-09-513-999C-16419	Sequence 16419, A
C 540	34	1.4	414	3	US-09-621-976-10253	Sequence 10253, A	C 612	32	1.3	170	3	US-09-513-999C-24363	Sequence 24363, A
C 541	34	1.4	422	3	US-09-513-999C-26937	Sequence 26937, A	C 613	32	1.3	184	3	US-09-513-999C-18456	Sequence 18456, A
C 543	34	1.4	423	3	US-09-513-999C-21120	Sequence 21120, A	C 614	32	1.3	195	3	US-09-513-999C-28277	Sequence 18277, A
C 544	34	1.4	438	3	US-09-621-976-9376	Sequence 9376, A	C 615	32	1.3	196	3	US-09-513-999C-24283	Sequence 24283, A
C 545	34	1.4	443	3	US-09-621-976-13015	Sequence 13015, A	C 616	32	1.3	198	3	US-09-513-999C-17441	Sequence 17441, A
C 546	34	1.4	456	3	US-09-621-976-1784	Sequence 1784, A	C 617	32	1.3	199	3	US-09-513-999C-17878	Sequence 17878, A
C 547	34	1.4	459	3	US-09-621-976-13163	Sequence 13163, A	C 618	32	1.3	203	3	US-09-621-976-10774	Sequence 10774, A
C 548	34	1.4	473	3	US-09-621-976-691	Sequence 691, App	C 619	32	1.3	204	3	US-09-513-999C-411	Sequence 411, App
C 549	34	1.4	474	3	US-09-149-476-13	Sequence 13, App	C 620	32	1.3	208	3	US-09-513-999C-17239	Sequence 17239, A
C 550	34	1.4	476	3	US-09-513-999C-13737	Sequence 13737, A	C 621	32	1.3	209	3	US-09-513-999C-9745	Sequence 9745, App
C 551	34	1.4	482	3	US-09-621-976-3258	Sequence 23258, A	C 622	32	1.3	210	3	US-09-513-999C-24761	Sequence 24761, A
C 552	34	1.4	483	3	US-09-621-976-3158	Sequence 3158, App	C 623	32	1.3	210	3	US-09-513-999C-24853	Sequence 24853, A
C 553	34	1.4	489	3	US-09-621-976-17360	Sequence 17360, A	C 624	32	1.3	213	3	US-09-513-999C-24765	Sequence 24765, A
C 554	34	1.4	489	3	US-09-621-976-652	Sequence 652, App	C 625	32	1.3	222	3	US-09-513-999C-9268	Sequence 9268, App
C 555	33	1.4	58	3	US-09-621-976-7983	Sequence 7983, App	C 626	32	1.3	228	3	US-09-513-999C-18833	Sequence 18833, A
C 556	33	1.4	122	3	US-09-513-999C-17927	Sequence 17927, A	C 627	32	1.3	228	3	US-09-513-999C-23505	Sequence 23505, A
C 557	33	1.4	122	3	US-09-513-999C-18025	Sequence 18025, A	C 628	32	1.3	229	3	US-09-513-999C-27124	Sequence 27124, A
C 558	33	1.4	122	3	US-09-513-999C-19887	Sequence 19887, A	C 629	32	1.3	240	2	US-09-513-999C-25865	Sequence 25865, A
C 559	33	1.4	135	3	US-09-513-999C-19072	Sequence 19072, A	C 630	32	1.3	244	3	US-09-513-999C-18146	Sequence 18146, A
C 560	33	1.4	141	3	US-09-513-999C-17707	Sequence 17707, A	C 631	32	1.3	250	3	US-09-513-999C-22302	Sequence 22302, A
C 561	33	1.4	152	3	US-09-513-999C-1766	Sequence 31766, A	C 632	32	1.3	256	3	US-09-513-999C-12740	Sequence 12740, A
C 562	33	1.4	165	3	US-09-513-999C-9875	Sequence 9875, App	C 633	32	1.3	257	3	US-09-621-976-12740	Sequence 12740, A
C 563	33	1.4	167	3	US-09-513-999C-20746	Sequence 20746, A	C 634	32	1.3	259	3	US-09-621-976-12928	Sequence 12928, A
C 564	33	1.4	169	3	US-09-513-999C-19604	Sequence 19604, A	C 635	32	1.3	260	3	US-09-621-976-10668	Sequence 10668, A
C 565	33	1.4	192	3	US-09-513-999C-19619	Sequence 19619, A	C 636	32	1.3	265	3	US-09-513-999C-19561	Sequence 19561, A
C 566	33	1.4	205	3	US-09-621-976-13679	Sequence 13679, A	C 637	32	1.3	270	3	US-09-513-999C-401	Sequence 401, App
C 567	33	1.4	231	3	US-09-513-999C-17699	Sequence 17699, A	C 638	32	1.3	270	3	US-09-513-999C-30655	Sequence 30625, App
C 568	33	1.4	241	3	US-09-513-999C-27485	Sequence 27485, A	C 639	32	1.3	271	3	US-09-513-999C-18481	Sequence 18481, A
C 569	33	1.4	246	3	US-09-513-999C-18467	Sequence 18467, A	C 640	32	1.3	271	3	US-09-513-999C-20383	Sequence 20383, A
C 570	33	1.4	266	3	US-09-513-999C-16791	Sequence 16791, A	C 641	32	1.3	271	3	US-09-513-999C-20475	Sequence 20475, A
C 571	33	1.4	279	5	US-09-513-999C-30494	Sequence 30494, A	C 642	32	1.3	280	3	US-09-513-999C-16271	Sequence 92, App
C 572	33	1.4	284	3	US-09-984-429-674	Sequence 674, App	C 643	32	1.3	285	3	US-09-513-999C-26731	Sequence 26731, A
C 573	33	1.4	289	3	US-09-513-999C-15510	Sequence 15510, A	C 644	32	1.3	287	3	US-09-513-999C-16287	Sequence 16287, A
C 574	33	1.4	300	4	US-09-513-999C-19193	Sequence 19193, A	C 645	32	1.3	289	3	US-09-621-976-10116	Sequence 10116, A
C 575	33	1.4	300	4	US-09-297-648-807	Sequence 807, App	C 646	32	1.3	290	5	US-09-854-867-2	Sequence 2, App
C 576	33	1.4	306	4	US-09-297-648-1778	Sequence 1778, App	C 647	32	1.3	290	5	US-09-573-080A-2	Sequence 2, App
C 577	33	1.4	316	3	US-09-513-999C-10156	Sequence 10156, A	C 648	32	1.3	293	3	US-09-621-976-10356	Sequence 10356, A
C 578	33	1.4	318	5	US-09-984-429-684	Sequence 684, App	C 649	32	1.3	293	3	US-09-621-976-10404	Sequence 10404, A
C 579	33	1.4	322	3	US-09-513-999C-17715	Sequence 17715, A	C 650	32	1.3	293	3	US-09-621-976-11002	Sequence 11002, A
C 580	33	1.4	324	3	US-09-513-999C-30653	Sequence 30653, A	C 651	32	1.3	293	3	US-09-621-976-11159	Sequence 11159, A
C 581	33	1.4	328	3	US-09-621-976-13343	Sequence 13343, A	C 652	32	1.3	293	3	US-09-621-976-13512	Sequence 13512, A
C 582	33	1.4	331	5	US-09-513-999C-14891	Sequence 14891, A	C 653	32	1.3	294	3	US-09-621-976-13512	Sequence 13512, A
C 583	33	1.4	354	3	US-09-984-429-569	Sequence 569, App	C 654	32	1.3	297	3	US-09-621-976-19140	Sequence 19140, App
C 584	33	1.4	354	3	US-09-513-999C-17301	Sequence 17301, A	C 655	32	1.3	300	4	US-09-513-999C-19347	Sequence 19347, A
C 585	33	1.4	362	3	US-09-513-999C-18284	Sequence 18284, A	C 656	32	1.3	300	4	US-09-297-648-565	Sequence 565, App
C 586	33	1.4	364	3	US-09-513-999C-18284	Sequence 18284, A	C 657	32	1.3	300	4	US-09-297-648-588	Sequence 588, App
C 587	33	1.4	380	2	US-08-126-587C-5	Sequence 5, App	C 658	32	1.3	302	3	US-09-621-976-12531	Sequence 12531, A
C 588	33	1.4	409	3	US-09-621-976-7840	Sequence 7840, App	C 659	32	1.3	302	3	US-09-621-976-12531	Sequence 12531, A
C 589	33	1.4	423	3	US-09-513-999C-2436	Sequence 2436, A	C 660	32	1.3	302	3	US-09-513-999C-22664	Sequence 22664, A
C 590	33	1.4	430	3	US-09-621-976-14807	Sequence 14807, A	C 661	32	1.3	302	3	US-09-513-999C-31881	Sequence 31881, A
C 591	33	1.4	442	3	US-09-621-976-8885	Sequence 8885, App	C 662	32	1.3	303	3	US-09-621-976-9840	Sequence 9840, App
C 592	33	1.4	459	3	US-09-513-999C-13732	Sequence 13732, A	C 663	32	1.3	306	3	US-09-621-976-11059	Sequence 11059, A
C 593	33	1.4	464	3	US-09-513-999C-25384	Sequence 25384, A	C 664	32	1.3	306	3	US-09-513-999C-24726	Sequence 24726, A
C 594	33	1.4	466	3	US-09-621-976-14636	Sequence 14636, A	C 665	32	1.3	306	3	US-09-513-999C-18429	Sequence 18429, A
C 595	33	1.4	476	3	US-09-513-999C-11011	Sequence 11011, A	C 666	32	1.3	312	3	US-09-513-999C-18429	Sequence 18429, A
C 596	33	1.4	478	3	US-09-621-976-3278	Sequence 3278, App	C 667	32	1.3	312	3	US-09-513-999C-35552	Sequence 35552, A
C 597	33	1.4	478	3	US-09-621-976-12603	Sequence 12603, A	C 668	32	1.3	312	5	US-09-984-429-664	Sequence 664, App
C 598	33	1.4	483	3	US-09-621-976-9339	Sequence 9339, App	C 669	32	1.3	313	3	US-09-513-999C-14780	Sequence 14780, A
C 599	32	1.3	51	3	US-09-443-199C-1171	Sequence 1171, App	C 670	32	1.3	313	3	US-09-513-999C-16661	Sequence 16661, A
C 600	32	1.3	79	3	US-09-513-999C-16049	Sequence 16049, A	C 671	32	1.3	317	3	US-09-621-976-11601	Sequence 11601, A
C 601	32	1.3	101	4	US-09-513-999C-16266	Sequence 16266, A	C 672	32	1.3	318	3	US-09-621-976-8557	Sequence 8557, App
C 602	32	1.3	127	3	US-10-298-192-10	Sequence 10, App	C 673	32	1.3	318	5	US-09-984-429-663	Sequence 663, App
C 603	32	1.3	128	3	US-09-513-999C-20796	Sequence 20796, A	C 674	32	1.3	319	3	US-09-621-976-13089	Sequence 13089, A
C 604	32	1.3	132	3	US-09-513-999C-30475	Sequence 30475, A	C 675	32	1.3	328	3	US-09-513-999C-3047	Sequence 3047, App
C 605	32	1.3	134	5	US-09-513-999C-18947	Sequence 18947, A	C 676	32	1.3	328	3	US-09-513-999C-9189	Sequence 9189, App
C 606	32	1.3	138	3	US-09-984-429-497	Sequence 497, App	C 677	32	1.3	329	3	US-09-621-976-14481	Sequence 14481, A
C 607	32	1.3	140	3	US-09-513-999C-15769	Sequence 15769, A	C 678	32	1.3	331	3	US-09-621-976-12648	Sequence 12648, A
C 608	32	1.3	140	3	US-09-513-999C-20643	Sequence 20643, A	C 679	32	1.3	341	5	US-09-984-429-544	Sequence 544, App
							C 680	32	1.3	341	3	US-09-404-879A-136	Sequence 136, App

681	32	1.3	341	3	US-09-338-933-136	Sequence 136, App	C 754	31	1.3	99	3	US-09-621-976-12273	Sequence 12273, A
682	32	1.3	341	3	US-09-215-681-136	Sequence 136, App	C 755	31	1.3	99	3	US-09-621-976-12455	Sequence 12455, A
683	32	1.3	341	3	US-09-216-003A-136	Sequence 136, App	C 756	31	1.3	101	3	US-09-513-999C-119827	Sequence 119827, A
684	32	1.3	341	3	US-09-667-857-136	Sequence 136, App	C 757	31	1.3	103	3	US-09-513-999C-20286	Sequence 20286, A
685	32	1.3	341	3	US-10-198-053-136	Sequence 136, App	C 758	31	1.3	106	3	US-09-621-976-11978	Sequence 11978, A
686	32	1.3	341	3	US-09-827-271-136	Sequence 136, App	C 759	31	1.3	108	3	US-09-621-976-11953	Sequence 11953, A
C 687	32	1.3	342	3	US-09-513-999C-17216	Sequence 1216, A	C 760	31	1.3	108	3	US-09-621-976-12369	Sequence 12369, A
C 688	32	1.3	344	3	US-09-621-976-8364	Sequence 8364, App	C 761	31	1.3	109	3	US-09-621-976-11741	Sequence 11741, A
C 689	32	1.3	345	3	US-09-385-982-164	Sequence 164, App	C 762	31	1.3	109	3	US-09-621-976-12517	Sequence 12517, A
C 690	32	1.3	345	3	US-09-513-999C-17205	Sequence 17205, A	C 763	31	1.3	111	3	US-09-621-976-11767	Sequence 11767, A
C 691	32	1.3	351	3	US-09-621-976-2073	Sequence 2073, App	C 764	31	1.3	111	3	US-09-621-976-12297	Sequence 12297, A
C 692	32	1.3	354	3	US-09-513-999C-17501	Sequence 17501, A	C 765	31	1.3	112	3	US-09-621-976-11643	Sequence 11643, A
C 693	32	1.3	356	3	US-09-621-976-1713	Sequence 1713, App	C 766	31	1.3	112	3	US-09-621-976-12116	Sequence 12116, A
C 694	32	1.3	361	3	US-09-621-976-12979	Sequence 12979, A	C 767	31	1.3	112	3	US-09-621-976-12111	Sequence 12111, A
C 695	32	1.3	361	3	US-09-621-976-12200	Sequence 12200, A	C 768	31	1.3	112	3	US-09-621-976-13539	Sequence 13539, A
C 696	32	1.3	364	3	US-09-621-976-13012	Sequence 13012, A	C 769	31	1.3	113	3	US-09-621-976-11948	Sequence 11948, A
C 697	32	1.3	364	3	US-09-621-976-13012	Sequence 13012, A	C 770	31	1.3	113	3	US-09-621-976-11677	Sequence 11677, A
C 698	32	1.3	379	3	US-09-621-976-14107	Sequence 14107, A	C 771	31	1.3	114	3	US-09-621-976-11677	Sequence 11677, A
C 699	32	1.3	380	3	US-09-621-976-12667	Sequence 12667, A	C 772	31	1.3	114	3	US-09-621-976-11709	Sequence 11709, A
C 700	32	1.3	386	3	US-09-621-976-13315	Sequence 13315, A	C 773	31	1.3	115	3	US-09-621-976-12111	Sequence 12111, A
C 701	32	1.3	387	3	US-09-621-976-11533	Sequence 11533, A	C 774	31	1.3	115	3	US-09-621-976-13534	Sequence 13534, A
C 702	32	1.3	391	3	US-09-621-976-17431	Sequence 17431, A	C 775	31	1.3	117	3	US-09-621-976-12066	Sequence 12066, A
C 703	32	1.3	395	3	US-09-513-999C-29227	Sequence 29227, A	C 776	31	1.3	119	3	US-09-621-976-13567	Sequence 13567, A
C 704	32	1.3	402	3	US-09-621-976-9257	Sequence 9257, App	C 777	31	1.3	120	3	US-09-621-976-12045	Sequence 12045, A
C 705	32	1.3	403	3	US-09-513-999C-506	Sequence 506, App	C 778	31	1.3	121	3	US-09-621-976-11812	Sequence 11812, A
C 706	32	1.3	412	3	US-09-949-016-131318	Sequence 131318, A	C 779	31	1.3	122	3	US-09-513-999C-18921	Sequence 18921, A
C 707	32	1.3	422	3	US-09-621-976-12655	Sequence 12655, A	C 780	31	1.3	122	3	US-09-621-976-11578	Sequence 11578, A
C 708	32	1.3	426	3	US-09-621-976-1401	Sequence 1401, App	C 781	31	1.3	125	3	US-09-621-976-11934	Sequence 11934, A
C 709	32	1.3	427	3	US-09-513-999C-34315	Sequence 34315, A	C 782	31	1.3	125	3	US-09-621-976-12432	Sequence 12432, A
C 710	32	1.3	429	3	US-09-621-976-12834	Sequence 12834, A	C 783	31	1.3	125	3	US-09-621-976-12432	Sequence 12432, A
C 711	32	1.3	430	3	US-09-513-999C-32133	Sequence 32123, A	C 784	31	1.3	125	3	US-09-621-976-13603	Sequence 13603, A
C 712	32	1.3	430	3	US-09-621-976-13061	Sequence 13061, A	C 785	31	1.3	126	3	US-09-621-976-11810	Sequence 11810, A
C 713	32	1.3	433	3	US-09-621-976-18046	Sequence 18046, A	C 786	31	1.3	126	3	US-09-513-999C-21194	Sequence 21194, A
C 714	32	1.3	439	3	US-09-621-976-14074	Sequence 14074, A	C 787	31	1.3	127	3	US-09-621-976-11639	Sequence 11639, A
C 715	32	1.3	441	3	US-09-513-999C-1832	Sequence 1832, App	C 788	31	1.3	127	3	US-09-621-976-11656	Sequence 11656, A
C 716	32	1.3	447	3	US-09-621-976-17439	Sequence 17439, A	C 789	31	1.3	128	3	US-09-513-999C-18681	Sequence 18681, A
C 717	32	1.3	448	3	US-09-949-016-138979	Sequence 138979, A	C 790	31	1.3	128	3	US-09-513-999C-22168	Sequence 22168, A
C 718	32	1.3	449	3	US-09-513-999C-32313	Sequence 32313, A	C 791	31	1.3	129	3	US-09-621-976-12043	Sequence 12043, A
C 719	32	1.3	452	3	US-09-621-976-1537	Sequence 1537, App	C 792	31	1.3	130	3	US-09-621-976-11758	Sequence 11758, A
C 720	32	1.3	454	3	US-09-621-976-2920	Sequence 2920, App	C 793	31	1.3	132	3	US-09-621-976-11649	Sequence 11649, A
C 721	32	1.3	454	3	US-09-621-976-12336	Sequence 12336, A	C 794	31	1.3	132	3	US-09-621-976-12354	Sequence 12354, A
C 722	32	1.3	461	3	US-09-404-879A-1	Sequence 1, App1.1	C 795	31	1.3	133	3	US-09-621-976-13532	Sequence 13532, A
C 723	32	1.3	461	3	US-09-338-933-1	Sequence 1, App1.1	C 796	31	1.3	134	3	US-09-621-976-12378	Sequence 12378, A
C 724	32	1.3	461	3	US-09-338-933-1	Sequence 1, App1.1	C 797	31	1.3	134	3	US-09-621-976-12378	Sequence 12378, A
C 725	32	1.3	461	3	US-09-215-681-1	Sequence 1, App1.1	C 798	31	1.3	134	3	US-09-621-976-13549	Sequence 13549, A
C 726	32	1.3	461	3	US-09-215-681-1	Sequence 1, App1.1	C 799	31	1.3	135	3	US-09-621-976-11952	Sequence 11952, A
C 727	32	1.3	461	3	US-09-215-681-1	Sequence 1, App1.1	C 800	31	1.3	136	3	US-09-621-976-11952	Sequence 11952, A
C 728	32	1.3	461	3	US-09-216-003A-1	Sequence 1, App1.1	C 801	31	1.3	137	3	US-09-621-976-11705	Sequence 11705, A
C 729	32	1.3	461	3	US-09-216-003A-3	Sequence 1, App1.1	C 802	31	1.3	137	3	US-09-621-976-12379	Sequence 12379, A
C 730	32	1.3	461	3	US-09-667-857-1	Sequence 1, App1.1	C 803	31	1.3	140	3	US-09-513-999C-17158	Sequence 17158, A
C 731	32	1.3	461	3	US-09-667-857-3	Sequence 3, App1.1	C 804	31	1.3	141	3	US-09-621-976-12027	Sequence 12027, A
C 732	32	1.3	461	3	US-10-198-053-1	Sequence 1, App1.1	C 805	31	1.3	142	3	US-09-621-976-12027	Sequence 12027, A
C 733	32	1.3	461	3	US-10-198-053-3	Sequence 3, App1.1	C 806	31	1.3	143	3	US-09-621-976-11896	Sequence 11896, A
C 734	32	1.3	461	3	US-09-827-2271-1	Sequence 1, App1.1	C 807	31	1.3	143	3	US-09-621-976-11942	Sequence 11942, A
C 735	32	1.3	465	3	US-09-827-2271-3	Sequence 3, App1.1	C 808	31	1.3	144	3	US-09-621-976-12352	Sequence 12352, A
C 736	32	1.3	472	3	US-09-621-976-1859	Sequence 1859, App	C 809	31	1.3	161	3	US-09-621-976-12022	Sequence 12022, A
C 737	32	1.3	473	3	US-09-621-976-8819	Sequence 8819, App	C 810	31	1.3	162	3	US-09-621-976-11580	Sequence 11580, A
C 738	32	1.3	480	3	US-09-621-976-1652	Sequence 1652, App	C 811	31	1.3	162	3	US-09-621-976-11739	Sequence 11739, A
C 739	32	1.3	480	3	US-09-621-976-10615	Sequence 10615, A	C 812	31	1.3	162	3	US-09-621-976-12221	Sequence 12221, A
C 740	32	1.3	481	3	US-09-621-976-3464	Sequence 3464, App	C 813	31	1.3	162	3	US-09-621-976-12335	Sequence 12335, A
C 741	32	1.3	481	3	US-09-513-999C-11967	Sequence 31967, A	C 814	31	1.3	162	3	US-09-621-976-12416	Sequence 12416, A
C 742	32	1.3	484	3	US-09-621-976-14663	Sequence 14663, A	C 815	31	1.3	162	3	US-09-621-976-13553	Sequence 13553, A
C 743	32	1.3	485	3	US-09-621-976-2118	Sequence 2118, App	C 816	31	1.3	163	3	US-09-621-976-11668	Sequence 11668, A
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ALIGNMENTS

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RESULT 1
US-09-167-322-8
; Sequence 8, Application US/09167322
; Patent No. 6365151
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GENERAL INFORMATION:
APPLICANT: Allegheny University of the Health
Sciences, Halpern, Michael S.
England, James M.
TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 base pairs
TYPE: nucleic acid
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STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-167-322-8
Query Match 13.2%; Score 313; DB 3; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.3e-132;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-167-322-9
; Sequence 9, Application US/09167322
; Patent No. 6365151
;
GENERAL INFORMATION:
APPLICANT: Allegheny University of the Health
Sciences, Halpern, Michael S.
England, James M.
TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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RESULT 3
US-09-200-355-1

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/ APPLICANT: Ecker, David J.
/ TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
/ FILE REFERENCE: IBIS0009
/ CURRENT APPLICATION NUMBER: US/09/200,355
/ CURRENT FILING DATE: 1996-11-25
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 1
/ LENGTH: 199
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ IS-09-200-355-1

```

Query Match	6.2%	Score 148;	DB 3;	Length 199;
Best Local Similarity	77.9%;	Pred. No. 2.6e-57;		
Matches 155; Conservative	43;	Mismatches 1;	Indels 0;	Gaps 0

OY		24	GAAACGTGGGAGATCTTTGGGGAGACCCCACTCACAAGCGCAAAAACCCGGATGTGTAGA	303
Db		1	GAAACUGGGGAUUCUUAGGGAGACCCCACUCCAAACCCGAAAAACCCGGAGUGGAGAGA	60
OY		304	GCAGCGAATTGTGCATAACCAATGTCTGTACTTATGATGTCGTGTAAACCACTCAC	363
Db		61	GCAGGGAAAUUGUCAUAUACAACAGUUCUGAACCUAGUGGUUCUUAACCACTCAC	120
OY		364	AGATTTCAGCTTCGGAAACAAGAGACCTCGTGTTAGACCAAACCATTGCTTTTGAAGTTAT	423
Db		121	AGAUUUCAGCUCUCCGAAACAAGAGACCCUGUUAAGCAAAAGCANUGCUUUTUGAAUGUAV	180
OY		424	TAAAGCTGTGTGTCAACA	442
Db		181	UAAAGUCUGUUGAGUCACA	199

RESULT 4
US-09-200-355-2
; Sequence 2, Application US/09200355
; Patent No. 6451524
; GENERAL INFORMATION:
; APPLICANT: Becker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids

```

1 FILE REFERENCE: IB150009
2 CURRENT APPLICATION NUMBER: US/09/200,355
3 CURRENT FILING DATE: 1998-11-25
4 NUMBER OF SEQ ID NOS: 4
5 SOFTWARE: PatentIn version 3.1
6 SEQ ID NO: 1

```

```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-200-355-2

```

[illegible]

RESULT 5
US-09-621-976-12751/c

```

? APPLICANT: Lomas MAINE EDWARDS, J.B.
? APPLICANT: Joberc, S.
? APPLICANT: Giordano, J.Y.
? TITLE OF INVENTION: ESTrs and Encoded Human Proteins
? FILE REFERENCE: GENSET .054PR2
? CURRENT APPLICATION NUMBER: US/09/621,976
? CURRENT FILING DATE: 2000-07-21
? NUMBER OF SEQ ID NOS: 19335
? SOFTWARE: Patent.pm
? SEQ ID NO 12751
? LENGTH: 397
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 250
? OTHER INFORMATION: n=a, g, c or t
?-S-09-621-976-12751
```

Query Match	3.3%;	Score 78;	DB 3;	Length 397;
Best Local Similarity	100.0%;	Pred. No. 1.7e-25;		
Matches 78;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

OY	2284	TGTGTTAGCAGGAAATGCTCGATCTCCTGAACCTGGATTCGCCCACTGGCCCTTCCCA	2344
Dδ	210	GTTGTTAGCAGGAAATGCTCGATCTCCTGAACCTGGATTCGCCCACTGGCCCTTCCCA	151
OY	2344	AGTGCTGGGATTACAAGC	2361
Dδ	150	AGTGCTGGGATTACAAGC	133

RESULT 6
US-09-073-567-49/c
; Sequence 49, Application US/09073567
; Patent No. 6013786
; GENERAL INFORMATION:
; APPLICANT: Jiaodong Chen
; APPLICANT: Sudhir Agrawal
; APPLICANT: Ruiwen Zhang

```

; TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDowell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,567
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield, Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 99,057-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; HYPOTHEICAL: NO
; ANTI-SENSE: YES
; US-09-073-567-49

```

```

Query Match          3.1%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e-23;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      665 AGGTACATCTGTGAGTGAAGACAGGTGTACCTTGAGAGTGGAGTCAAAAGACCT 724
Db      73  AGGTACATCTGTGAGTGAAGACAGGTGTACCTTGAGAGTGGAGTCAAAAGACCT 14
Qy      725 TGTACAAGAGCTT 737
Db      13  TGTACAAGAGCTT 1

```

```

RESULT 7
US-09-541-848-49/C
; Sequence 49, Application US/09541848
; Patent No. 6946447
; GENERAL INFORMATION:
; APPLICANT: CHEN, Jiantong
; APPLICANT: AGRAWAL, Sudhir
; APPLICANT: ZHANG, Ruiwen
; TITLE OF INVENTION: MD-M2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 29924/98057C
; CURRENT APPLICATION NUMBER: US/09/541,848
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 09/383,507
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/073,567
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 08/916,834
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-541-848-49

```

```

Query Match          3.1%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e-23;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      665 AGGTACATCTGTGAGTGAAGACAGGTGTACCTTGAGAGTGGAGTCAAAAGACCT 724
Db      73  AGGTACATCTGTGAGTGAAGACAGGTGTACCTTGAGAGTGGAGTCAAAAGACCT 14
Qy      725 TGTACAAGAGCTT 737
Db      13  TGTACAAGAGCTT 1

```

```

RESULT 8
US-09-621-976-8284/C
; Sequence 8284, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8284
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-8284

```

```

Query Match          2.8%; Score 67; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2295 GATGTCCTCATCTCTGACCTCGTGATCCGCCCACTCGGCTCCCAAAAGTCTGGGAT 2354
Db      480 GATGTCCTCATCTCTGACCTCGTGATCCGCCCACTCGGCTCCCAAAAGTCTGGGAT 421
Qy      2355 TACAGGC 2361
Db      420 TACAGGC 414

```

```

RESULT 9
US-09-621-976-15415/C
; Sequence 15415, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15415
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-15415

```

```

Query Match          2.5%; Score 60; DB 3; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.6e-17;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2260 TTTTAGTAGACAGAGGGTTTCAACCGTGTAGCCAGGATGATCTCGATCTCGACCTCG 2319
|||||
DB 201 TTTTACTAGACAGAGGGTTTCAACCGTGTAGCCAGGATGATCTCGATCTCGACCTCG 142

RESULT 10
US-09-621-976-17159/c
; Sequence 17159, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO. 17159
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17159

Query Match 2.5%; Score 60; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.6e-17;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2304 GATCTCCTGACCTCGATCGGCGCCGCCACCTCGGCTCCCAAAGTGTGGATTACAGGGCAT 2363
|||||
DB 172 GATCTCCTGACCTCGATCGGCGCCGCCACCTCGGCTCCCAAAGTGTGGATTACAGGGCAT 113

RESULT 11
US-09-513-999C-18362
; Sequence 18362, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO. 18362
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-18362

Query Match 2.4%; Score 58; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.2e-16;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGAGGGTTTCAACCGTGTAGCCAGGATGATCTCGATCTCGACCTCG 2317
|||||
DB 67 TTTTAGTAGACAGAGGGTTTCAACCGTGTAGCCAGGATGATCTCGATCTCGACCTCG 124

RESULT 12
US-09-621-976-14420/c
; Sequence 14420, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO. 14420
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 417,454
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-14420

Query Match 2.4%; Score 58; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2275 GGTTTCAACCGTGTAGCCAGGATGATCTCGATCTCGACCTCGATCGGCGCCACT 2332
|||||
DB 341 GGTTTCAACCGTGTAGCCAGGATGATCTCGATCTCGACCTCGATCGGCGCCACT 284

RESULT 13
US-09-513-999C-32581
; Sequence 32581, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO. 32581
; LENGTH: 149
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 149
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-32581

Query Match 2.3%; Score 55; DB 3; Length 149;
Best Local Similarity 100.0%; Pred. No. 5.1e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCAACCGTGTAGCCAGGATGATCTCGATCTCGACCTCGATCGGCGCC 2328
|||||
DB 91 GGGTTTCAACCGTGTAGCCAGGATGATCTCGATCTCGACCTCGATCGGCGCC 145

RESULT 14
US-09-513-999C-27025
; Sequence 27025, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961


```
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 27025
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 162
; OTHER INFORMATION: s=g or c
; NAME/KEY: misc_feature
; LOCATION: 170
; OTHER INFORMATION: s=g or c
; US-09-513-999C-27025
```

```
Query Match 2.3%; Score 55; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 5.1e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2274 GGGTTTACCGTGTAGCCAGATGTCGATCTCCTGACCTCGTATCCGCC 2328
Db 66 GGGTTTACCGTGTAGCCAGATGTCGATCTCCTGACCTCGTATCCGCC 120
```

```
RESULT 15
US-09-513-999C-22797/C
; Sequence 22797, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22797
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-22797
```

```
Query Match 2.3%; Score 55; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 5e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2274 GGGTTTACCGTGTAGCCAGATGTCGATCTCCTGACCTCGTATCCGCC 2328
Db 125 GGGTTTACCGTGTAGCCAGATGTCGATCTCCTGACCTCGTATCCGCC 71
```

```
RESULT 16
US-09-513-999C-22123
; Sequence 22123, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
```

```
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22123
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-22123
```

```
Query Match 2.3%; Score 55; DB 3; Length 192;
Best Local Similarity 100.0%; Pred. No. 5e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2274 GGGTTTACCGTGTAGCCAGATGTCGATCTCCTGACCTCGTATCCGCC 2328
Db 88 GGGTTTACCGTGTAGCCAGATGTCGATCTCCTGACCTCGTATCCGCC 142
```

```
RESULT 17
US-09-984-429-629/C
; Sequence 629, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 629
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-984-429-629
```

```
Query Match 2.3%; Score 55; DB 5; Length 258;
Best Local Similarity 100.0%; Pred. No. 5e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2274 GGGTTTACCGTGTAGCCAGATGTCGATCTCCTGACCTCGTATCCGCC 2328
Db 62 GGGTTTACCGTGTAGCCAGATGTCGATCTCCTGACCTCGTATCCGCC 8
```

```
RESULT 18
US-09-621-976-13784/C
; Sequence 13784, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
```

```

; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13784
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13784

Query Match      2.3%; Score 55; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2274 GGGTTTCAACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTATCCGCC 2328
Db      125 GGGTTTCAACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTATCCGCC 71

RESULT 19
US-09-984-429-627/c
; Sequence 627, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 627
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-627

Query Match      2.3%; Score 55; DB 5; Length 294;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2274 GGGTTTCAACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTATCCGCC 2328
Db      102 GGGTTTCAACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTATCCGCC 48

RESULT 20
US-09-984-429-678/c
; Sequence 678, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```

```

; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 638
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-678

Query Match      2.3%; Score 55; DB 5; Length 300;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2274 GGGTTTCAACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTATCCGCC 2328
Db      94 GGGTTTCAACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTATCCGCC 40

RESULT 21
US-09-984-429-638/c
; Sequence 638, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 638
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-638
```

US-09-984-429-638

Query Match 2.3%; Score 55; DB 5; Length 301;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2274 GGGTTTACCGGTGTTAGCCAGATGATGTCGATCTCTGACCTCGATCCGCC 2328
Db 107 GGGTTTACCGGTGTTAGCCAGATGATGTCGATCTCTGACCTCGATCCGCC 53

RESULT 22
US-09-984-429-618/c
; Sequence 618, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 618
; LENGTH: 316
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-618

Query Match 2.3%; Score 55; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2274 GGGTTTACCGGTGTTAGCCAGATGATGTCGATCTCTGACCTCGATCCGCC 2328
Db 116 GGGTTTACCGGTGTTAGCCAGATGATGTCGATCTCTGACCTCGATCCGCC 62

RESULT 23
US-09-621-976-9777/c
; Sequence 9777, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9777
; LENGTH: 322
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 86
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9777

Query Match 2.3%; Score 55; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2274 GGGTTTACCGGTGTTAGCCAGATGATGTCGATCTCTGACCTCGATCCGCC 2328
Db 146 GGGTTTACCGGTGTTAGCCAGATGATGTCGATCTCTGACCTCGATCCGCC 92

RESULT 24
US-09-984-429-679/c
; Sequence 679, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 679
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-679

Query Match 2.3%; Score 55; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2274 GGGTTTACCGGTGTTAGCCAGATGATGTCGATCTCTGACCTCGATCCGCC 2328
Db 109 GGGTTTACCGGTGTTAGCCAGATGATGTCGATCTCTGACCTCGATCCGCC 55

RESULT 25
US-09-513-999C-34128/c
; Sequence 34128, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; Patent No. 6783961
; CURRENT APPLICATION NUMBER: US/09/513,999C

```

; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 34128
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 190
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 293
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 299
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 305
; OTHER INFORMATION: r=a or g
; US-09-513-999C-34128

```

```

Query Match      2.3%; Score 55; DB 3; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2274 GGGTTTACCGGTGTAGCCAGAGATGTCCTCATCTCTGACCTCGTATCCGCCCC 2328
Db      282 GGGTTTACCGGTGTAGCCAGAGATGTCCTCATCTCTGACCTCGTATCCGCCCC 228

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RESULT 26

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; US-09-984-429-521/c
; Sequence 521, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 521
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-984-429-521

```

```

Query Match      2.3%; Score 55; DB 5; Length 370;

```

```

Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2274 GGGTTTACCGGTGTAGCCAGAGATGTCCTCATCTCTGACCTCGTATCCGCCCC 2328
Db      156 GGGTTTACCGGTGTAGCCAGAGATGTCCTCATCTCTGACCTCGTATCCGCCCC 102

```

RESULT 27

```

; US-09-621-976-13869/c
; Sequence 13869, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Joderc, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13869
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-13869

```

```

Query Match      2.3%; Score 55; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2274 GGGTTTACCGGTGTAGCCAGAGATGTCCTCATCTCTGACCTCGTATCCGCCCC 2328
Db      189 GGGTTTACCGGTGTAGCCAGAGATGTCCTCATCTCTGACCTCGTATCCGCCCC 135

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RESULT 28

```

; US-09-949-016-80631
; Sequence 80631, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMERPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80631
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-80631

```

```

Query Match      2.3%; Score 55; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2274 GGGTTTACCGGTGTAGCCAGAGATGTCCTCATCTCTGACCTCGTATCCGCCCC 2328
Db      83 GGGTTTACCGGTGTAGCCAGAGATGTCCTCATCTCTGACCTCGTATCCGCCCC 137

```

RESULT 29

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US-09-880-107-445

```

```
; Sequence 445, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 445
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 AA218727
; US-09-880-107-445

Query Match          2.3%; Score 54; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2274 GGGTTACCGGTGTTAGCCAGATGTCGATCTCTCGACTCGATCGGCC 2327
Db      171 GGGTTACCGGTGTTAGCCAGATGTCGATCTCTCGACTCGATCGGCC 224

RESULT 30
US-09-984-429-643/C
; Sequence 643, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 643
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98)..(98)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-984-429-643
```

```
Query Match          2.2%; Score 53; DB 5; Length 301;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2276 GTTTCACCGGTGTTAGCCAGATGTCGATCTCTCGACTCGATCGGCC 2328
Db      97 GTTTCACCGGTGTTAGCCAGATGTCGATCTCTCGACTCGATCGGCC 45

RESULT 31
US-09-621-976-13091/C
; Sequence 13091, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13091
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-13091

Query Match          2.2%; Score 53; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2275 GGTTCACCGGTGTTAGCCAGATGTCGATCTCTCGACTCGATCGGCC 2327
Db      287 GGTTCACCGGTGTTAGCCAGATGTCGATCTCTCGACTCGATCGGCC 235

RESULT 32
US-09-513-999C-32057/C
; Sequence 32057, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 32057
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 215
; OTHER INFORMATION: s=g or c
; US-09-513-999C-32057

Query Match          2.2%; Score 51; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.3e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2274 GGGTTACCGGTGTTAGCCAGATGTCGATCTCTCGACTCGATCGGCC 2324
Db      75 GGGTTACCGGTGTTAGCCAGATGTCGATCTCTCGACTCGATCGGCC 25
```

```
RESULT 33
US-09-297-648-1408
; Sequence 1408, Application US/09297648
; Patent No. 6964868
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhardt, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassan, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Cirkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, William Lee
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: No. 6964868e1 Human Genes and Gene Expression
; FILE REFERENCE: 2300-1481
; CURRENT APPLICATION NUMBER: US/09/297,648
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,666
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,515
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/105,234
; NUMBER OF SEQ ID NOS: 5252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1408
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-297-648-1408

Query Match      2.2%; Score 51; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2274 GGGTTACCGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 2324
Db      12 GGGTTACCGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 62

RESULT 34
US-09-621-976-14124/c
; Sequence 14124, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
```

```
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14124
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14124

Query Match      2.2%; Score 51; DB 3; Length 315;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2274 GGGTTACCGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 2324
Db      301 GGGTTACCGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 251

RESULT 35
US-09-621-976-8313/c
; Sequence 8313, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8313
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8313

Query Match      2.2%; Score 51; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2274 GGGTTACCGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 2324
Db      395 GGGTTACCGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 345

RESULT 36
US-10-131-827-4749
; Sequence 4749, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4749
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4749
```

Query Match 2.1%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1747 GACACCAATTCAATGATGTTGCTAACTATTTCCCTAGTGACCTGT 1796
Db 1 GACACCAATTCAATGATGTTGCTAACTATTTCCCTAGTGACCTGT 50

RESULT 37
US-10-131-831-4749
; Sequence 4749, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Mohlemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE REFERENCE: 50661200121
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4749
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-4749

Query Match 2.1%; Score 50; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1747 GACACCAATTCAATGATGTTGCTAACTATTTCCCTAGTGACCTGT 1796
Db 1 GACACCAATTCAATGATGTTGCTAACTATTTCCCTAGTGACCTGT 50

RESULT 38
US-09-513-999C-32786
; Sequence 32786, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 32786
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-32786

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Best Local Similarity 100.0%; Pred. No. 9.8e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 39
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; Sequence 23250, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 23250
; LENGTH: 133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-23250

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Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 GGGTTACCGGTGTTAGCCAGATGCTCTCATCTCTCTGATC 74

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; Sequence 22153, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22153
; LENGTH: 215
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 140
; OTHER INFORMATION: k=g or t
US-09-513-999C-22153

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Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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• Tue Aug 8 11:14:49 2006

us-09-966-724b-2.011go.rml

Page 19

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Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

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Minimum DB seq length: 5

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Post-processing: Listing first 1000 summaries

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SUMMARIES

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122	58	2.4	239	4	AAI62870	AAI62870 Human gen	195	57	2.4	422	4	AAK79346	Aak79346 Human imm
123	58	2.4	270	4	ABK42329	ABk42329 Genomic s	C 196	57	2.4	429	5	ABV10402	Abv10402 Human pro
124	58	2.4	270	4	ABK42330	ABk42330 Genomic s	197	57	2.4	463	5	ADL42591	AdL42591 Human ova
125	58	2.4	270	9	ADB60486	ADB60486 Connectiv	C 198	57	2.4	466	4	AAI03506	AAI03506 Human rep
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C 269	55	2.3	287	4	AAK76576	Aak76576 Human imm	C 342	55	2.3	308	4	AAK75667	Aak75667 Human imm
C 270	55	2.3	287	4	AAK65493	Aak65493 Human imm	C 343	55	2.3	308	4	AAK75667	Aak75667 Human imm
C 271	55	2.3	287	14	ADY78745	AdY78745 Aluy subf	C 344	55	2.3	308	4	AAK75667	Aak75667 Human imm
C 272	55	2.3	287	14	ADY78748	AdY78748 Aluy subf	C 345	55	2.3	308	5	AAK75667	Aak75667 Human imm
C 273	55	2.3	288	4	AAK66381	Aak66381 Human imm	C 346	55	2.3	308	8	ABZ74179	AbZ74179 Secreted
C 274	55	2.3	288	11	ADZ57847	AdZ57847 Human imm	C 347	55	2.3	308	8	ADA98708	Ada98708 Human sec
C 275	55	2.3	290	4	AAK65530	Aak65530 Human imm	C 348	55	2.3	308	8	ADA44412	Ada44412 Human sec
C 276	55	2.3	290	4	AAI62895	Aai62895 Human gen	C 349	55	2.3	308	10	ABZ67745	AbZ67745 Human sec
C 277	55	2.3	293	4	AAI62841	Aai62841 Human gen	C 350	55	2.3	310	4	AAK82057	AAK82057 Human imm
C 278	55	2.3	294	4	AAK71496	Aak71496 Human imm	C 351	55	2.3	310	4	AAK65531	Aak65531 Human imm
C 279	55	2.3	294	4	AAK68338	Aak68338 Human imm	C 352	55	2.3	310	4	AAK65503	Aak65503 Human imm
C 280	55	2.3	294	4	AAK72748	Aak72748 Human imm	C 353	55	2.3	310	4	AAK77227	AAK77227 Human imm
C 281	55	2.3	294	4	AAK67727	Aak67727 Human imm	C 354	55	2.3	310	4	AAK77227	AAK77227 Human imm
C 282	55	2.3	294	4	AAK84093	Aak84093 Human imm	C 355	55	2.3	311	4	AAI62896	Aai62896 Human gen
C 283	55	2.3	294	5	ABA21131	AbA21131 Human ner	C 356	55	2.3	311	4	AAK65494	Aak65494 Human imm
C 284	55	2.3	294	5	ADA41531	Ada41531 Human sec	C 357	55	2.3	311	5	ABA15631	AbA15631 Human gen
C 285	55	2.3	294	8	ACC50874	Acc50874 Human sec	C 358	55	2.3	314	4	AAK76575	Aak76575 Human ner
C 286	55	2.3	294	10	ADA57659	Ada57659 Human sec	C 359	55	2.3	314	4	AAK71376	Aak71376 Human imm
C 287	55	2.3	294	12	ADJ12773	Adj12773 DNA fragm	C 360	55	2.3	314	4	AAI06326	Aai06326 Human imm
C 288	55	2.3	296	5	ABA20541	AbA20541 Human ner	C 361	55	2.3	314	4	AAI06326	Aai06326 Human imm
C 289	55	2.3	297	4	AAK65522	Aak65522 Human imm	C 362	55	2.3	316	4	AAI62889	Aai62889 Human gen
C 290	55	2.3	297	4	AAI35818	Aai35818 Human mus	C 363	55	2.3	316	4	AAK67726	Aak67726 Human imm
C 291	55	2.3	297	4	AAI62863	Aai62863 Human gen	C 364	55	2.3	316	4	AAK71495	Aak71495 Human imm
C 292	55	2.3	297	8	ABX58806	AbX58806 CDNA enco	C 365	55	2.3	316	4	AAK84090	Aak84090 Human imm
C 293	55	2.3	297	12	ADJ28556	Adj28556 Human mus	C 366	55	2.3	316	8	ABZ74071	AbZ74071 Secreted
C 294	55	2.3	298	4	AAK83322	Aak83322 Human imm	C 367	55	2.3	316	8	ADA4385	Ada4385 Human sec
C 295	55	2.3	299	4	AAK65533	Aak65533 Human imm	C 368	55	2.3	316	12	ADJ12764	Adj12764 DNA fragm
C 296	55	2.3	299	4	AAK71491	Aak71491 Human imm	C 369	55	2.3	318	5	ABA21135	AbA21135 Human ner
C 297	55	2.3	299	4	AAI32648	Aai32648 Human gen	C 370	55	2.3	322	4	AAK90995	Aak90995 Human dig
C 298	55	2.3	299	4	AAI62898	Aai62898 Human gen	C 371	55	2.3	322	4	AAK71484	Aak71484 Human imm
C 299	55	2.3	299	8	ABZ74206	AbZ74206 Secreted	C 372	55	2.3	322	4	AAK84420	Aak84420 Human imm
C 300	55	2.3	299	8	ABZ74193	AbZ74193 Secreted	C 373	55	2.3	322	4	AAK83275	Aak83275 Human imm
C 301	55	2.3	299	8	ABZ74107	AbZ74107 Secreted	C 374	55	2.3	322	4	AAK83275	Aak83275 Human imm
C 302	55	2.3	299	8	ADA98722	Ada98722 Human sec	C 375	55	2.3	322	4	AAK84073	Aak84073 Human imm
C 303	55	2.3	299	8	ADA98735	Ada98735 Human sec	C 376	55	2.3	322	4	AAK84419	Aak84419 Human imm
C 304	55	2.3	299	8	ADA44421	Ada44421 Human sec	C 377	55	2.3	322	4	AAK67711	AAK67711 Human imm
C 305	55	2.3	299	10	ABZ67772	AbZ67772 Human sec	C 378	55	2.3	322	4	AAK85224	AAK85224 Human imm
C 306	55	2.3	299	10	ABZ67759	AbZ67759 Human sec	C 379	55	2.3	322	4	AAK82750	Aak82750 Human imm
C 307	55	2.3	300	4	AAK71479	Aak71479 Human imm	C 380	55	2.3	322	4	AAI19650	Aai19650 Human exp
C 308	55	2.3	300	4	AAK86793	Aak86793 Human imm	C 381	55	2.3	322	4	AAI02925	Aai02925 Human rep
C 309	55	2.3	300	4	AAK71292	Aak71292 Human imm	C 382	55	2.3	322	5	ABA18115	AbA18115 Human gen
C 310	55	2.3	300	4	AAK67699	Aak67699 Human imm	C 383	55	2.3	322	5	AAK32030	Aak32030 Human liv

C 384	55	2.3	322	6	ABN90385	Abn90385 Human liv	C 457	54	2.3	243	4	AAK6798	AAK6798 Human imm
C 385	55	2.3	322	8	ABZ74102	ABZ74102 Secreced	458	54	2.3	280	4	AAK89056	AAK89056 Human dig
C 386	55	2.3	322	8	ADA44416	ADA4416 Human sec	459	54	2.3	280	5	AAK89056	AAK89056 Human dig
C 387	55	2.3	322	11	ADJ15298	Adj15298 Human liv	460	54	2.3	280	4	ADBJ32612	ADBJ32612 Human b
C 388	55	2.3	322	12	ADJ12825	Adj12825 DNA fragm	461	54	2.3	283	4	AAJ02835	AAJ02835 Human nov
C 389	55	2.3	324	4	AAJ06324	AAJ06324 Human rep	462	54	2.3	283	5	AAJ02865	AAJ02865 Human rep
C 390	55	2.3	325	4	AAK85270	AAK85270 Human imm	463	54	2.3	283	11	ADJ09492	Adj09492 Human pro
C 391	55	2.3	326	4	AAK82942	AAK82942 Human imm	464	54	2.3	286	4	AAK68557	AAK68557 Human imm
C 392	55	2.3	326	4	AAK82941	AAK82941 Human imm	465	54	2.3	292	8	ADA41537	Ada41537 Human sec
C 393	55	2.3	327	4	AAK74122	AAK74122 Human imm	466	54	2.3	292	8	ACC50880	ACC50880 Human sec
C 394	55	2.3	328	3	AAK30053	AAK30053 Human sec	467	54	2.3	292	10	ADA57665	Ada57665 BAC fragm
C 395	55	2.3	331	4	AAK78782	AAK78782 Human imm	468	54	2.3	297	4	AAK72356	AAK72356 Human imm
C 396	55	2.3	331	4	AAK70954	AAK70954 Human imm	469	54	2.3	298	8	ADA41599	Ada41599 Human sec
C 397	55	2.3	332	4	AAK90745	AAK90745 Human dig	470	54	2.3	298	9	ADB91891	ADB91891 Human sec
C 398	55	2.3	332	4	AAK68510	AAK68510 Human imm	471	54	2.3	300	4	AAK71675	AAK71675 Human imm
C 399	55	2.3	332	4	AAJ06012	AAJ06012 Human rep	472	54	2.3	301	4	AAK84092	AAK84092 Human imm
C 400	55	2.3	332	4	ABJ98577	ABJ98577 Human tes	473	54	2.3	302	4	AAK71674	AAK71674 Human imm
C 401	55	2.3	337	8	AAJ37420	AAJ37420 Human mus	474	54	2.3	303	4	AAK71441	AAK71441 Human imm
C 402	55	2.3	337	8	ABX60408	ABX60408 cDNA enco	475	54	2.3	303	4	AAJ36178	AAJ36178 Human mus
C 403	55	2.3	347	12	ADJ31158	Adj31158 Human mus	476	54	2.3	303	4	AAJ36170	AAJ36170 Human mus
C 404	55	2.3	347	4	AAK81654	AAK81654 Human imm	477	54	2.3	303	4	AAJ28342	AAJ28342 Genomic s
C 405	55	2.3	358	9	ACH50498	ACH50498 Human leu	478	54	2.3	303	5	ABA19144	ABA19144 Human ner
C 406	55	2.3	370	12	ADJ12667	Adj12667 DNA fragm	479	54	2.3	303	8	ABX59158	ABX59158 cDNA enco
C 407	55	2.3	378	5	ABV13490	ABV13490 Human pro	480	54	2.3	303	8	ABX59165	ABX59165 cDNA enco
C 408	55	2.3	385	5	ABV14869	ABV14869 Human pro	481	54	2.3	303	10	ADG41538	ADG41538 Human tes
C 409	55	2.3	398	14	ACL55126	ACL55126 Human col	482	54	2.3	303	11	ADJ197312	Adj197312 Human tes
C 410	55	2.3	404	6	ABL67851	ABL67851 Ovary can	483	54	2.3	303	12	ADJ29916	Adj29916 Human mus
C 411	55	2.3	408	5	ABV34605	ABV34605 Human pro	484	54	2.3	308	4	AAK87658	AAK87658 Human imm
C 412	55	2.3	417	4	AAH10519	AAH10519 Human CDN	485	54	2.3	308	4	AAK77873	AAK77873 Human imm
C 413	55	2.3	427	8	ABZ74217	ABZ74217 Secreced	486	54	2.3	308	4	AAK77873	AAK77873 Human imm
C 414	55	2.3	427	8	ADA98746	ADA98746 Human sec	487	54	2.3	308	4	AAK72213	AAK72213 Human imm
C 415	55	2.3	427	10	ABZ67783	ABZ67783 Human sec	488	54	2.3	308	8	ACC50934	ACC50934 Human sec
C 416	55	2.3	429	5	ADJ176153	Adj176153 Human ova	489	54	2.3	308	8	ABZ71532	ABZ71532 Secreced
C 417	55	2.3	429	5	ADJ69818	ADJ69818 Human ova	490	54	2.3	308	9	ADB91903	ADB91903 Human sec
C 418	55	2.3	441	4	AAK86113	AAK86113 Human imm	491	54	2.3	308	10	ADCT4691	ADCT4691 Human sec
C 419	55	2.3	441	4	AAK86111	AAK86111 Human imm	492	54	2.3	309	4	AAJ35832	AAJ35832 Human mus
C 420	55	2.3	441	4	AAJ04060	AAJ04060 Human rep	493	54	2.3	309	8	ABX58820	ABX58820 cDNA enco
C 421	55	2.3	441	5	AAJ04061	AAJ04061 Human rep	494	54	2.3	314	12	ADJ29570	Adj29570 Human mus
C 422	55	2.3	441	5	AAJ04046	AAJ04046 DNA enco	495	54	2.3	314	4	AAK66997	AAK66997 Human imm
C 423	55	2.3	441	5	AAJ04047	AAJ04047 DNA enco	496	54	2.3	316	4	AAK75434	AAK75434 Human imm
C 424	55	2.3	441	5	ABV05700	ABV05700 Human pro	497	54	2.3	324	5	AAJ02832	AAJ02832 Human rep
C 425	55	2.3	441	11	ADJ09652	Adj09652 Human pro	498	54	2.3	324	5	AAJ02832	AAJ02832 Human rep
C 426	55	2.3	441	11	ADJ09653	Adj09653 Human pro	499	54	2.3	324	11	ADJ09489	Adj09489 Human pro
C 427	55	2.3	442	9	ACH24731	ACH24731 Human adu	500	54	2.3	326	5	ABV09591	ABV09591 Human pro
C 428	55	2.3	447	6	ABN61857	ABN61857 Human can	501	54	2.3	333	4	AAK79198	AAK79198 Human imm
C 429	55	2.3	449	5	ABV38956	ABV38956 Human pro	502	54	2.3	375	5	ABV39735	ABV39735 Human pro
C 430	55	2.3	449	5	ABV53736	ABV53736 Human pro	503	54	2.3	375	5	ABV30767	ABV30767 Human pro
C 431	55	2.3	451	5	ADJ39067	ADJ39067 Human ova	504	54	2.3	407	5	ABV12806	ABV12806 Human pro
C 432	55	2.3	459	12	ADN13569	ADN13569 Human pro	505	54	2.3	411	6	ABL66140	ABL66140 Human pro
C 433	55	2.3	461	4	AAK82763	AAK82763 Human imm	506	54	2.3	412	9	ACH29052	ACH29052 Gene #445
C 434	55	2.3	463	4	AAJ36479	AAJ36479 Human car	507	54	2.3	412	9	ACH29052	ACH29052 Human adu
C 435	55	2.3	463	4	AAJ36478	AAJ36478 Human car	508	54	2.3	447	5	ABV03637	ABV03637 Human pro
C 436	55	2.3	463	10	ADJ47173	ADJ47173 Human car	509	54	2.3	458	5	ABV3935	ABV3935 Human pro
C 437	55	2.3	463	10	ADJ47172	ADJ47172 Human car	510	54	2.3	458	5	ABV42808	ABV42808 Human pro
C 438	55	2.3	463	13	ADJ08590	ADJ08590 Human car	511	54	2.3	463	4	AAK88748	AAK88748 Human dig
C 439	55	2.3	463	13	ADJ08591	ADJ08591 Human car	512	54	2.3	463	4	AAK31782	AAK31782 Human liv
C 440	55	2.3	480	5	ADJ62669	ADJ62669 Human ova	513	54	2.3	463	6	ABN60297	ABN60297 Human can
C 441	55	2.3	486	5	ABV49991	ABV49991 Human pro	514	54	2.3	463	6	ABN60137	ABN60137 Human liv
C 442	55	2.3	496	5	AAJ65878	AAJ65878 DNA enco	515	54	2.3	463	11	ADJ14904	ADJ14904 Human liv
C 443	55	2.3	497	9	ACH27615	ACH27615 Human adu	516	54	2.3	476	6	ABV87857	ABV87857 Human col
C 444	55	2.3	101	4	ABK43115	ABK43115 Genomic s	517	54	2.3	298	4	AAK90251	AAK90251 Human tes
C 445	55	2.3	101	4	AAK90943	AAK90943 Human dig	518	53	2.2	105	4	AAK79088	AAK79088 Human imm
C 446	55	2.3	101	5	AAK51978	AAK51978 Human liv	519	53	2.2	123	4	AAK79091	AAK79091 Human imm
C 447	55	2.3	101	6	ABN90333	ABN90333 Human liv	520	53	2.2	134	4	AAK81169	AAK81169 Human imm
C 448	55	2.3	101	9	ADJ61271	ADJ61271 Connectiv	521	53	2.2	289	4	AAK74211	AAK74211 Human imm
C 449	55	2.3	101	11	ADJ15246	ADJ15246 Human liv	522	53	2.2	293	4	AAJ05082	AAJ05082 Human rep
C 450	55	2.3	116	4	AAK75304	AAK75304 Human imm	523	53	2.2	293	4	ABL97975	ABL97975 Human tes
C 451	55	2.3	116	4	AAK74678	AAK74678 Human imm	524	53	2.2	298	4	AAK90251	AAK90251 Human dig
C 452	55	2.3	116	4	AAK74679	AAK74679 Human imm	525	53	2.2	298	5	AAJ39880	AAJ39880 Genomic s
C 453	55	2.3	158	4	AAJ62839	AAJ62839 Human gen	526	53	2.2	298	9	ADB32840	ADB32840 Human nov
C 454	55	2.3	186	4	AAK85783	AAK85783 Human imm	527	53	2.2	301	4	AAK67724	AAK67724 Human imm
C 455	55	2.3	204	4	AAK85791	AAK85791 Human imm	528	53	2.2	301	4	AAK84088	AAK84088 Human imm
C 456	55	2.3	240	4	AAK71189	AAK71189 Human imm	529	53	2.2	301	12	ADJ12789	Adj12789 DNA fragm

C 530	53	2.2	339	5	ABV38767	Human pro	C 603	51	2.2	300	4	AAK71494	AAK71494	Human imm
C 531	53	2.2	394	5	ABV48163	Human pro	C 604	51	2.2	300	4	AAK76791	AAK76791	Human imm
C 532	53	2.2	416	5	ABV18377	Human pro	C 605	51	2.2	300	4	AAK84083	AAK84083	Human imm
C 533	53	2.2	439	5	ABV08877	Human pro	C 606	51	2.2	300	4	AAK67719	AAK67719	Human imm
C 534	53	2.2	498	9	ACH43429	Human toe	C 607	51	2.2	300	4	AAK69602	AAK69602	Human imm
C 535	53	2.2	500	6	ABN64113	Human can	C 608	51	2.2	300	8	AD274082	AD274082	Human sec
C 536	52	2.2	235	4	AAK68600	Human imm	C 609	51	2.2	300	8	ADA44396	ADA44396	Human sec
C 537	52	2.2	235	4	AAK65499	Human imm	C 610	51	2.2	303	4	AAK80840	AAK80840	Human imm
C 538	52	2.2	238	4	AAI99111	Human exc	C 611	51	2.2	307	4	AAK83623	AAK83623	Human imm
C 539	52	2.2	238	4	AAK65760	Human imm	C 612	51	2.2	308	8	AB274197	AB274197	Human imm
C 540	52	2.2	238	5	AAI63461	Human kid	C 613	51	2.2	308	8	AB274198	AB274198	Human sec
C 541	52	2.2	309	5	ABAI9091	Human ner	C 614	51	2.2	308	8	ADA98727	ADA98727	Human sec
C 542	52	2.2	320	5	ABAI7067	Human ner	C 615	51	2.2	308	8	ADA98726	ADA98726	Human sec
C 543	52	2.2	354	4	AAH98762	Human EST	C 616	51	2.2	308	10	AB267764	AB267764	Human sec
C 544	52	2.2	368	14	ACL58916	Human col	C 617	51	2.2	308	10	AB267763	AB267763	Human sec
C 545	52	2.2	394	4	AAI85259	Human pol	C 618	51	2.2	310	4	AAK85375	AAK85375	Human imm
C 546	52	2.2	395	5	AAI65301	Novel hum	C 619	51	2.2	313	8	AB274177	AB274177	Human sec
C 547	52	2.2	407	6	ABL83907	Human ova	C 620	51	2.2	313	8	ADA98706	ADA98706	Human sec
C 548	52	2.2	461	5	ABV58360	Human pro	C 621	51	2.2	313	10	AB267743	AB267743	Human sec
C 549	52	2.2	487	5	ABV48273	Human pro	C 622	51	2.2	314	4	AAK69299	AAK69299	Human imm
C 550	52	2.2	118	4	AAI05636	Human rep	C 623	51	2.2	314	4	AAK86803	AAK86803	Human imm
C 551	51	2.2	119	4	AAK86641	Human imm	C 624	51	2.2	314	5	ABAI0684	ABAI0684	Human imm
C 552	51	2.2	128	4	AAK82487	Human imm	C 625	51	2.2	314	5	ABAI7726	ABAI7726	Human ner
C 553	51	2.2	129	4	AAK73560	Human imm	C 626	51	2.2	318	5	ABAI18466	ABAI18466	Human ner
C 554	51	2.2	129	4	AAK87162	Human imm	C 627	51	2.2	319	5	AAK86995	AAK86995	Human imm
C 555	51	2.2	163	4	AAK81159	Human imm	C 628	51	2.2	323	8	AB274180	AB274180	Human imm
C 556	51	2.2	163	4	AAK78885	Human imm	C 629	51	2.2	323	8	ADA98709	ADA98709	Human sec
C 557	51	2.2	167	8	AB274228	Secreted	C 630	51	2.2	323	10	AB267746	AB267746	Human sec
C 558	51	2.2	167	8	ADA98757	Human sec	C 631	51	2.2	326	4	AAI03402	AAI03402	Human rep
C 559	51	2.2	167	10	AB267794	Human sec	C 632	51	2.2	326	5	AAI03400	AAI03400	Human rep
C 560	51	2.2	174	10	ACD97602	Human col	C 633	51	2.2	326	5	ABAI19502	ABAI19502	Human ner
C 561	51	2.2	186	4	AAK72166	Human imm	C 634	51	2.2	329	5	AAI37625	AAI37625	Human ner
C 562	51	2.2	194	4	AAI36061	Human mus	C 635	51	2.2	329	5	ABAI21063	ABAI21063	Human mus
C 563	51	2.2	194	4	ABX59049	CDNA enco	C 636	51	2.2	329	8	ABX60613	ABX60613	Human ner
C 564	51	2.2	194	12	ADJ29799	Human mus	C 637	51	2.2	329	12	ADJ31363	ADJ31363	Human mus
C 565	51	2.2	196	4	AAK79620	Human imm	C 638	51	2.2	335	5	AAI99076	AAI99076	Human exc
C 566	51	2.2	199	4	AAK80837	Human imm	C 639	51	2.2	335	5	AAI63426	AAI63426	Human kid
C 567	51	2.2	201	13	ADS38357	Human aut	C 640	51	2.2	342	6	ABI85299	ABI85299	Human ova
C 568	51	2.2	229	4	AAK65532	Human imm	C 641	51	2.2	358	8	AB274216	AB274216	Human sec
C 569	51	2.2	229	4	AAI62897	Human gen	C 642	51	2.2	358	8	ADA98745	ADA98745	Human sec
C 570	51	2.2	231	3	AAK27982	Human sec	C 643	51	2.2	358	10	AB267782	AB267782	Human sec
C 571	51	2.2	254	4	AA626722	Human gen	C 644	51	2.2	364	14	AED26410	AED26410	Human sec
C 572	51	2.2	254	8	ABX74071	Human nov	C 645	51	2.2	372	4	AAK64160	AAK64160	Human imm
C 573	51	2.2	270	4	AAK86794	Human imm	C 646	51	2.2	392	5	ABV40657	ABV40657	Human pro
C 574	51	2.2	270	4	AAK67703	Human imm	C 647	51	2.2	392	5	ABV44065	ABV44065	Human pro
C 575	51	2.2	270	5	AAK78884	Human imm	C 648	51	2.2	401	4	AAK95622	AAK95622	Human neu
C 576	51	2.2	270	5	ABAI9080	Human ner	C 649	51	2.2	401	4	AAK97115	AAK97115	Human neu
C 577	51	2.2	270	5	ABAI9080	Human ner	C 650	51	2.2	401	6	ABT00392	ABT00392	Human neu
C 578	51	2.2	270	8	AB274104	Secreted	C 651	51	2.2	401	6	ABT01885	ABT01885	Human neu
C 579	51	2.2	270	8	ADA41540	Human sec	C 652	51	2.2	401	11	ADW70711	ADW70711	Human neu
C 580	51	2.2	270	8	ACC50883	Human sec	C 653	51	2.2	421	9	ACH48623	ACH48623	Human leu
C 581	51	2.2	270	8	ADA44418	Human sec	C 654	51	2.2	424	5	ABV59242	ABV59242	Human pro
C 582	51	2.2	280	10	ADA57668	Human sec	C 655	51	2.2	428	5	AB207094	AB207094	Human pro
C 583	51	2.2	280	14	ACL54518	AD257668 BAC fragm	C 656	51	2.2	442	13	ACF89303	ACF89303	Human ner
C 584	51	2.2	290	4	AAK80835	AD54518 Human col	C 657	51	2.2	461	6	ABI85524	ABI85524	Human ova
C 585	51	2.2	291	4	AAK85376	Human imm	C 658	51	2.2	475	12	ADN12992	ADN12992	Human pro
C 586	51	2.2	292	4	ABK42960	Genomic s	C 659	51	2.2	484	5	ABV57673	ABV57673	Human pro
C 587	51	2.2	292	4	ABK42957	Genomic s	C 660	51	2.2	489	9	ACH13366	ACH13366	Human adu
C 588	51	2.2	292	9	ADB61116	Connectiv	C 661	51	2.2	490	4	AA532394	AA532394	Human cdn
C 589	51	2.2	292	9	ADB61113	Connectiv	C 662	51	2.2	491	5	AA572613	AA572613	DNA encod
C 590	51	2.2	293	4	AAK71486	Human imm	C 663	51	2.2	50	6	AB204758	AB204758	Human leu
C 591	51	2.2	293	4	AAK81170	Human imm	C 664	51	2.2	50	12	ADP10274	ADP10274	50-mex O1
C 592	51	2.2	293	4	AAK71427	Human imm	C 665	51	2.2	95	3	AAK28711	AAK28711	Human sec
C 593	51	2.2	293	4	AAK86637	Human imm	C 666	51	2.2	102	4	AAK77190	AAK77190	Human imm
C 594	51	2.2	293	8	AB274074	Human imm	C 667	51	2.2	102	4	AAK77191	AAK77191	Human imm
C 595	51	2.2	293	8	ADA44388	Secreted	C 668	51	2.2	105	4	AAK75547	AAK75547	Human imm
C 596	51	2.2	298	4	AAK81139	Human sec	C 669	51	2.2	105	4	AAK83439	AAK83439	Human imm
C 597	51	2.2	298	5	AB211129	Human imm	C 670	51	2.2	105	4	AAI04571	AAI04571	Human imm
C 598	51	2.2	298	5	AB210683	Human ner	C 671	51	2.2	105	4	ABU97494	ABU97494	Human rep
C 599	51	2.2	298	8	AB274092	Secreted	C 672	51	2.2	108	4	AAK79902	AAK79902	Human tes
C 600	51	2.2	298	8	ADA44406	Human sec	C 673	51	2.2	111	4	AAK74636	AAK74636	Human imm
C 601	51	2.2	299	4	AAK80829	Human imm	C 674	51	2.2	111	4	AAK74634	AAK74634	Human imm
C 602	51	2.2	300	2	AA213939	Human gen	C 675	51	2.2	111	4	AAK74635	AAK74635	Human imm

C 676	50	2.1	129	4	AAK79389	Human	imm	749	49	2.1	275	6	ABL85792	AD185792	Human	ova
C 677	50	2.1	133	3	AAC19175	Human	sec	750	49	2.1	275	6	ABL85671	AD185671	Human	ova
C 678	50	2.1	139	8	ABZ74222	Secreted		751	49	2.1	275	6	ABL85919	AD185919	Human	ova
C 679	50	2.1	139	8	ADA98751	Human	sec	C 752	49	2.1	276	4	AAK84515	AAK84515	Human	imm
C 680	50	2.1	139	10	ABZ67788	Human	sec	C 753	49	2.1	276	4	AAK84516	AAK84516	Human	imm
C 681	50	2.1	148	4	AAK32635	Human	gen	C 754	49	2.1	276	4	AAK84516	AAK84516	Human	imm
C 682	50	2.1	163	4	AAK87060	Human	imm	C 755	49	2.1	276	4	AAK84516	AAK84516	Human	imm
C 683	50	2.1	204	4	AAK87640	Human	imm	C 756	49	2.1	282	4	AAK72354	AAK72354	Human	rep
C 684	50	2.1	215	3	AAC18078	Human	sec	C 757	49	2.1	282	4	AAK66312	AAK66312	Human	imm
C 685	50	2.1	223	4	AAI62892	Human	gen	C 758	49	2.1	282	4	AAK66312	AAK66312	Human	imm
C 686	50	2.1	246	4	AAK65764	Human	imm	C 759	49	2.1	287	4	ABA07123	ABA07123	Human	pan
C 687	50	2.1	252	3	AAC24019	Human	sec	C 760	49	2.1	287	4	ABA07124	ABA07124	Human	pan
C 688	50	2.1	252	3	AAC23998	Human	sec	C 761	49	2.1	287	4	AAK89337	AAK89337	Human	dig
C 689	50	2.1	252	3	ABK42146	Genomic s		C 762	49	2.1	301	5	ABV00850	ABV00850	Human	pro
C 690	50	2.1	252	9	ADB60302	Connectiv		C 763	49	2.1	301	5	ABV00850	ABV00850	Human	pro
C 691	50	2.1	262	5	ABV18445	Human	pro	C 764	49	2.1	302	5	ABA20685	ABA20685	Human	ner
C 692	50	2.1	264	4	AAI06058	Human	rep	C 765	49	2.1	314	2	AAQ59748	AAQ59748	Human	bra
C 693	50	2.1	264	4	ABL98623	Human	tes	C 766	49	2.1	316	5	ABA16536	ABA16536	Human	ner
C 694	50	2.1	272	4	AAI06059	Human	rep	C 767	49	2.1	317	3	AAA16104	AAA16104	Human	col
C 695	50	2.1	272	4	ABL98624	Human	tes	C 768	49	2.1	331	4	AAK64191	AAK64191	Human	col
C 696	50	2.1	281	5	ABA15591	Human	ner	C 769	49	2.1	334	6	ABL66958	ABL66958	Human	imm
C 697	50	2.1	285	4	ASA42009	Genomic s		C 770	49	2.1	353	14	ACL60381	ACL60381	Human	ova
C 698	50	2.1	287	4	AAK75892	Human	imm	C 771	49	2.1	364	6	ABL85304	ABL85304	Human	ova
C 699	50	2.1	288	4	ABA08134	Human	imm	C 772	49	2.1	371	14	ADW06702	ADW06702	Human	pro
C 700	50	2.1	288	12	ADN41748	Novel hum		C 773	49	2.1	374	5	ABV00713	ABV00713	Human	pro
C 701	50	2.1	301	4	AAK71489	Human	imm	C 774	49	2.1	378	5	ABV00563	ABV00563	Human	pro
C 702	50	2.1	301	4	AAK75869	Human	imm	C 775	49	2.1	399	4	AAI85423	AAI85423	Human	pol
C 703	50	2.1	301	5	ABA18117	Human	ner	C 776	49	2.1	425	13	ACR86513	ACR86513	Human	SIR
C 704	50	2.1	301	12	ADJ12790	DNA	fragm	C 777	49	2.1	425	13	ACR86513	ACR86513	Human	SIR
C 705	50	2.1	308	4	AAK84180	Human	imm	C 778	49	2.0	111	3	AAK14117	AAK14117	Human	sec
C 706	50	2.1	308	4	AAK84177	Human	imm	C 779	49	2.0	121	12	ADR933693	ADR933693	Polynucle	
C 707	50	2.1	310	4	AAK67523	Human	imm	C 780	49	2.0	137	3	AAK23582	AAK23582	Human	sec
C 708	50	2.1	317	4	AAI04900	Human	rep	C 781	49	2.0	168	4	AAK86647	AAK86647	Human	imm
C 709	50	2.1	317	4	ABL97794	Human	tes	C 782	49	2.0	206	6	ABL80499	ABL80499	Human	ova
C 710	50	2.1	321	4	AAK66221	Human	imm	C 783	49	2.0	218	4	AAK81174	AAK81174	Human	imm
C 711	50	2.1	323	12	ADJ12815	DNA	fragm	C 784	49	2.0	242	4	AAK65763	AAK65763	Human	imm
C 712	50	2.1	337	5	ABV48229	Human	pro	C 785	49	2.0	242	5	ABA21134	ABA21134	Human	ner
C 713	50	2.1	361	4	AAK37052	Novel hum		C 786	49	2.0	242	8	ADAA1529	ADAA1529	Human	sec
C 714	50	2.1	364	4	AAK37052	Novel hum		C 787	49	2.0	242	8	ACCS0872	ACCS0872	Human	sec
C 715	50	2.1	365	4	AAI83467	Human	pol	C 788	49	2.0	242	10	ADA57657	ADA57657	BAC	fragm
C 716	50	2.1	377	5	ABV10381	Human	pro	C 789	49	2.0	242	12	ADJ12760	ADJ12760	DNA	fragm
C 717	50	2.1	378	5	ABV19229	Human	pro	C 790	49	2.0	268	4	AAK71312	AAK71312	Human	imm
C 718	50	2.1	378	5	ABV09882	Human	pro	C 791	49	2.0	273	4	AAK65431	AAK65431	Human	imm
C 719	50	2.1	380	5	ABV30901	Human	pro	C 792	49	2.0	275	4	AAI05692	AAI05692	Human	rep
C 720	50	2.1	380	5	ABV09727	Human	pro	C 793	49	2.0	285	4	AAI05692	AAI05692	Human	rep
C 721	50	2.1	387	14	ACL54687	Human	col	C 794	49	2.0	298	4	AAK89542	AAK89542	Human	dig
C 722	50	2.1	393	5	ABV09732	Human	pro	C 795	49	2.0	309	4	ABK42588	ABK42588	Genomic s	
C 723	50	2.1	400	5	ABV39012	Human	imm	C 796	49	2.0	309	9	ABK42589	ABK42589	Genomic s	
C 724	50	2.1	405	4	AAK71027	Human	imm	C 797	49	2.0	309	9	ADB60745	ADB60745	Connectiv	
C 725	50	2.1	411	4	AAI05066	Human	rep	C 798	49	2.0	309	9	ADB60744	ADB60744	Connectiv	
C 726	50	2.1	411	4	ABL97959	Human	tes	C 799	49	2.0	321	5	ABA17411	ABA17411	Human	ner
C 727	50	2.1	416	5	ABV30906	Human	pro	C 800	49	2.0	321	5	ABA17412	ABA17412	Human	ner
C 728	50	2.1	416	5	ABV31056	Human	pro	C 801	49	2.0	322	4	AAK62536	AAK62536	Human	imm
C 729	50	2.1	416	5	ABV31552	Human	pro	C 802	49	2.0	333	4	AAI21815	AAI21815	Human	bre
C 730	50	2.1	418	5	ACH25986	Human	adu	C 803	49	2.0	361	4	AAK67648	AAK67648	Human	imm
C 731	50	2.1	429	6	ABL84458	Human	ova	C 804	49	2.0	375	4	AAK67647	AAK67647	Human	imm
C 732	50	2.1	431	5	ABV00558	Human	pro	C 805	49	2.0	405	14	ADW82760	ADW82760	MAP3X9	ma
C 733	50	2.1	442	5	ACH27646	Human	adu	C 806	49	2.0	440	4	AAK82754	AAK82754	Human	imm
C 734	50	2.1	443	5	ABV05822	Human	pro	C 807	49	2.0	478	3	AAK98012	AAK98012	Human	col
C 735	50	2.1	444	5	ACH21861	Human	adu	C 808	49	2.0	496	6	ABN65242	ABN65242	Human	can
C 736	50	2.1	454	5	ABV57254	Human	pro	C 809	49	2.0	497	3	AAZ65926	AAZ65926	Human	map
C 737	50	2.1	458	5	ACH39382	Human	pro	C 810	49	2.0	114	4	AAK65723	AAK65723	Human	imm
C 738	50	2.1	465	6	ABK44737	CDNA	enco	C 811	49	2.0	114	4	AAK65719	AAK65719	Human	imm
C 739	50	2.1	471	6	ABN60735	Human	can	C 812	49	2.0	114	4	AAK82374	AAK82374	Human	imm
C 740	50	2.1	488	5	ABV47991	Human	pro	C 813	49	2.0	114	4	AAK82373	AAK82373	Human	imm
C 741	50	2.1	102	5	AAK90358	Human	dig	C 814	49	2.0	114	4	AAK82376	AAK82376	Human	imm
C 742	50	2.1	102	5	AAK39914	Genomic s		C 815	49	2.0	114	4	AAK65718	AAK65718	Human	imm
C 743	50	2.1	102	5	AAK39914	Genomic s		C 816	49	2.0	195	4	AAK89723	AAK89723	Human	dig
C 744	50	2.1	106	4	AAK86494	Human	imm	C 817	49	2.0	204	3	AAK27124	AAK27124	Human	sec
C 745	50	2.1	106	4	AAK86494	Human	imm	C 818	49	2.0	266	4	AAK89720	AAK89720	Human	dig
C 746	50	2.1	121	4	AAK83492	Human	ner	C 819	49	2.0	277	4	AAI03102	AAI03102	Human	rep
C 747	50	2.1	237	4	AAK68259	Human	imm	C 820	49	2.0	277	4	AAI03102	AAI03102	Human	rep
C 748	50	2.1	249	3	AAK12905	Human	sec	C 821	49	2.0	277	4	ABL97435	ABL97435	Human	tes

C 822	47	2.0	277	4	ABL97436	Ab197436 Human tes	895	45	1.9	147	11	AD197253	Ad197253 Human res
C 823	47	2.0	281	4	AAK67696	AAK67696 Human imm	896	45	1.9	147	11	AD197254	Ad197254 Human res
C 824	47	2.0	281	4	ADJ12814	AdJ12814 DNA fragm	C 897	45	1.9	187	8	ABZ73999	Abz73999 Secreted
C 825	47	2.0	296	5	ABA19501	AbA19501 Human ner	C 898	45	1.9	187	10	ADCC20711	Adcc20711 Human sec
C 826	47	2.0	297	14	ACL54796	AcI54796 Human col	C 899	45	1.9	191	12	ADH73466	Adh73466 Human Ali
C 827	47	2.0	300	4	AAK89751	AAK89750 Human dig	C 900	45	1.9	201	13	ADSA4257	Adsa4257 Human aut
C 828	47	2.0	300	4	AAK89750	AAK89750 Human dig	C 901	45	1.9	237	3	AAK23528	AAK23528 Human sec
C 829	47	2.0	307	13	ACF83404	AcF83404 Human SIR	C 902	45	1.9	265	4	AAI24545	AAI24545 Human bre
C 830	47	2.0	315	5	ABA16659	AbA16659 Human ner	C 903	45	1.9	266	4	AAI199176	AAI199176 Human exc
C 831	47	2.0	316	5	ABV00723	ABV00723 Human pro	C 904	45	1.9	266	4	AAK69770	AAK69770 Human imm
C 832	47	2.0	333	5	AAI16258	AAI16258 Human bre	C 905	45	1.9	266	4	AAK65703	AAK65703 Human imm
C 833	47	2.0	347	5	ABV04436	ABV04436 Human pro	C 906	45	1.9	266	5	AAI63526	AAI63526 Human kid
C 834	47	2.0	347	6	ABL84980	AbL84980 Human ova	C 907	45	1.9	279	3	AAOC8419	AAOC8419 Human sec
C 835	47	2.0	386	5	AD167897	AdI67897 Human ova	C 908	45	1.9	279	6	ABV96400	ABV96400 Human pan
C 836	47	2.0	386	5	AD174274	AdI74274 Human ova	C 909	45	1.9	295	4	AAI199175	AAI199175 Human exc
C 837	47	2.0	391	4	AAAS39252	AAAS39252 Novel hum	C 910	45	1.9	295	4	AAK69769	AAK69769 Human imm
C 838	47	2.0	391	4	AAI81397	AAI81397 Human pol	C 911	45	1.9	295	5	AAK65702	AAK65702 Human imm
C 840	47	2.0	412	4	AAK56256	AAK56256 Human imm	C 912	45	1.9	295	5	AAI63525	AAI63525 Human kid
C 841	47	2.0	422	5	ADL39511	AdL39511 Human ova	C 913	45	1.9	297	3	AAK70687	AAK70687 Human imm
C 842	47	2.0	426	5	ABV11010	ABV11010 Human pro	C 914	45	1.9	303	3	AAK24437	AAK24437 Human sec
C 843	47	2.0	430	6	ABL77255	ABL77255 Human ova	C 915	45	1.9	303	4	AAK86626	AAK86626 Human imm
C 844	47	2.0	447	5	ABV21148	ABV21148 Human pro	C 916	45	1.9	309	3	AAK61557	AAK61557 Genetic s
C 845	47	2.0	447	5	ABV23499	ABV23499 Human pro	C 917	45	1.9	315	6	ABL84753	ABL84753 Human ova
C 846	47	2.0	473	5	ABV32159	ABV32159 Human pro	C 918	45	1.9	322	4	AAK70481	AAK70481 Human imm
C 847	47	2.0	478	9	ACH39416	ACH39416 Human foe	C 919	45	1.9	336	4	AAI23673	AAI23673 Human bre
C 848	47	2.0	480	6	ABN61750	ABN61750 Human can	C 920	45	1.9	337	14	ACL60368	ACL60368 Human col
C 849	47	2.0	480	9	ACH24912	ACH24912 Human adu	C 921	45	1.9	350	4	AAI191502	AAI191502 Human pol
C 850	47	2.0	480	14	ACL60088	ACL60088 Human col	C 922	45	1.9	353	4	AAI14811	AAI14811 Human bre
C 851	47	2.0	481	14	ACL62985	ACL62985 Human col	C 923	45	1.9	353	5	ABV01381	ABV01381 Human pro
C 852	47	2.0	485	9	ACH24636	ACH24636 Human adu	C 924	45	1.9	372	5	ABV13850	ABV13850 Human pro
C 853	47	2.0	500	4	AAI25180	AAI25180 Human bre	C 925	45	1.9	379	5	ABV34962	ABV34962 Human pro
C 854	46	1.9	95	4	AAK85116	AAK85116 Human imm	C 926	45	1.9	379	5	ABV43811	ABV43811 Human pro
C 855	46	1.9	106	4	AAI04297	AAI04297 Human rep	C 927	45	1.9	384	4	AAK67754	AAK67754 Human imm
C 856	46	1.9	109	4	AAK71805	AAK71805 Human imm	C 928	45	1.9	393	4	AAK67752	AAK67752 Human imm
C 857	46	1.9	121	12	ADK91573	AdK91573 Polynucle	C 929	45	1.9	393	4	AAK67753	AAK67753 Human imm
C 858	46	1.9	121	12	ADK91575	AdK91575 Polynucle	C 930	45	1.9	393	4	AAK67753	AAK67753 Human imm
C 859	46	1.9	204	4	AAK85792	AAK85792 Human imm	C 931	45	1.9	401	5	ABV04681	ABV04681 Human pro
C 860	46	1.9	204	4	AAI62860	AAI62860 Human gen	C 932	45	1.9	402	5	ABV12344	ABV12344 Human pro
C 861	46	1.9	226	4	AAK67708	AAK67708 Human imm	C 933	45	1.9	402	5	AAK66105	AAK66105 Novel hum
C 862	46	1.9	227	3	AAK14388	AAK14388 Human sec	C 934	45	1.9	403	4	AAI23620	AAI23620 Human bre
C 863	46	1.9	259	4	AAK81441	AAK81441 Human imm	C 935	45	1.9	407	14	ACL63022	ACL63022 Human col
C 864	46	1.9	282	4	AAI36569	AAI36569 Human mus	C 936	45	1.9	410	4	AAI191465	AAI191465 Human pro
C 865	46	1.9	282	8	ABX59557	ABX59557 CDNA enco	C 937	45	1.9	417	5	ABV03175	ABV03175 Human pro
C 866	46	1.9	282	12	ADJ30307	AdJ30307 Human mus	C 938	45	1.9	417	8	ACA04834	ACA04834 CDNA enco
C 867	46	1.9	293	4	AAK79251	AAK79251 Human imm	C 939	45	1.9	419	14	ADX38182	ADX38182 Human can
C 868	46	1.9	347	13	ACF90672	AcF90672 Human SIR	C 940	45	1.9	421	4	AAI19681	AAI19681 Human bre
C 869	46	1.9	355	5	ABV01212	ABV01212 Human pro	C 941	45	1.9	428	14	ACL59953	ACL59953 Human col
C 870	46	1.9	394	5	ABV10550	ABV10550 Human pro	C 942	45	1.9	434	5	ABV50314	ABV50314 Human pro
C 871	46	1.9	395	4	AAI89981	AAI89981 Human pol	C 943	45	1.9	435	4	AAK64271	AAK64271 Human imm
C 872	46	1.9	396	5	ABV35076	ABV35076 Human pro	C 944	45	1.9	440	6	ABN65698	ABN65698 Human can
C 873	46	1.9	396	5	ABV43922	ABV43922 Human pro	C 945	45	1.9	443	5	ABV33488	ABV33488 Human pro
C 874	46	1.9	409	13	ACF89707	AcF89707 Human SIR	C 946	45	1.9	443	5	ABV42411	ABV42411 Human pro
C 875	46	1.9	410	5	ABV01233	ABV01233 Human pro	C 947	45	1.9	447	9	AAI192053	AAI192053 Human pol
C 876	46	1.9	414	4	AAI89811	AAI89811 Human pro	C 948	45	1.9	447	9	ACH38868	ACH38868 Human foe
C 877	46	1.9	420	5	ABV40521	ABV40521 Human pro	C 949	45	1.9	449	6	ABI83516	ABI83516 Human ova
C 878	46	1.9	420	5	ABV31720	ABV31720 Human pro	C 950	45	1.9	453	5	AD175286	AD175286 Human ova
C 879	46	1.9	437	5	ABV01418	ABV01418 Human pro	C 951	45	1.9	453	5	AD168931	AD168931 Human ova
C 880	46	1.9	446	13	ACF89708	AcF89708 Human pro	C 952	45	1.9	462	9	ACH19276	ACH19276 Human adu
C 881	46	1.9	493	5	ABV04799	ABV04799 Human SIR	C 953	45	1.9	463	6	ABT09995	ABT09995 Human bre
C 882	46	1.9	498	9	ACH24451	ACH24451 Human adu	C 954	45	1.9	468	4	AAI10101	AAI10101 Human bre
C 883	45	1.9	122	4	AAK72590	AAK72590 Human imm	C 955	45	1.9	472	4	AAK48361	AAK48361 Human lun
C 884	45	1.9	126	4	AAK71426	AAK71426 Human imm	C 956	45	1.9	474	4	AAK88655	AAK88655 Human dig
C 885	45	1.9	130	4	AAI36471	AAI36471 Human mus	C 957	45	1.9	474	9	ACH19395	ACH19395 Human adu
C 886	45	1.9	130	12	ABX59459	ABX59459 CDNA enco	C 958	45	1.9	477	12	ADQ21162	ADQ21162 Human sof
C 887	45	1.9	130	12	ADJ30209	AdJ30209 CDNA enco	C 959	45	1.9	480	5	ABV56354	ABV56354 Human pro
C 888	45	1.9	131	5	ABA20488	ABA20488 Human ner	C 960	45	1.9	482	9	ACH38395	ACH38395 Human end
C 889	45	1.9	133	4	AAK67352	AAK67352 Human imm	C 961	45	1.9	482	11	ACN88154	ACN88154 Breast ca
C 890	45	1.9	146	4	AAK82713	AAK82713 Human imm	C 962	45	1.9	483	11	ACN86300	ACN86300 Breast ca
C 891	45	1.9	147	4	AAK28283	AAK28283 Genomic s	C 963	45	1.9	488	4	AAK82612	AAK82612 Human imm
C 892	45	1.9	147	4	AAK28284	AAK28284 Genomic s	C 964	45	1.9	488	4	AAK82613	AAK82613 Human imm
C 893	45	1.9	147	10	ADG41480	AdG41480 Human res	C 965	45	1.9	495	8	ACA04569	ACA04569 CDNA enco
C 894	45	1.9	147	10	ADG41479	AdG41479 Human res	C 966	45	1.9	76	3	AAI13689	AAI13689 Human sec
							C 967	44	1.9	102	12	ADN41817	ADn41817 Novel hum

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C 968 44 1.9 104 4 AAK69303 Human imm
C 969 44 1.9 107 4 AAK74844 Human imm
C 970 44 1.9 115 4 AAK89203 Human imm
C 971 44 1.9 115 4 AAK90088 Human imm
C 972 44 1.9 115 4 AAK80878 Human imm
C 973 44 1.9 115 4 AAL06348 Human rep
C 974 44 1.9 115 5 AAS39747 Genomic s
C 975 44 1.9 128 4 ADB32707 Human nov
C 976 44 1.9 128 4 AAS32510 Human gen
C 977 44 1.9 128 4 AAS32508 Human gen
C 978 44 1.9 128 4 AAS32513 Human gen
C 979 44 1.9 131 4 AAK80864 Human imm
C 980 44 1.9 131 4 AAK85677 Human imm
C 981 44 1.9 131 4 AAK86568 Human imm
C 982 44 1.9 131 4 AAK68094 Human imm
C 983 44 1.9 131 4 AAK72017 Human imm
C 984 44 1.9 131 4 AAK66835 Human imm
C 985 44 1.9 138 5 ABA17054 Human ner
C 986 44 1.9 138 5 ABA17055 Human ner
C 987 44 1.9 142 4 AAK84532 Human imm
C 988 44 1.9 143 4 AAK65842 Human imm
C 989 44 1.9 147 3 AAK16174 Human sec
C 990 44 1.9 148 3 AAK16023 Human sec
C 991 44 1.9 152 4 AAK87062 Human imm
C 992 44 1.9 154 4 AAK72589 Human imm
C 993 44 1.9 172 4 AAK81214 Human imm
C 994 44 1.9 172 4 AAK66061 Human imm
C 995 44 1.9 179 4 AAK66062 Human imm
C 996 44 1.9 179 4 AAK66065 Human imm
C 997 44 1.9 182 4 AAK67721 Human imm
C 998 44 1.9 182 4 AAK81143 Human imm
C 999 44 1.9 182 4 AAK32651 Human gen
C1000 44 1.9 188 3 AAK16228 Human sec
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ALIGNMENTS

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RESULT 1
ADXL5874
ID ADXL5874 standard; DNA; 327 BP.
AC ADXL5874;
XX
DT 05-MAY-2005 (first entry)
XX
DE wild-type human double minute 2 protein (17-125) DNA SEQ ID NO:1.
XX
KW double minute 2; ds; cancer; cytosstatic; neoplasm; X-ray crystallography;
KM protein solubilization; mutagenesis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..327
FT /tag= a
FT /product= "double minute 2"
FT /partial
FT /note= "no start/stop codon given"
XX
PN US2005037383-A1.
XX
PD 17-FEB-2005.
XX
PF 09-APR-2004; 2004US-00822254.
XX
PR 10-APR-2003; 2003US-0461787P.
PR 24-FEB-2004; 2004US-0547265P.
XX
XX (SCHE ) SCHERING CORP.
PA
XX Taremi SS, Xie G, Hesson T, Duca JS, Strickland C, Windsor WT,
PI Madison VS, Zhang R, Reichert P;
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XX
DR WPI: 2005-180390/19.
DR P-PSDB; ADXL5875.
XX
PT Novel modified human double minute 2 protein polypeptide, comprising
PT amino acid sequence differing from its corresponding wild-type, useful
PT for identifying compounds used as anticancer agents.
XX
PS Disclosure; SEQ ID NO 1; 49pp; English.
XX
CC The invention relates to a novel modified human Double Minute 2 protein
CC (Hdm2) polypeptide (1) comprising a fully defined sequence of 109 amino
CC acids (S1) as given in the specification, differing from the
CC corresponding wild-type Hdm2 (17-125) amino acid sequence (ADXL5875). A
CC polypeptide of the invention is useful for identifying an agent for use
CC as an inhibitor of Hdm2. The polypeptide, crystal of the polypeptide or
CC polypeptide-compound complex (PPC) is useful for designing, selecting
CC and/or optimizing a potential inhibitor of the polypeptide. The
CC polypeptide or PPC is useful for evaluating the ability of a potential
CC inhibitor to associate with the polypeptide or PPC. The polypeptide,
CC crystal of the polypeptide or PPC is useful for identifying, selecting
CC and/or designing compounds useful as anticancer agents. The polypeptide
CC is useful in designing high affinity inhibitors of Hdm2 that are useful
CC in the treatment of cancers. The present sequence encodes the wild-type
CC human Double Minute 2 protein (Hdm2) polypeptide of the invention.
XX
SQ Sequence 327 BP; 106 A; 56 C; 69 G; 96 T; 0 U; 0 Other;
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Query Match 13.8%; Score 327; DB 14; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.3e-147;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 360 TCACAGATTCAGCTTCGGAACAAGAGACCCTGGTTAGACCAAGCATTGCTTTGAAG 419
Db 1 TCACAGATTCAGCTTCGGAACAAGAGACCCTGGTTAGACCAAGCATTGCTTTGAAG 60
QY 420 TTATTAAGTCTGTTGGTGACAAAAAGACATTATACATGAAAGAGTTCTTTTAT 479
Db 61 TTATTAAGTCTGTTGGTGACAAAAAGACATTATACATGAAAGAGTTCTTTTAT 120
QY 480 CTTGGCCAGTATATATTAAGACTTAAACGTTATATGATGAGAAAGCAACATATGTATAT 539
Db 121 CTTGGCCAGTATATATTAAGACTTAAACGTTATATGATGAGAAAGCAACATATGTATAT 180
QY 540 TGTTCAAATGATCTCTTAGAGATTTGTTGGCGTGGCAAGCTCTCTGTGAAGAGCAC 599
Db 181 TGTTCAAATGATCTCTTAGAGATTTGTTGGCGTGGCAAGCTCTCTGTGAAGAGCAC 240
QY 600 AGGAAATATATATACATGATCTACAGAACTTGGTAGTATCATCAGCAGAAATCATCG 659
Db 241 AGGAAATATATATACATGATCTACAGAACTTGGTAGTATCATCAGCAGAAATCATCG 300
QY 660 GACTCAGGTACATCTGTGAGTGAGAAC 686
Db 301 GACTCAGGTACATCTGTGAGTGAGAAC 327
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RESULT 2
AAT71257
ID AAT71257 standard; DNA; 399 BP.
AC AAT71257;
XX
DT 30-MAR-1998 (first entry)
XX
DE Human mdm2-D gene.
XX
KW Cognate transgene; human; mdm2; lymphoma; cellular immunogen; cancer;
KW self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
KW colon carcinoma; immunotherapy; proto-oncogene; ss.
XX
XX Homo sapiens.
OS
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PN WO9725860-A1.
XX 24-JUL-1997.
XX
XX 13-JAN-1997; 97WO-US000582.
XX
XX PR 19-JAN-1996; 96US-0010262P.
XX
XX (UVAL-) UNIV ALLEGHENY HEALTH SCI.
XX
XX PI Halpern MS, England JM;
XX DR WPI; 1997-38493/35.
XX
XX Proto-oncogene immunogen - used in vaccine for the prevention and
XX treatment of cancer.
XX
XX Disclosure; Page 60; 81pp; English.
XX
XX This sequence represents the human mdm2-D cognate transgene (CTG).
XX Deletion of amino acids 9-155 of the encoded protein renders the CTG non-
XX transforming. This sequence can be used in the cellular immunogen of the
XX invention. The cellular immunogen of the invention is for immunising
XX against the product of a target proto-oncogene, over-expression of which
XX is associated with cancer, comprises host cells transfected with a
XX construct containing at least one transgene related to the proto-oncogene
XX and driven by a strong promoter. The product of the transgene induces
XX immunoreactivity to host self-determinants on the product of proto-
XX oncogene. The cellular immunogens are used for protective vaccination
XX against cancer (e.g. carcinoma of breast or colon, or various lymphomas)
XX and for immunotherapy of cancer. Use of the immunogen eliminates the need
XX to isolate immunogenic, HLA host-matched peptides. The method is not
XX based on immune recognition of a determinant defined by a cancer-specific
XX mutation and generates a systemic (anti-metastatic) response
SQ Sequence 399 BP; 133 A; 82 C; 84 G; 100 T; 0 U; 0 Other;
Query Match 13.2%; Score 313; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-140;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1475 ACAAGAAAGTGAAGACTATTCTCAGCCATCACTTCTAGTAGCATTATTATAGAGCCA 1534
DB 87 ACAAGAAAGTGAAGACTATTCTCAGCCATCACTTCTAGTAGCATTATTATAGAGCCA 146
QY 1535 AGAAGATGTGAAGAGTTTGAAGGAGAAAGAAAGCAAGCAAGAGAGTGTGAATC 1594
DB 147 AGAAGATGTGAAGAGTTTGAAGGAGAAAGCAAGCAAGAGAGTGTGAATC 206
QY 1535 TAGTTGGCCCTTATAGCATTTGAACCTTGTGTGATTGTCAAGTCCAGCTTAAAGATG 1654
DB 207 TAGTTGGCCCTTATAGCATTTGAACCTTGTGTGATTGTCAAGTCCAGCTTAAAGATG 266
QY 1655 TTGCATTGTCCATGAGCAAGAGCATCTTATGCGCTTACATGAGCAAGAGCT 1714
DB 267 TTGCATTGTCCATGAGCAAGAGCATCTTATGCGCTTACATGAGCAAGAGCT 326
QY 1715 AAAAGAAAGAAATAGCCCTGCCAGATGTAGACAAACCAATTCAAATGATGTGCTAAC 1774
DB 327 AAAAGAAAGAAATAGCCCTGCCAGATGTAGACAAACCAATTCAAATGATGTGCTAAC 386
QY 1775 TTATTTCCTCTAG 1787
DB 387 TTATTTCCTCTAG 399
RESULT 3
AAZ60819
ID AAZ60819 standard; DNA; 399 BP.
XX AAZ60819;
AC
XX 16-MAY-2000 (first entry)
DT

XX
DE Nucleotide sequence of a cognate transgene of mdm-2.
XX
XX Cognate transgene; CTG; tumorigenic; cellular immunogen; immunisation;
XX KW proto-oncogene; malignancy; allogenic cell; vaccine; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200004927-A1.
XX
XX 03-FEB-2000.
XX
XX 08-JUL-1999; 99WO-US015594.
XX
XX 24-JUL-1998; 98US-0093965P.
XX
XX (UVAL-) UNIV ALLEGHENY HEALTH SCI.
XX (HALP/) HALPERN M S.
XX (ENGL/) ENGLAND J M.
XX
XX PI Halpern MS, England JM;
XX DR WPI; 2000-182543/16.
XX
XX Cellular immunogens comprising allogenic donor cells transfected with a
XX construct comprising a proto-oncogene cognate, useful as cancer vaccines.
XX
XX Disclosure; Page 69; 77pp; English.
XX
XX The present sequence represents a cognate transgene (CTG) which is
XX rendered non-tumorigenic by deletion of amino acids 9-155. The CTG is
XX used in the course of the invention. The specification describes a
XX cellular immunogen for immunizing a host against the effects of the
XX product of a target proto-oncogene which is associated with a
XX malignancy. The cellular immunogen comprises allogenic cells transfected
XX with transgene construct comprising a transgene cognate to target proto-
XX oncogene and a strong promoter. The cellular immunogen is useful for
XX vaccinating a host against cancer by inserting the transgene construct
XX into the body of the host for the expression of the transgene. The method
XX of the invention is designed to target mutation-driven non-self
XX determinants. The cellular immunogens induce reactivity for self-
XX expressed proto-oncogenes
SQ Sequence 399 BP; 133 A; 82 C; 84 G; 100 T; 0 U; 0 Other;
Query Match 13.2%; Score 313; DB 3; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-140;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1475 ACAAGAAAGTGAAGACTATTCTCAGCCATCACTTCTAGTAGCATTATTATAGAGCCA 1534
DB 87 ACAAGAAAGTGAAGACTATTCTCAGCCATCACTTCTAGTAGCATTATTATAGAGCCA 146
QY 1535 AGAAGATGTGAAGAGTTTGAAGGAGAAAGCAAGCAAGAGAGTGTGAATC 1594
DB 147 AGAAGATGTGAAGAGTTTGAAGGAGAAAGCAAGCAAGAGAGTGTGAATC 206
QY 1595 TAGTTGGCCCTTATAGCATTTGAACCTTGTGTGATTGTCAAGTCCAGCTTAAAGATG 1654
DB 207 TAGTTGGCCCTTATAGCATTTGAACCTTGTGTGATTGTCAAGTCCAGCTTAAAGATG 266
QY 1655 TTGCATTGTCCATGAGCAAGAGCATCTTATGCGCTTACATGAGCAAGAGCT 1714
DB 267 TTGCATTGTCCATGAGCAAGAGCATCTTATGCGCTTACATGAGCAAGAGCT 326
QY 1715 AAAAGAAAGAAATAGCCCTGCCAGATGTAGACAAACCAATTCAAATGATGTGCTAAC 1774
DB 327 AAAAGAAAGAAATAGCCCTGCCAGATGTAGACAAACCAATTCAAATGATGTGCTAAC 386
QY 1775 TTATTTCCTCTAG 1787
DB 387 TTATTTCCTCTAG 399

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RESULT 4
AD15878
ID AD15878 standard; DNA; 327 BP.
XX
AC AD15878;
XX
DT 05-MAY-2005 (first entry)
XX
DE Modified human double minute 2 protein Y76H encoding DNA SEQ ID NO:5.
XX
KM double minute 2; ds; cancer; cytostatic; neoplasm; X-ray crystallography;
KM protein solubilization; mutant; mutagenesis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..327
FT /*tag= a
FT /product= "double minute 2 variant"
FT /partial
FT /note= "no start/stop codon given"
XX
PN US2005037383-A1.
XX
PD 17-FEB-2005.
XX
PF 09-APR-2004; 2004US-00822254.
XX
PR 10-APR-2003; 2003US-0461787P.
PR 24-FEB-2004; 2004US-0547265P.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Taremi SS, Xie G, Hesson T, Duca JS, Strickland C, Windsor WT;
PI Madison VS, Zhang R, Reichert P;
XX
DR WPI; 2005-180390/19.
DR P-PSDB; ADX15879.
XX
PT Novel modified human double minute 2 protein polypeptide, comprising
PT amino acid sequence differing from its corresponding wild-type, useful
PT for identifying compounds used as anticancer agents.
XX
PS Claim 7; SEQ ID NO 5; 49pp; English.
XX
CC The invention relates to a novel modified human Double Minute 2 protein
CC (Hdm2) polypeptide (I) comprising a fully defined sequence of 109 amino
CC acids (S1) as given in the specification, differing from the
CC corresponding wild-type Hdm2 (17-125) amino acid sequence (ADX15875). A
CC polypeptide of the invention is useful for identifying an agent for use
CC as an inhibitor of Hdm2. The polypeptide, crystal of the polypeptide or
CC polypeptide-compound complex (PPC) is useful for designing, selecting
CC and/or optimizing a potential inhibitor of the polypeptide. The
CC polypeptide or PPC is useful for evaluating the ability of a potential
CC inhibitor to associate with the polypeptide or PPC. The polypeptide,
CC crystal of the polypeptide or PPC is useful for identifying, selecting
CC and/or designing compounds useful as anticancer agents. The polypeptide
CC is useful in designing high affinity inhibitors of Hdm2 that are useful
CC in the treatment of cancers. The present sequence encodes a modified
CC human Double Minute 2 protein (Hdm2) polypeptide of the invention.
XX
SQ Sequence 327 BP; 106 A; 57 C; 69 G; 95 T; 0 U; 0 Other;
Query Match 11.6%; Score 276; DB 14; Length 327;
Best Local Similarity 99.7%; Pred. No. 1.1e-122;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 360 TCACAGATTCGAGCTCGGAACAGAGACCCGTTACACCAAGCCATTGCTTTGAG 419
Db 1 TCACAGATTCGAGCTCGGAACAGAGACCCGTTACACCAAGCCATTGCTTTGAG 60

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Oy 420 TTATTTAAAGTCTGTGGTGACAAAGACACTTATATATGAAGAGGTTCTTTTAT 479
Db 61 TTATTTAAAGTCTGTGGTGACAAAGACACTTATATATGAAGAGGTTCTTTTAT 120
Oy 480 CTTGGCCAGTATATTAAGTCTAAACGATTAATGATGGAAGCAACAATATGTATAT 539
Db 121 CTTGGCCAGTATATTAAGTCTAAACGATTAATGATGGAAGCAACAATATGTATAT 180
Oy 540 TGTTCAAATGATCTTTAGAGATTTTGTGGCGTGCAGACTTCTGTGAAAGACAC 599
Db 181 TGTTCAAATGATCTTTAGAGATTTTGTGGCGTGCAGACTTCTGTGAAAGACAC 240
Oy 600 AGGAAATATATACCATGATCTACAGAACTTGTAGTACTGATCAATCAGCAAGAAATCATCG 659
Db 241 AGGAAATATATACCATGATCTACAGAACTTGTAGTACTGATCAATCAGCAAGAAATCATCG 300
Oy 660 GACTCAGGTACATCTGTGAGTGAAGAC 686
Db 301 GACTCAGGTACATCTGTGAGTGAAGAC 327

RESULT 5
AD15880
ID AD15880 standard; DNA; 327 BP.
XX
AC AD15880;
XX
DT 05-MAY-2005 (first entry)
XX
DE Modified human double minute 2 protein F55Y encoding DNA SEQ ID NO:7.
XX
KM double minute 2; ds; cancer; cytostatic; neoplasm; X-ray crystallography;
KM protein solubilization; mutant; mutagenesis.
XX
OS Homo sapiens.
XX
PI Taremi SS, Xie G, Hesson T, Duca JS, Strickland C, Windsor WT;
PI Madison VS, Zhang R, Reichert P;
XX
DR WPI; 2005-180390/19.
DR P-PSDB; ADX15881.
XX
PT Novel modified human double minute 2 protein polypeptide, comprising
PT amino acid sequence differing from its corresponding wild-type, useful
PT for identifying compounds used as anticancer agents.
XX
PS Claim 7; SEQ ID NO 7; 49pp; English.
XX
CC The invention relates to a novel modified human Double Minute 2 protein
CC (Hdm2) polypeptide (I) comprising a fully defined sequence of 109 amino
CC acids (S1) as given in the specification, differing from the
CC corresponding wild-type Hdm2 (17-125) amino acid sequence (ADX15875). A
CC polypeptide of the invention is useful for identifying an agent for use
CC as an inhibitor of Hdm2. The polypeptide, crystal of the polypeptide or
CC polypeptide-compound complex (PPC) is useful for designing, selecting

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CC and/or optimizing a potential inhibitor of the polypeptide. The
CC polypeptide or PPC is useful for evaluating the ability of a potential
CC inhibitor to associate with the polypeptide or PPC. The polypeptide,
CC crystal of the polypeptide or PPC is useful for identifying, selecting
CC and/or designing compounds useful as anticancer agents. The polypeptide
CC is useful in designing high affinity inhibitors of Hdm2 that are useful
CC in the treatment of cancers. The present sequence encodes a modified
CC human Double Minute 2 protein (Hdm2) polypeptide of the invention.

XX Sequence 327 BP; 107 A; 56 C; 69 G; 95 T; 0 U; 0 Other;

Query Match 11.6%; Score 276; DB 14; Length 327;

Best Local Similarity 99.7%; Pred. No. 1.1e-122;

Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 360 TCACGATTCCAGCTTCGGACAAAGACCCCTGGTTAGCCAAAGCATGCTTTGGAAG 419
DB 1 TCACGATTCCAGCTTCGGACAAAGACCCCTGGTTAGCCAAAGCATGCTTTGGAAG 60

QY 420 TTATTAAGTCTGTGTGACAAAAGACACTTATCATGTAAGAGGTTCTTTTAT 479
DB 61 TTATTAAGTCTGTGTGACAAAAGACACTTATCATGTAAGAGGTTCTTTTAT 120

QY 480 CTTGGCCAGTATATTATGACTTAACGATTATGATGAGAACAAACATATTGTAT 539
DB 121 CTTGGCCAGTATATTATGACTTAACGATTATGATGAGAACAAACATATTGTAT 180

QY 540 TGTTCATATGATCTTCTAGAGATTGTTGGCGTCCAGAGCTTCTGTGAAAGAGCAG 599
DB 181 TGTTCATATGATCTTCTAGAGATTGTTGGCGTCCAGAGCTTCTGTGAAAGAGCAG 240

QY 600 AGGAAATATATACCATGATCTACAGAACTTGATAGTCAATCAGACGAATCATCG 659
DB 241 AGGAAATATATACCATGATCTACAGAACTTGATAGTCAATCAGACGAATCATCG 300

QY 660 GACTCAGGTACATCTGTGAGTGAAGAC 686
DB 301 GACTCAGGTACATCTGTGAGTGAAGAC 327

RESULT 6
AAT99094
ID AAT99094 standard; DNA; 309 BP.

XX AAT99094;

XX 30-MAR-1998 (first entry)

XX Human mdm2-E gene.

XX Cognate transgene; human; mdm2; lymphoma; cellular immunogen; cancer;
XX self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
XX colon carcinoma; immunotherapy; proto-oncogene; ss.

OS Homo sapiens.

PN W09725860-A1.

XX 24-JUL-1997.

PF 13-JAN-1997; 97WO-US000582.

PR 19-JAN-1996; 96US-0010262P.

XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.

PA Halpern MS, England JM;

XX WPI; 1997-38493/35.

XX Proto-oncogene immunogen - used in vaccine for the prevention and
XX treatment of cancer.

PS Disclosure; Page 60-61; 81pp; English.

XX This sequence represents the human mdm2-E cognate transgene (CTG).
CC Deletion of amino acids 9-155 of the encoded protein renders the CTG non-
CC transforming. This sequence can be used in the cellular immunogen of the
CC invention. The cellular immunogen of the invention is for immunising
CC against the product of a target proto-oncogene, over-expression of which
CC is associated with cancer, comprises host cells transfected with a
CC construct containing at least one transgene related to the proto-oncogene
CC and driven by a strong promoter. The product of the transgene induces
CC immunoreactivity to host self-determinants on the product of proto-
CC oncogene. The cellular immunogens are used for protective vaccination
CC against cancer (e.g. carcinoma of breast or colon, or various lymphomas)
CC and for immunotherapy of cancer. Use of the immunogen eliminates the need
CC to isolate immunogenic, HLA host-matched peptides. The method is not
CC based on immune recognition of a determinant defined by a cancer-specific
CC mutation and generates a systemic (anti-metastatic) response

XX Sequence 309 BP; 100 A; 57 C; 53 G; 99 T; 0 U; 0 Other;

Query Match 9.5%; Score 225; DB 2; Length 309;

Best Local Similarity 100.0%; Pred. No. 5.6e-98;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGCGAATACCAACATGCTGTACCTTCTGATGCTGTGAACCACTCAGATTGCA 371
DB 1 ATGCGAATACCAACATGCTGTACCTTCTGATGCTGTGAACCACTCAGATTGCA 60

QY 372 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCATGCTTTGAAGTTTAAGTCT 431
DB 61 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCATGCTTTGAAGTTTAAGTCT 120

QY 432 GTTGTGCAAAAAGACACTTATATCTATGAAGAGTCTTTTATCTTGCCAGTAT 491
DB 121 GTTGTGCAAAAAGACACTTATATCTATGAAGAGTCTTTTATCTTGCCAGTAT 180

QY 492 ATTATGACTTAACGATTATATGATGAGAGCAACAATATTGTA 536
DB 181 ATTATGACTTAACGATTATATGATGAGAGCAACAATATTGTA 225

RESULT 7
AAZ60820
ID AAZ60820 standard; DNA; 309 BP.

XX AAZ60820;

XX 16-MAY-2000 (first entry)

XX Nucleotide sequence of a cognate transgene of mdm-2.

XX Cognate transgene; CTG; tumorigenic; cellular immunogen; immunisation;
XX proto-oncogene; malignancy; allogenic cell; vaccine; cancer; ss.

OS Homo sapiens.

PN W0200004927-A1.

XX 03-FEB-2000.

PF 08-JUL-1999; 99WO-US015594.

PR 24-JUL-1998; 98US-0093965P.

XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.

PA (HALP/) HALPERN M S.

XX (ENGL/) ENGLAND J M.

PI Halpern MS, England JM;

XX WPI; 2000-182543/16.
XX Cellular immunogens comprising allogenic donor cells transfected with a

PT construct comprising a proto-oncogene cognate, useful as cancer vaccines.
XX Disclosure; Page 70; 77pp; English.
XX
CC The present sequence represents a cognate transgene (CTG) which is
CC rendered non-tumorigenic by deletion of amino acids 9-155. The CTG is
CC used in the course of the invention. The specification describes a
CC cellular immunogen for immunizing a host against the effects of the
CC product of a target proto-oncogene which is associated with a
CC malignancy. The cellular immunogen comprises allogenic cells transfected
CC with transgene construct comprising a transgene cognate to target proto-
CC oncogene and a strong promoter. The cellular immunogen is useful for
CC vaccinating a host against cancer by inserting the transgene construct
CC into the body of the host for the expression of the transgene. The method
CC of the invention is designed to target mutation-driven non-self
CC determinants. The cellular immunogens induce reactivity for self-
CC determinants in the over expressed product of tumour associated and over
CC expressed proto-oncogenes
XX
SQ Sequence 309 BP; 100 A; 57 C; 53 G; 99 T; 0 U; 0 Other;
Query Match 9.5%; Score 225; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.6e-96;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 312 ATGTGCAATACCAACATGTCTGTACTTACTGATGCTGCTGTAACCACTCAGATTCCA 371
DB 1 ATGTGCAATACCAACATGTCTGTACTTACTGATGCTGCTGTAACCACTCAGATTCCA 60
QY 372 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
DB 61 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
QY 432 GTTGTGACAAAGAAAGACCTTATCTATGAAAGGTTCTTTTATCTGGCAGATAT 491
DB 121 GTTGTGACAAAGAAAGACCTTATCTATGAAAGGTTCTTTTATCTGGCAGATAT 180
QY 492 ATTATGACTAAACGATTATATGATGAGAAGCAACAATATTGTA 536
DB 101 ATTATGACTAAACGATTATATGATGAGAAGCAACAATATTGTA 225
RESULT 8
ADX15882
ID ADX15882 standard; DNA; 327 BP.
XX
AC ADX15882;
XX
DT 05-MAY-2005 (first entry)
DE Modified human double minute 2 protein F55Y/Y76H DNA SEQ ID NO:9.
XX
KW double minute 2; ds; cancer; cytostatic; neoplasm; X-ray crystallography;
KW protein solubilization; mutant; mutagenesis.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..327
FT /*tag= a
FT /product= "double minute 2 variant"
FT /partial
FT /note= "no start/stop codon given"
XX
PN US200503783-A1.
XX
PD 17-FEB-2005.
XX
PF 09-APR-2004; 2004US-00822254.
XX
PR 10-APR-2003; 2003US-0461787P.
PR 24-FEB-2004; 2004US-0547265P.
XX

PA (SCHE) SCHERING CORP.
XX
XX Taremi SS, Xie G, Heeson T, Duca JS, Strickland C, Windsor WT;
PI Madison VS, Zhang R, Reichert P;
XX
XX WPI; 2005-180390/19.
DR P-PsDB; ADX15883.
XX
PT Novel modified human double minute 2 protein polypeptide, comprising
PT amino acid sequence differing from its corresponding wild-type, useful
PT for identifying compounds used as anticancer agents.
XX
PS Claim 7; SEQ ID NO 9; 499p; English.
XX
CC The invention relates to a novel modified human Double Minute 2 protein
CC (Hdm2) polypeptide (I) comprising a fully defined sequence of 109 amino
CC acids (SI) as given in the specification, differing from the
CC corresponding wild-type Hdm2 (17-125) amino acid sequence (ADX15875). A
CC polypeptide of the invention is useful for identifying an agent for use
CC as an inhibitor of Hdm2. The polypeptide, crystal of the polypeptide or
CC polypeptide-compound complex (PPC) is useful for designing, selecting
CC and/or optimizing a potential inhibitor of the polypeptide. The
CC polypeptide or PPC is useful for evaluating the ability of a potential
CC inhibitor to associate with the polypeptide or PPC. The polypeptide,
CC crystal of the polypeptide or PPC is useful for identifying, selecting
CC and/or designing compounds useful as anticancer agents. The polypeptide
CC is useful in designing high affinity inhibitors of Hdm2 that are useful
CC in the treatment of cancers. The present sequence encodes a modified
CC human Double Minute 2 protein (Hdm2) polypeptide of the invention.
XX
SQ Sequence 327 BP; 107 A; 57 C; 69 G; 94 T; 0 U; 0 Other;
Query Match 9.5%; Score 225; DB 14; Length 327;
Best Local Similarity 99.4%; Pred. No. 5.6e-98;
Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 360 TCACAGATTCACGCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTGAAG 419
DB 1 TCACAGATTCACGCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTGAAG 60
QY 420 TTATTTAAGTCTGTGTGTGCAAAAAGACACTTATCTATGAAAGGTTCTTTTAT 479
DB 61 TTATTTAAGTCTGTGTGTGCAAAAAGACACTTATCTATGAAAGGTTCTTTTAT 120
QY 480 CTTGACCGATATATTATGACTTAAACGATTATATGATGAGAAGCAACAATATTGTAAT 539
DB 121 CTTGACCGATATATTATGACTTAAACGATTATATGATGAGAAGCAACAATATTGTAAT 180
QY 540 TGTTCAAATGATCTTCTAGAGATTTGTTGGCGTGCAGCTTCTGTGAAAAGACAC 599
DB 181 TGTTCAAATGATCTTCTAGAGATTTGTTGGCGTGCAGCTTCTGTGAAAAGACAC 240
QY 600 AGGAAAATATATATACATGATTTACAGAACTTGGTATGATCATCAGCAGGATTCATCG 659
DB 241 AGGAAAATATATATACATGATTTACAGAACTTGGTATGATCATCAGCAGGATTCATCG 300
QY 660 GACTCAGGTACATCTGTGAGTGAAGAC 686
DB 301 GACTCAGGTACATCTGTGAGTGAAGAC 327
RESULT 9
ADK66041
ID ADK66041 standard; DNA; 211 BP.
XX
AC ADK66041;
XX
DT 06-MAY-2004 (first entry)
DE Standardized polynucleotide system polynucleotide #9.
XX
KW ss; standardized polynucleotide system; medical diagnosis;
KW functional genomics; sample analysis; pharmacogenomics; sample analysis.
KW


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XX OS Unidentified.
XX PN DE10209071-A1.
XX PD 25-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01009071.
XX PR 28-FEB-2002; 2002DE-01009071.
XX PA (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
XX PI Koehler T, Rost A;
XX DR WPI; 2003-732912/70.
XX PT Standardized polynucleotide system, useful for quantitative, real-time
XX PT determination of nucleic acid, comprises stabilized standards, primers
XX PT and probe.
XX PS Claim 1; Page 7; 38pp; German.
XX CC The present invention relates to a standardized polynucleotide system,
XX CC which comprises at least one carrier nucleic acid, at least 3
XX CC oligonucleotides, as primers and target-specific, fluorescently labeled
XX CC probe and optionally at least one set of stabilized controls (standard
XX CC RNA or DNA) of known concentration and instructions. The system comprises
XX CC any of 20 sets of one control, two primers and one target-specific probe.
XX CC The standardized polynucleotide system can be used for quantitative, real-
XX CC time detection of target nucleic acids, especially analysis of genes or
XX CC gene products, e.g. for individualized medical diagnosis, in veterinary
XX CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,
XX CC pharmaceutical testing, analysis of food or environmental samples and
XX CC also for ultra-sensitive detection of proteins by immuno-PCR. The present
XX CC sequence is a polynucleotide used in the system of the invention.
XX SQ Sequence 211 BP; 73 A; 38 C; 52 G; 48 T; 0 U; 0 Other;

Query Match      8.9%; Score 211; DB 10; Length 211;
Best Local Similarity 100.0%; Pred. No. 3.4e-91;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1531 GCCAAGAGATGTGAAGAGTTGGAAGGAAAGAACCCAGACAAAGAGAGATGTGG 1590
Db 1 GCCAAGAGATGTGAAGAGTTGGAAGGAAAGAACCCAGACAAAGAGAGATGTGG 60
QY 1591 AATCTAGTTGGCCCTTATGACATTGAACCTGTGTGATTTGTCAAGGTGACCTAAA 1650
Db 61 AATCTAGTTGGCCCTTATGACATTGAACCTGTGTGATTTGTCAAGGTGACCTAAA 120
QY 1651 ATGGTTGATTTGTCATGCGCAAAACAGACATCTTATGCGCTTTTACATGTGCAAGA 1710
Db 121 ATGGTTGATTTGTCATGCGCAAAACAGACATCTTATGCGCTTTTACATGTGCAAGA 180
QY 1711 AGCTAAAGAAAAGAAATTAAGCCCTTCCCACT 1741
Db 181 AGCTAAAGAAAAGAAATTAAGCCCTTCCCACT 211

RESULT 10
AAA62123
ID AAA62123 standard; RNA; 199 BP.
XX AC AAA62123;
XX DT 20-JUN-2001 (first entry)
XX DE mdm2 long transcript found in cancerous cells.
XX KW mdm2; disease prediction; cancer; p53; human; ss.
XX OS Homo sapiens.
```

```
XX Key Location/Qualifiers
XX FH misc_structure 5..50
XX FT /tag= f
XX FT /standard_name= "Unique Exon1 structure"
XX FT 5..10
XX FT /tag= a
XX FT /bound_moiety= "mdm2 long transcript"
XX FT /note= "Forms double-stranded region with bases 45-50 of
XX FT mdm2 long transcript"
XX FT 13..17
XX FT /tag= b
XX FT /bound_moiety= "mdm2 long transcript"
XX FT /note= "Forms double-stranded region with bases 37-41 of
XX FT mdm2 long transcript"
XX FT 20..33
XX FT /tag= c
XX FT /tag= d
XX FT /bound_moiety= "mdm2 long transcript"
XX FT /note= "Forms double-stranded region with bases 13-17 of
XX FT mdm2 long transcript"
XX FT 45..50
XX FT /tag= e
XX FT /bound_moiety= "mdm2 long transcript"
XX FT /note= "Forms double-stranded region with bases 5-10 of
XX FT mdm2 long transcript"
XX FT 53..98
XX FT /tag= g
XX FT /standard_name= "Unique Exon1/ Exon3 junction structure"
XX FT 101..114
XX FT /tag= h
XX FT 116..118
XX FT /tag= i
XX FT /bound_moiety= "mdm2 long transcript"
XX FT /note= "Forms double-stranded region with bases 141-143
XX FT of mdm2 long transcript"
XX FT 124..137
XX FT /tag= j
XX FT 141..143
XX FT /tag= k
XX FT /bound_moiety= "mdm2 long transcript"
XX FT /note= "Forms double-stranded region with bases 116-118
XX FT of mdm2 long transcript"
XX FT 148..158
XX FT /tag= l
XX FT 161..164
XX FT /tag= m
XX FT /bound_moiety= "mdm2 long transcript"
XX FT /note= "Forms double-stranded region with bases 191-194
XX FT of mdm2 long transcript"
XX FT 169..185
XX FT /tag= n
XX FT 191..194
XX FT /tag= o
XX FT /bound_moiety= "mdm2 long transcript"
XX FT /note= "Forms double-stranded region with bases 161-164
XX FT of mdm2 long transcript"
XX PN WO200031110-A1.
XX PD 02-JUN-2000.
XX PF 22-NOV-1999; 99WO-US027710.
XX PR 25-NOV-1998; 98US-0020035.
XX PR 25-NOV-1998; 98US-0110024P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ;
XX DR WPI; 2000-400027/34.
```

XX Identifying a target nucleic acid sequence predictive of preselected
PT disease states such as a cancerous state, by comparing members of a set
PT of mRNA molecules, from a common gene, containing different sequences and
PT structures.
XX
XX Example 1; Fig 2; 38pp; English.
XX
CC The mdm2 oncogene is implicated in a variety of human cancers. The
CC protein encoded by mdm2 gene binds to p53 protein and thereby inhibits
CC p53's function. p53 is a tumour suppressor. Cancer cells contain a
CC specific form of mdm2 RNA, which is not found in normal cells. The
CC present sequence is the cancer-specific mdm2 RNA. The present sequence
CC has two unique structures: "unique Exon1 structure", and "unique Exon1/
CC Exon3 junction structure". These structures are not found in the mdm2 RNA
CC of normal cells (see ABA62124). The present sequence is predictive of
CC cancer and detection of the present sequence may therefore be used as a
CC method of predicting disease. Other diseases which may be identified by
CC using a similar method to detect other RNA molecules are
CC hyperproliferative conditions, lupus erythematosus, psoriasis,
CC inflammation, cardiovascular disease, pain, arthritis, obesity, trauma,
CC Huntington's disease or neurological disorders
XX
SQ Sequence 199 BP; 56 A; 49 C; 51 G; 0 T; 43 U; 0 Other;
Query Match 8.4%; Score 199; DB 3; Length 199;
Best Local Similarity 78.4%; Pred. No. 2.2e-85;
Matches 156; Conservative 43; Mismatches 0; Indels 0; Gaps 0;
OY 244 GAAACTGGGAGCTTGAAGGAGACCCCGAGTCCAAAGCCGAGATGTTGAGGA 303
DB 1 GAAACUGGGGAGUCUGGAGGAGCCCGAGCUCGCAAGCCGAGAAACCCGAGUGGAGAGA 60
OY 304 GCAGGCAAAATGTCATACCAACATGCTGTATACCTACGATGAGTGTCTTAACCACTTCAC 363
DB 61 GCAGGCAAAATGTCATACCAACATGCTGTATACCTACGATGAGTGTCTTAACCACTTCAC 120
OY 364 AGATTCGAGCTTCGGAACAAGACCCCTGTTAGACCAAGCCATTCCTTTGAAGTTAT 423
DB 121 AGAATCCAGCUCUCGGAACAAGACCCCTGTTAGACCAAGCCATTCCTTTGAAGTTAT 180
OY 424 TAAAGTCTGTTGTGACACA 442
DB 181 UAAAGUCUGUGUGGACACA 199
RESULT 11
ADC22295
ID ADC22295 standard; DNA; 176 BP.
XX
XX ADC22295;
XX
DT 18-DEC-2003 (first entry)
XX
DE Protein binding domain nucleotide sequence SEQ ID NO:144.
XX
XX recombinant fusion protein; fusion protein; binding; detection;
KW localisation domain; binding domain;
KW subcellular compartment localisation; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003012068-A2.
XX
PD 13-FEB-2003.
XX
PF 01-AUG-2002; 2002WO-US024572.
XX
PR 01-AUG-2001; 2001US-0309395P.
XX
PR 13-DEC-2001; 2001US-0341589P.
XX
PA (CELL-) CELLOMICS INC.
XX

PI Bright G, Premkumar DR, Chen Y;
XX
XX WPI: 2003-248174/24.
DR P-PDB: ADC22294.
XX
XX New recombinant fusion protein comprising detection and first
PT localisation domains and a binding domain for the molecule of interest,
PT useful for detecting binding of a molecule of interest.
XX
XX Disclosure; SEQ ID NO 144; 101pp; English.
XX
XX The present invention describes a recombinant fusion protein (1) for
CC detecting binding of a molecule of interest. (1) comprises: (a) a
CC detection domain; (b) a first localisation domain; and (c) a binding
CC domain for the molecule of interest. The detection domain, the first
CC localisation domain and the binding domain for the molecule of interest
CC constituting the recombinant fusion protein for detecting binding of a
CC molecule of interest are operably linked. The binding domain for the
CC molecule of interest is separated from the first localisation domain by 0
CC -20 amino acid residues. The first localisation domain and the binding
CC domain for the molecule of interest both do not occur in a single non-
CC recombinant protein with the same spacing as in the recombinant fusion
CC protein for detecting binding of a molecule of interest. Also described:
CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;
CC (2) a recombinant expression vector comprising the nucleic acid control
CC sequences operably linked to the recombinant nucleic acid molecule; (3) a
CC genetically engineered host cell transfected with the recombinant
CC expression vector; (4) a kit for detecting binding of the molecule of
CC interest; and (5) a method for identifying compounds that alter the
CC binding of the molecule of interest. The recombinant fusion protein is
CC useful for detecting binding of a molecule of interest. The recombinant
CC fusion protein eliminates the need to construct two or more chimeric
CC proteins and enables the monitoring of biochemical events in live, intact
CC or fixed cells. The present sequence is used in the exemplification of
CC the present invention.
XX
SQ Sequence 176 BP; 60 A; 25 C; 35 G; 56 T; 0 U; 0 Other;
Query Match 7.4%; Score 176; DB 10; Length 176;
Best Local Similarity 100.0%; Pred. No. 3e-74;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 435 GGTGCACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCAGTATAT 494
DB 1 GTGCACAAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCAGTATAT 60
OY 495 ATGACTAAAGATTTATGATGAGAACACAAATATTTGTTCAAAAGATCTT 554
DB 61 ATGACTAAAGATTTATGATGAGAACACAAATATTTGTTCAAAAGATCTT 120
OY 555 CTAGAGATTTGTTGGCGTGCCAAAGCTTCTGTGAAAGAGCACAGAAATATA 610
DB 121 CTAGAGATTTGTTGGCGTGCCAAAGCTTCTGTGAAAGAGCACAGAAATATA 176
RESULT 12
ABV94129
ID ABV94129 standard; CDNA; 319 BP.
XX
XX ABV94129;
XX
DT 08-JAN-2003 (first entry)
XX
DE Breast carcinoma related nucleotide sequence SEQ ID NO:120.
XX
XX Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200246467-A2.
XX
PD 13-JUN-2002.
XX

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XX 07-DEC-2001; 2001WO-1B002811.
PF 08-DEC-2000; 2000US-0254090P.
PR 07-DEC-2001; 2001US-00007926.
XX (IPSO-) IPSOGEN.
XX Bertucci F, Houlgate R, Birnbaum D, Nguyen C, Viens P, Fert V;
XX WPI; 2002-619023/66.
XX Novel polynucleotide library useful in molecular characterization of a
XX carcinoma, comprising a pool of polynucleotide sequences or its
XX subsequences which are either underexpressed or overexpressed in tumor
XX cells.
XX Claim 1; Page 189; 401pp; English.
XX The present invention describes a polynucleotide library (I) useful in
XX the molecular characterization of a carcinoma, comprising a pool of
XX polynucleotides or its subsequences which are either underexpressed or
XX overexpressed in tumor cells, and correspond to any of the
XX polynucleotide sequences chosen from the 468 sequences given in ABY94010
XX to ABY94477. Also described: (1) a polynucleotide array (II) useful for
XX the prognosis or diagnostic of tumor, comprising (1); and (2) detecting
XX (M1) differentially expressed polynucleotide sequences which are
XX correlated with a cancer, involves obtaining a polynucleotide sample from
XX a patient, and reacting the polynucleotide sample obtained with a probe
XX immobilised on a solid support, where the probe comprises any combination
XX of the polynucleotide sequences of (1) or its expression products encoded
XX by polynucleotide sequences of (1), and detecting the reaction product.
XX (1) have cytosolic activities and can be used as anti-tumour agents. (1)
XX is useful in molecular characterization of a carcinoma. (1) and (II) are
XX useful for the prognosis or diagnostic of tumour, in differentiating a
XX normal cell from a cancer cell, detecting a hormone sensitive tumour
XX cell, differentiating a tumour with lymph nodes from a tumour without
XX lymph nodes, differentiating antitaxylene-sensitive tumours from
XX antitaxylene-insensitive tumours, and classifying good and poor prognosis
XX primary breast tumours. (1) is useful for large-scale molecular
XX characterisation of breast cancer that help in prediction, prognosis and
XX cancer treatment, and for detecting differentially expressed genes that
XX correlated with a cancer
XX Sequence 319 BP; 100 A; 50 C; 44 G; 123 T; 0 U; 2 Other;
SO
Query Match 7.0%; Score 167; DB 6; Length 319;
Best Local Similarity 100.0%; Pred. No. 6.7e-70;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1773 ACTTATTTCCCTAGTGAAGTCTCTATATAGAAATTAATATTTCTAATATATACCC 1832
DB 2 ACTTATTTCCCTAGTGAAGTCTCTATATAGAAATTAATATTTCTAATATATACCC 61
QY 1833 TAGGAATTAGCAACCTGAATTTATTCACATATATCAAGTGAAGAAATGCCCAATT 1892
DB 62 TAGGAATTAGCAACCTGAATTTATTCACATATATCAAGTGAAGAAATGCCCAATT 121
QY 1893 CACATAGATTTCTTCTTTAGTATATATGACCTACTTGGTAGGG 1939
DB 122 CACATAGATTTCTTCTTTAGTATATATGACCTACTTGGTAGGG 168

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KM mdm2; disease prediction; cancer; p53; human; ss.
XX Homo sapiens.
OS Key
XX misc_binding
XX Location/Qualifiers
XX 2..8
XX /tag= a
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 10..28
XX /tag= b
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 29..38
XX /tag= c
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 2-8 of
XX mdm2 short transcript"
XX 40..46
XX /tag= d
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 2-8 of
XX mdm2 short transcript"
XX 54..67
XX /tag= e
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 116-118
XX of mdm2 short transcript"
XX 72..110
XX /tag= f
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 short transcript"
XX 116..118
XX /tag= g
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 short transcript"
XX 124..137
XX /tag= h
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 short transcript"
XX 141..143
XX /tag= i
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 short transcript"
XX 148..158
XX /tag= j
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 short transcript"
XX 161..164
XX /tag= k
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 short transcript"
XX 169..185
XX /tag= l
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 short transcript"
XX 191..194
XX /tag= m
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 short transcript"
XX 199..200
XX /tag= n
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 short transcript"
XX 2000031110-A1.
XX 02-JUN-2000.
XX 22-NOV-1999; 99WO-US027710.
XX 25-NOV-1998; 98US-00200355.
XX 25-NOV-1998; 98US-0110024P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ;
XX WPI; 2000-400027/34.
XX Identifying a target nucleic acid sequence predictive of preselected
XX disease states such as a cancerous state, by comparing members of a set
XX of mRNA molecules, from a common gene, containing different sequences and
XX structures.
XX Example 1; Fig 2; 38pp; English.
XX The mdm2 oncogene is implicated in a variety of human cancers. The

```

CC protein encoded by mdm2 gene binds to p53 protein and thereby inhibits
CC p53's function. p53 is a tumour suppressor. Cancer cells contain a
CC specific form of mdm2 RNA, which is not found in normal cells (AA62123).
CC The present sequence is the mdm2 RNA which is found in normal cells. The
CC present sequence has a unique structure: "Exon2/ Exon3 junction
CC structure". These structures are not found in the mdm2 RNA of cancerous
CC cells. The sequence of AA62123 is predictive of cancer and detection of
CC the presence of AA62123 may therefore be used as a method of predicting
CC disease. Other diseases which may be identified by using a similar method
CC to detect other RNA molecules are hyperproliferative conditions, lupus
CC erythematosus, psoriasis, inflammation, cardiovascular disease, pain,
CC arthritis, obesity, trauma, Huntington's disease or neurological
CC disorders
XX
SQ Sequence 199 BP; 50 A; 49 C; 49 G; 0 T; 51 U; 0 Other;
Query Match 5.8%; Score 138; DB 3; Length 199;
Best Local Similarity 73.9%; Pred. No. 7.4e-56;
Matches 102; Conservative 36; Mismatches 0; Indels 0; Gaps 0;
QY 305 CAGGCAATGTCATACCAATGTCCTGTAACCTATGTCGTGAACCACTCA 364
Db 62 CAGGCAAAUGUGCAADUACCAUGUCUGUACCUAGUGUGUAAACCACTCA 121
QY 365 GATTCAGACTTCGGAACAGAGACCCCTGTTAGACCAAGCATGCTTTGAAGTAT 424
Db 122 GAUUCGACGUCUGGAACAGAGACCCUGUUAAGCAAGCAUUGCUUUGAAGUUAU 181
QY 425 AAAGCTGTTGGTGCACA 442
Db 182 AAAGUCUGUGUGGCACA 199
RESULT 14
ADX15884
ID ADX15884 standard; DNA; 327 BP.
XX
AC ADX15884;
XX
DT 05-MAY-2005 (first entry)
XX
DE Modified human double minute 2 protein HK5 encoding DNA SEQ ID NO:11.
XX
KM double minute 2; ds; cancer; cytostatic; neoplasm; X-ray crystallography;
KM protein solubilization; mutant; mutagenesis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..327
FT /tag= a
FT /product= "double minute 2 variant"
FT /partial
FT /note= "no start/stop codon given"
XX
PN US2005037383-A1.
XX
PD 17-FEB-2005.
XX
PR 09-APR-2004; 2004US-00822254.
XX
PR 10-APR-2003; 2003US-0461787P.
PR 24-FEB-2004; 2004US-0547265P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Taremi SS, Xie G, Hesson T, Duca JS, Strickland C, Windsor WT;
PI Madison VS, Zhang R, Reichert P;
XX
DR WPI; 2005-180390/19.
DR P-PSDB; ADX15885.
XX
PT Novel modified human double minute 2 protein polypeptide, comprising

PT amino acid sequence differing from its corresponding wild-type, useful
XX for identifying compounds used as anticancer agents.
XX
PS Claim 7; SEQ ID NO 11; 49pp; English.
XX
CC The invention relates to a novel modified human Double Minute 2 protein
CC (Hdm2) polypeptide (I) comprising a fully defined sequence of 109 amino
CC acids (S1) as given in the specification, differing from the
CC corresponding wild-type Hdm2 (117-125) amino acid sequence (ADX15875). A
CC polypeptide of the invention is useful for identifying an agent for use
CC as an inhibitor of Hdm2. The polypeptide, crystal of the polypeptide or
CC polypeptide-compound complex (PPC) is useful for designing, selecting
CC and/or optimizing a potential inhibitor of the polypeptide. The
CC polypeptide or PPC is useful for evaluating the ability of a potential
CC inhibitor to associate with the polypeptide or PPC. The polypeptide,
CC crystal of the polypeptide or PPC is useful for identifying, selecting
CC and/or designing compounds useful as anticancer agents. The polypeptide
CC is useful in designing high affinity inhibitors of Hdm2 that are useful
CC in the treatment of cancers. The present sequence encodes a modified
CC human Double Minute 2 protein (Hdm2) polypeptide of the invention.
XX
SQ Sequence 327 BP; 117 A; 53 C; 70 G; 87 T; 0 U; 0 Other;
Query Match 4.6%; Score 109; DB 14; Length 327;
Best Local Similarity 100.0%; Pred. No. 8e-42;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 578 AAGCTTCTCTGTGAAGAGCACAGAAATTAATCAATGATTCACAGAACTGGTA 637
Db 219 AAGCTTCTCTGTGAAGAGCACAGAAATTAATCAATGATTCACAGAACTGGTA 278
QY 638 AGTCATCAGCAGGAATCATCGACTCAGGTACATCTGTGAGTGAAC 686
Db 279 AGTCATCAGCAGGAATCATCGACTCAGGTACATCTGTGAGTGAAC 327
RESULT 15
AAK81934/C
ID AAK81934 standard; DNA; 297 BP.
XX
AC AAK81934;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36746.
XX
KM Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI, 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 36746; 3071pp + Sequence Listing; English.

AA54951 to AA64702 encode the human immune/hematopoietic antigen (I)
amino acid sequences given in AA62170 to AA61921. (I) have cytosolic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AA64703

CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 297 BP, 93 A, 68 C, 88 G, 48 T, 0 U, 0 Other;
Query Match 4.3%; Score 102; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 110 TTTTAGTAGACACAGGGTTTACCGTGTAGCCAGAGTGTCTGATCTCTGACCTCGT 51
OY 2320 GATCGCCACCTCGGCTCCCAAGTGTGGGATTACAGGC 2361
Db 50 GATCGCCACCTCGGCTCCCAAGTGTGGGATTACAGGC 9
RESULT 16
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ID AAK81936 standard; DNA; 324 BP.
XX
AC AAK81936;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36748.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
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PR 05-JAN-2001; 2001US-02559678P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Roosen CA, Barash SC, Ruben SM,
XX
XX WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 36748; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK7694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
XX
SQ Sequence 324 BP; 100 A; 72 C; 98 G; 54 T; 0 U; 0 Other;

Query Match 4.3%; Score 102; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2260 TTTTAGTAGAGACAGAGGTTTACCGTGTAGCCAGATGATGTCATCTCCGACCTGGT 2319
DB 137 TTTTAGTAGAGACAGAGGTTTACCGTGTAGCCAGATGATGTCATCTCCGACCTGGT 78
OY 2320 GATCCGCCACCTCGGCTCCCAAGAGTGTGGGATTAACGGC 2361
DB 77 GATCCGCCACCTCGGCTCCCAAGAGTGTGGGATTAACGGC 36

RESULT 17
AAK81937/C
ID AAK81937 standard; DNA; 325 BP.
XX
XX AAK81937;
AC
XX
DT 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36749.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
XX WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
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PR 17-NOV-2000; 2000US-0249300P.

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PR 01-DEC-2000; 2000US-0250391P.
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PR 05-DEC-2000; 2000US-0251988P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 36749; 3071bp + Sequence listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytosstatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 325 BP; 100 A; 71 C; 97 G; 57 T; 0 U; 0 Other;
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XX Query Match 4.3%; Score 102; DB 4; Length 325;
XX Best Local Similarity 100.0%; Pred. No. 2e-38;
XX Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2260 TTTTAGTAGAGACAGGGTTTACCGGTGTACCGAGATGCTCGATCTCTGACCTGCT 2319
Db 138 TTTTAGTAGAGACAGGGTTTACCGGTGTACCGAGATGCTCGATCTCTGACCTGCT 79
Qy 2320 GATCGCCACCTCGGCTCCCAAGTGTGGGATTACAGGC 2361
Db 78 GATCGCCACCTCGGCTCCCAAGTGTGGGATTACAGGC 37
RESULT 18
AAK81935/C
ID AAK81935 standard; DNA; 331 BP.
XX
XX AAK81935;
AC
DT 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36747.
DE Human immune/haematopoietic; immune/haematopoietic antigen; cancer;
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
KW
XX
OS Homo sapiens.
XX

PN WO200157182-A2.
XX 09-AUG-2001.
PD 17-JAN-2001; 2001WO-US001354.
XX
PF
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
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PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Baraah SC, Ruben SM;

XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 36747; 3071bp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytotoxic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC to AAK87694 represent human immune/haematopoietic-derived cells. AAK64703
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 331 BP; 102 A; 72 C; 99 G; 58 T; 0 U; 0 Other;
Query Match 4.3%; Score 102; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2260 TTTTATGAGACAGAGGTTTACCGTGTAGCCAGAGTGTGATCTCCGACCTGT 2319
Db 138 TTTTATGAGACAGAGGTTTACCGTGTAGCCAGAGTGTGATCTCCGACCTGT 79
QY 2320 GATCCGCCACCTCGGCTCCCAAAGTGTCTGGATTACAGC 2361
Db 78 GATCCGCCACCTCGGCTCCCAAAGTGTCTGGATTACAGC 37
RESULT 19
AAK81933/C
ID AAK81933 standard; DNA; 331 BP.
XX
AC AAK81933;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36745.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
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PR 05-JAN-2001; 2001US-0255678P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX
XX Disclosure; SEQ ID NO 36745; 3071bp + Sequence Listing; English.
XX
XX AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostratic
CC activity, and can be used in gene therapy and vaccine production. (II)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells: AAK64703
CC to AAK64794 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 331 BP, 102 A; 72 C; 99 G; 58 T; 0 U; 0 Other;
Query Match 4.3%; Score 102; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2260 TTTTAGTAGACAGAGGTTTACCGGTGTAGCCAGAGTGTCTGATCTCTGACTCGT 2319
DB 118 TTTTAGTAGACAGAGGTTTACCGGTGTAGCCAGAGTGTCTGATCTCTGACTCGT 79
QY 2320 GATCGCCCACTCGGCTTCCCAAGTGTGTGGATTACAGGC 2361
DB 78 GATCGCCCACTCGGCTTCCCAAGTGTGTGGATTACAGGC 37
RESULT 20
ID AAL36256 standard; DNA; 309 BP.
XX
XX AAL36256;
AC 08-JAN-2002 (first entry)
XX
DT Human musculoskeletal system related polynucleotide SEQ ID NO 2621.
XX
DE
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antilucer;
XX vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein;
XX musculoskeletal system; ds.
XX
OS Homo sapiens.
XX
XX W020015367-Al.
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001338.
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 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-451937/48.
 PT Isolated polypeptide for treating, preventing and/ or prognosing
 PT disorders related to the musculoskeletal system including musculoskeletal
 PT cancers and also for testing and detection e.g. diagnosis.
 XX
 PS Example 2; SEQ ID NO 2621; 781bp + Sequence listing; English.
 XX
 CC The invention relates to novel genes (AAL34663-AAL37666) and proteins
 CC (ABB03087-ABB04109) associated with the musculoskeletal system useful for
 CC preventing, treating or ameliorating medical conditions e.g. by protein
 CC or gene therapy. The genes are isolated from a range of human tissues
 CC disclosed in the specification. The nucleic acids, proteins, antibodies
 CC and (ant)agonists are useful in the diagnosis, treatment and prevention
 CC of: (a) Cancer, e.g. breast and ovarian cancer and other cancers of the
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
 CC myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
 CC bacterial, fungal and parasitic infections. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 309 BP; 42 A; 95 C; 80 G; 92 T; 0 U; 0 Other;

Query Match 3.7%; Score 88; DB 4; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1.2e-31;
 Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2274 GGGTTTCACCGGTGATAGCCAGATGTCGATTCCTGACCTCGTATCCGCCACCTC 2333
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 DB 200 GGGTTTCACCGGTGATAGCCAGATGTCGATTCCTGACCTCGTATCCGCCACCTC 259

OY 2334 GGCCTCCCAAGTGCCTGGGATTCACAGGC 2361
 |||||
 DB 260 GGCCTCCCAAGTGCCTGGGATTCACAGGC 287

RESULT 21
 ABX59244
 ID ABX59244 standard; cDNA; 309 BP.
 XX ABX59244;
 XX
 AC 26-FEB-2003 (first entry)
 XX
 DT
 XX
 DE cDNA encoding novel human musculoskeletal system antigen #1568.
 XX
 KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
 KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
 KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
 KW post-operative tissue repair; limb regeneration; neuronal growth;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW AIDS-related complex; chondrocyte growth; bone regeneration;
 KW periodontal regeneration; tissue transport; bone graft; skin aging;
 KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
 KW cell growth; organ transplant; cell differentiation; body height; weight;
 KW hair colour; eye colour; skin; percentage of adipose tissue;
 KW pigmentation; cosmetic surgery; metabolism; biohythm; cardiac rhythm;
 KW depression; tendency for violence; pain; reproductive capability;
 KW hormone level; endocrine level; appetite; libido; memory; stress;
 KW storage capability; fat content; lipid content; protein content;
 KW carbohydrate content; vitamin content; cofactor content;
 KW nutritional component.
 KW
 XX Homo sapiens.
 OS
 XX
 XX US2002147140-A1.
 PN
 XX
 PD 10-OCT-2002.
 XX
 XX
 PF 17-JAN-2001; 2001US-00764877.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
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 PR 01-NOV-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
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 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX
 XX (ROSE// ROSEN C A.
 XX (RUBE// ROSEN S M.
 XX (BARA// BARASH S C.
 XX
 XX Rosen CA, Ruben SM, Barash SC;
 DR WPI, 2003-128199/12.
 XX
 XX Isolated nucleic acid molecules encoding musculoskeletal system
 XX associated polypeptides, useful for detecting disorders, e.g. cancer.
 XX
 XX Disclosure, SEQ ID NO 2621, 321pp; English.
 XX
 XX The invention describes an isolated nucleic acid molecule comprising a
 XX sequence encoding musculoskeletal system associated polypeptides useful
 XX for detecting disorders, e.g., cancer or cancer metastases, in animals or
 XX humans. The nucleic acid stimulates re-vascularisation of ischemic
 XX tissues associated with conditions such as thrombosis, arteriosclerosis,
 XX and other cardiovascular conditions; treats wounds due to injuries,
 XX burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
 XX and limb regeneration; stimulates neuronal growth; can treat and prevent
 XX neuronal damage occurring in certain disorders or neurodegenerative
 XX conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-
 XX related complex; stimulates chondrocyte growth, thus they can be used to
 XX enhance bone and periodontal regeneration and aid in tissue transports or
 XX bone grafts; prevents skin aging due to sunburn by stimulating
 XX keratinocyte growth; prevents hair loss, since FGF family members
 XX activate hair-forming cells and promotes melanocyte growth; stimulates
 XX growth and differentiation of hematopoietic cells and bone marrow cells
 XX when used in combination with other cytokines; maintains organs before
 XX transplantation or for supporting cell culture of primary tissues;
 XX induces tissue of mesodermal origin to differentiate in early embryos;
 XX increases or decreases the differentiation or proliferation of embryonic
 XX stem cells, besides, haematopoietic lineage; modulates mammalian
 XX characteristics, such as, body height, weight, hair colour, eye colour,
 XX skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,
 XX cosmetic surgery); modulates mammalian metabolism; changes mammal's metal
 XX state or physical state by influencing biorhythms; cardiac rhythms,
 XX depression, tendency for violence, tolerance for pain, reproductive
 XX capabilities, hormonal or endocrine levels, appetite, libido, memory, or
 XX stress; increases or decreases storage capabilities, fat content, lipid,
 XX protein, carbohydrate, vitamins, minerals, cofactors or other nutritional
 XX components. This sequence encodes a novel human musculoskeletal system
 XX antigen. Note: The sequence data for this patent did not form part of the
 XX printed specification, but was obtained in electronic format directly
 XX from the US patent office at
 XX ftp.segdata.uspto.gov/sequence.html?docID=20020147140

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XX SQ Sequence 309 BP; 42 A; 95 C; 80 G; 92 T; 0 U; 0 Other;
Query Match 3.7%; Score 88; DB 8; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 200 GGGTTTACCGTGTATAGCAGATGATGTCGATCTCCGACTCGATCCGATCCGCCACTC 259
QY 2334 GGCCTCCCAAGTCTGGATTACAGGC 2361
Db 260 GGCCTCCCAAGTCTGGATTACAGGC 287

RESULT 22
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XX AC ADJ2994;
XX DT 20-MAY-2004 (first entry)
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2621.
XX KW musculoskeletal system; cytosratic; osteopathic; cancer; osteoporosis;
XX gene therapy; vaccine; human; ds.
XX OS Homo sapiens.
XX PN US2004009488-A1.
XX PD 15-JAN-2004.
XX PF 13-SEP-2002; 2002US-00242515.
XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
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PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
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PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251088P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0256748P.
PR 17-JAN-2001; 2001US-00764877.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI, 2004-090458/09.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX
XX Disclosure; SEQ ID NO 2621; 289pp; English.
XX
XX The invention relates to a novel isolated musculoskeletal system-
CC associated nucleic acid molecule. The nucleic acid of the invention
CC demonstrates cytostatic and osteopathic activities and may be useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
CC possibly via gene therapy or vaccine production. The current sequence is
CC that of the human musculoskeletal system-associated genomic DNA of the
CC invention. The current sequence is not shown within the specification per
CC se but is available on the USPTO web-site
CC http://seqdata.uspto.gov/sequence.html?docID=20040009488.
XX
XX Sequence 309 BP; 42 A; 95 C; 80 G; 92 T; 0 U; 0 Other;
SQ
Query Match 3.7%; Score 88; DB 12; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTCAACCGTGTAGCAGAGATGTCGATCTCTGACCTCGTGAATCCGCCACCTC 2333
DB 200 GGGTTTCAACCGTGTAGCAGAGATGTCGATCTCTGACCTCGTGAATCCGCCACCTC 259
QY 2334 GGCCTCCCAAAAGTGTGGGATTACAGGC 2361
DB 260 GGCCTCCCAAAAGTGTGGGATTACAGGC 287

RESULT 23
AEF22010
ID AEF22010 standard; DNA; 140 BP.
XX
XX AEF22010;
XX

DT 09-MAR-2006 (first entry)
XX
XX Human non-basal transcription modulator splice variant DNA #152.
DE
XX Cytostatic; diagnosis; transcription factor; neoplasm; ds.
XX
XX Homo sapiens.
OS
XX WO2006005042-A2.
XX
XX 12-JAN-2006.
PD
XX 30-JUN-2005; 2005WO-US023708.
PF
XX 30-JUN-2004; 2004US-0584784P.
PR
XX (CEMI-) CEMINES INC.
XX
XX Shen D, Neuman T, Palm K;
XX
XX WPI, 2006-100776/10.
XX
XX Diagnosing cancer, useful for treating cancer, e.g. lung, breast,
PT prostate, skin, gastrointestinal cancer, comprises determining the
PT expression of at least one splice variant of each of the basal
PT transcription factors.
XX
XX Disclosure; Page 68; 131pp; English.
XX
XX The invention relates to a method of diagnosing cancer which comprises
CC determining the expression of at least one splice variant of each of the
CC basal transcription factors, where expression of each of the basal
CC transcription factor splice variants is distinguished from expression of
CC its wildtype isoform, and where the expression pattern of the basal
CC transcription factor splice variants is indicative of cancer. The methods
CC and bioactive agents are useful for treating cancer, e.g. lung cancer,
CC gastrointestinal cancer, breast cancer, prostate cancer, skin cancer,
CC sarcoma, endocrine cancer, neural cancer, bladder cancer, cervical
CC cancer, renal cancer and hematopoietic cancer. The present sequence
CC represents a human non-basal transcription modulator splice variant DNA.
XX
XX Sequence 140 BP; 50 A; 26 C; 26 G; 38 T; 0 U; 0 Other;
SQ
Query Match 3.6%; Score 85; DB 15; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.3e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1387 TTCCGATTGTAAAAAACTATAGCATGATTCACAGAGATCATGTGTGGAATAATG 1446
DB 56 TTCCGATTGTAAAAAACTATAGCATGATTCACAGAGATCATGTGTGGAATAATG 115
QY 1447 ATGATTAATTAACACAGACTTCACA 1471
DB 116 ATGATTAATTAACACAGACTTCACA 140

RESULT 24
AAK85766/C
ID AAK85766 standard; DNA; 173 BP.
XX
XX AAK85766;
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40578.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS
XX Homo sapiens.
XX
XX WO200157182-A2.
XX

PD 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
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PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
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PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
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PR 22-AUG-2000; 2000US-0227182P.
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PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
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PR 12-SEP-2000; 2000US-0231968P.
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PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
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PR 21-SEP-2000; 2000US-0234274P.
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PR 25-SEP-2000; 2000US-0234998P.
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PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246476P.
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PR 08-NOV-2000; 2000US-0246524P.
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PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246529P.
PR 08-NOV-2000; 2000US-0246609P.
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PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249254P.
PR 17-NOV-2000; 2000US-0249255P.
PR 17-NOV-2000; 2000US-0249257P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250319P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0251989P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251899P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-483426/52.
DR

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides.
PT Useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure: SEQ ID NO 40578; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I) may be
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK67694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169.
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 173 BP; 41 A; 47 C; 56 G; 29 T; 0 U; 0 Other;

Query Match 3.5%; Score 82; DB 4; Length 173;
Best Local Similarity 100.0%; Pred. No. 9.5e-29;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCAGATGTCGATCCTCGACTCGTATCGGCCACCTC 2333
|||
DB 103 GGGTTTCACCGTGTAGCAGATGTCGATCCTCGACTCGTATCGGCCACCTC 44
|||
QY 2334 GGCCTCCCAAGTGTGGATT 2355
|||
DB 43 GGCCTCCCAAGTGTGGATT 22
|||

RESULT 25
AAK85765/c
ID AAK85765 standard; DNA; 173 BP.
XX
AC AAK85765;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:40577.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.

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PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
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PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
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PR 14-AUG-2000; 2000US-0225279P.
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PR 22-AUG-2000; 2000US-0226681P.
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PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
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PR 05-SEP-2000; 2000US-0229509P.
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PR 08-SEP-2000; 2000US-0232081P.
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PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
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PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
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PR 02-OCT-2000; 2000US-0237038P.
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PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.

CC	20-OCT-2000;	2000US-0241825P.
PR	01-NOV-2000;	2000US-024617P.
PR	08-NOV-2000;	2000US-0246474P.
PR	08-NOV-2000;	2000US-0246475P.
PR	08-NOV-2000;	2000US-0246476P.
PR	08-NOV-2000;	2000US-0246477P.
PR	08-NOV-2000;	2000US-0246478P.
PR	08-NOV-2000;	2000US-0246523P.
PR	08-NOV-2000;	2000US-0246524P.
PR	08-NOV-2000;	2000US-0246525P.
PR	08-NOV-2000;	2000US-0246526P.
PR	08-NOV-2000;	2000US-0246527P.
PR	08-NOV-2000;	2000US-0246528P.
PR	08-NOV-2000;	2000US-0246532P.
PR	08-NOV-2000;	2000US-0246609P.
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PR	08-NOV-2000;	2000US-0246611P.
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PR	17-NOV-2000;	2000US-0249209P.
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PR	01-DEC-2000;	2000US-0250160P.
PR	01-DEC-2000;	2000US-0250391P.
PR	05-DEC-2000;	2000US-0251030P.
PR	05-DEC-2000;	2000US-0251988P.
PR	05-DEC-2000;	2000US-0256719P.
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PR	08-DEC-2000;	2000US-0251869P.
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PR	05-JAN-2001;	2001US-0253678P.
XX		
PA	(HMDA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
XX	WPI; 2001-483426/52.	
DR		
XX		
PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and metastasis.	
XX		
PS	Diaclosure; SEQ ID NO 40577; 3071pp + Sequence Listing; English.	
XX		
CC	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)	
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of (I) by expressing inactive proteins or to	
CC	supplement the patients own production of (I). Additionally, (I)	
CC	polynucleotides may be used to produce the secreted (I), by inserting the	
CC	nucleic acids into a host cell and culturing the cell to express the	

CC	protein.(II) proteins and polynucleotides may be used to prevent.
CC	diagnose and treat immune/haematopoietic-related diseases, especially
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC	to AAK87694 represent human immune/haematopoietic antigen genomic
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM62169
CC	represent sequences used in the exemplification of the present invention
XX	
SQ	Sequence 173 BP; 41 A; 47 C; 56 G; 29 T; 0 U; 0 Other;
Query Match	3.5%; Score 82; DB 4; Length 173;
Best Local Similarity	100.0%; Pred. No. 9.5e-29;
Matches	82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	2274 GGGTTTACCGCTGTTAGCCAGGAATGTTCATCTCTCCTGACTTGATCCGCCCACTC 2333 DB 103 GGCTTTACCCGTGTAGGCAGAAATGCTCGATCTCTGACTCGTGTATCGCCCACTC 44
OY	2334 GGCTTCCCAGAATGCTGGGATT 2355 DB 43 GGCTTCCCAGAATGCTGGGATT 22
RESULT 26	
ID	ADY59447 standard; cDNA; 80 BP.
XX	
AC	ADY59447;
XX	
DT	19-MAY-2005 (first entry)
DE	Polynucleotide of the invention SD36.
XX	
KW	ss; diagnosis; tumor; cytostatic; neoplasm; DNA microarray.
XX	
OS	Unidentified.
XX	
PN	CN1472338-A.
XX	
PD	04-FEB-2004.
XX	
Pf	01-AUG-2002; 2002CN-00125892.
XX	
PR	01-AUG-2002; 2002CN-00125892.
XX	
PA	(JUNXUAN BIOLOGICAL TECHNOLOGY CO LTD SHE.
XX	
PI	Liang P, Ding Y, Zhang X;
XX	
DR	WPI; 2004-317417/30.
XX	
PS	Tumor related gene testing method.
XX	
PS	Disclosure; Page 7; 14pp; Chinese.
XX	
CC	The invention relates to a novel process for detecting a tumor associated
CC	gene in order to diagnose early tumor. The method comprises artificially
CC	synthesizing a specific cDNA fragment as a probe, on a solid support to
CC	form a DNA array of a tumor associated gene, reverse transcription and
CC	labeling, hybridizing the labeled specimen cDNA fragment and tumor
CC	associated gene DNA array, and direct quantitative analysis. The present
CC	sequence is used in the invention.
XX	
SQ	Sequence 80 BP; 26 A; 17 C; 15 G; 22 T; 0 U; 0 Other;
Query Match	3.4%; Score 80; DB 13; Length 80;
Best Local Similarity	100.0%; Pred. No. 8.8e-28;
Matches	80; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	827 AGATGAATTAATCTGCTGACGACAAGAAAAGCCACAATCTGATATTTCCTTTC 886 DB 1 AGATGAATTAATCTGCTGACGACAAGAAAAGCCACAATCTGATATTTCCTTTC 60
OY	887 CTTTGATGAAGCTGGCTC 906

```
Db          61 CTTGATGAAAGCCTGCCTC 80
|||||
RESULT 27
AAK69176/c
ID AAK69176 standard; DNA; 140 BP.
XX
AC AAK69176;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23988.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW Cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WC200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220966P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
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XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 23988; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 140 BP; 36 A; 38 C; 42 G; 24 T; 0 U; 0 Other;
Query Match 3.2%; Score 77; DB 4; Length 140;
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QY 2345 GTGCTGGGATTATACAGGC 2361
DB 36 GTGCTGGGATTATACAGGC 20
RESULT 28
ID ABA18531/C
XX ABA18531 standard; DNA; 140 BP.
XX
XX ABA18531;
XX
XX 23-JAN-2002 (first entry)
XX
XX Human nervous system related polynucleotide SEQ ID NO 10862.
XX
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisticking; antianaemic; antiarthritic; cancer;

KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; de-
OS Homo sapiens.
XX
XX WO200159063-A2.
XX
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 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX PI
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.
 XX
 PS Disclosure; SEQ ID NO 10862; 1701bp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (AB114678-AB118001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 140 BP; 36 A; 38 C; 42 G; 24 T; 0 U; 0 Other;
 Query Match 3.2%; Score 77; DB 5; Length 140;
 Best Local Similarity 100.0%; Pred. No. 2.5e-26;
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 Db 36 GTGCTGGGATTACAGGC 20
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 ID ABA19693 standard; DNA; 140 BP.
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 AC ABA19693;
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 DT 23-JAN-2002 (first entry)
 XX
 DE Human nervous system related polynucleotide SEQ ID NO 12024.
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 KW Human; nootropic; neuroprotective; cytoskeletal; dermatological; virucide;
 KW immunosuppressive; anti-inflamatory; anti-HIV; antibacterial; vulnerary;
 KW antiparasitic; antidiabetic; antianemic; antiallergic; cancer;
 KW antineumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; anticancer; anticonvulsant; antifungal;
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX
 OS Homo sapiens.
 XX
 XX W0200159063-A2.
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PF 17-JAN-2001; 2001WO-US001334.
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PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
PR 01-DEC-2000; 2000US-0251160P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
DR Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX
PT

PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
XX
PS Disclosure; SEQ ID NO 12024; 1701bp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABBI4678-ABBI18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 140 BP; 36 A; 38 C; 42 G; 24 T; 0 U; 0 Other;
Query Match 3.2%; Score 77; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2285 TGTTAGCCAGATGCTCTGATCTCTGACCTCTGATCCGCCACCTCGGCTCCCAAA 2344
DB 96 TGTTAGCCAGATGCTCTGATCTCTGACCTCTGATCCGCCACCTCGGCTCCCAAA 37
QY 2345 GTGCTGGATTACAGCC 2361
DB 36 GTGCTGGATTACAGCC 20
RESULT 30
AAK35141/c
ID AAK35141 standard; DNA; 73 BP.
AC AAK35141;
XX
DT 01-JUN-1999 (first entry)
XX
DE Nucleotide sequence SEQ ID 49.
XX
KM MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KM inhibition; tumour growth; DNA-damaging agent; camptothecin;
KM DNA/RNA hybrid; ss.
XX
OS Synthetic.
XX
FN MO9910486-A2.
XX
PD 04-MAR-1999.
XX
PF 18-AUG-1998; 98WO-US017147.
XX
PR 22-AUG-1997; 97US-00916384.
PR 06-MAY-1998; 98US-00073567.
XX
PA (HYBR-) HYBRIDON INC.
XX
PI Chen J, Agrawal S, Zhang R;
XX
DR WPI; 1999-254219/21.
XX
XX New MDM2-specific antisense oligonucleotides.
PS Disclosure; Page 57; 59pp; English.
XX

CC The specification describes antisense oligonucleotides that inhibit MDM2
CC protein expression. The antisense oligonucleotides can be used to
CC activate a tumour suppressor. The antisense oligonucleotides are used to
CC inhibit tumour growth in a mammal, including a human, particularly in
CC conjunction with a DNA-damaging agent such as camptothecin. The present
CC sequence appears in the specification
XX
SQ Sequence 73 BP; 17 A; 23 C; 11 G; 22 T; 0 U; 0 Other;
Query Match 3.1%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 665 AGTACATCTGTGATGAGACAGGTGTACCTTGAAGTGGAGTGTCAAAAGACCT 724
DB 73 AGTACATCTGTGATGAGACAGGTGTACCTTGAAGTGGAGTGTCAAAAGACCT 14
QY 725 TGTACAGAGCTT 737
DB 13 TGTACAGAGCTT 1
RESULT 31
AAD65023/c
ID AAD65023 standard; DNA; 73 BP.
AC AAD65023;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) non-coding antisense oligonucleotide.
XX
KM MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KM therapeutic; antisense therapy; human; antisense; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
EN US2003119765-A1.
XX
PD 26-JUN-2003.
XX
PF 03-APR-2000; 2000US-00541848.
XX
PR 22-AUG-1997; 97US-00916384.
PR 06-MAY-1998; 98US-00073567.
PR 26-AUG-1999; 99US-00383507.
XX
PA (CHEN/) CHEN J.
PA (AGRA/) AGRRAWAL S.
PA (ZHANG/) ZHANG R.
PI Chen J, Agrawal S, Zhang R;
XX
DR WPI; 2003-863445/80.
XX
XX Inhibiting expression of mouse double-minute (MDM2) using anti-MDM2
XX antisense oligonucleotides, useful for screening potential therapeutic
XX agents and evaluating therapeutic effectiveness in treating tumors and/or
XX cancers.
PS Disclosure; SEQ ID NO 49; 0pp; English.
XX
XX The present invention provides methods for inhibiting expression of mouse
XX double-minute (MDM2) using anti-MDM2 antisense oligonucleotides. The
XX methods and compositions of the present invention are useful as
XX analytical and diagnostic tools for screening potential therapeutic

CC agents in the treatment of tumours and/or cancers. They may also be
CC useful in evaluating the therapeutic effectiveness of anti-human-MDM2
CC antisense oligonucleotides in the treatment of human colorectal cancers.
CC The present sequence is human mouse double minute (MDM2) non-coding
CC oligonucleotide
XX
SQ Sequence 73 BP; 17 A; 23 C; 11 G; 22 T; 0 U; 0 Other;
Query Match 3.1%; Score 73; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 665 AGGTACATCTGTGAGTGAAGACAGTGTCACTTGAAGTGGAGTCAAAAGACCT 724
DB 73 AGGTACATCTGTGAGTGAAGACAGTGTCACTTGAAGTGGAGTCAAAAGACCT 14
OY 725 TGTACAGAGCTT 737
DB 13 TGTACAGAGCTT 1
AC AAI99125; AAI99125 standard; DNA; 149 BP.
XX AAI99125;
XX 07-JAN-2002 (first entry)
DE Human excretory related polynucleotide SEQ ID NO 889.
XX
XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virocidic;
XX immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
XX antiParkinsonian; antistickling; antianaemic; antitubercic; cancer;
XX antitumumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX antiallergic; antidiabetic; antituber; anticonvulsant; antifungal;
XX antiparasitic; cardiac; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine;
XX excretory system; ds.
XX
XX Homo sapiens.
XX
XX WO200155313-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001323.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217486P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
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PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
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PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
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PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
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PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
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PR 02-OCT-2000; 2000US-0237039P.
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PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
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PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241832P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
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PR 08-NOV-2000; 2000US-0246524P.
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PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
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PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
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PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 06-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-465569/50.
XX
XX Isolated nucleic acid molecule encoding excretory system antigen is used
PT in preventing, treating or ameliorating a medical condition.
XX
XX Example 2; SEQ ID NO 889; 574pp + Sequence Listing; English.
XX
XX The invention relates to novel excretory system related human
CC polynucleotides (AA198567-AA199503) and the encoded proteins (AAM99594-
CC AAM99913) useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy, especially disorders related
CC to the excretory system. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment and
CC prevention of: (a) cancer, e.g. breast and ovarian cancer and other
CC cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal
CC tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's
CC disease, allergies, autoimmune haemolytic anaemia, autoimmune
CC thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis,
CC rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders
CC such as myocardial ischaemias; (d) wound healing; (e) neurological
CC diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases
CC such as viral, bacterial, fungal and parasitic infections. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 149 BP; 47 A; 35 C; 41 G; 26 T; 0 U; 0 Other;
SQ

Query Match

3.0%; Score 72; DB 4; Length 149;

Best Local Similarity 100.0%; Pred. No. 6,66-24;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2284 GTGTAGCCAGAGTGTCTCATCTCTGACCTGTGATCCGCCACCTCGGCTCCCA 2343
DB 116 GTGTAGCCAGAGTGTCTCATCTCTGACCTGTGATCCGCCACCTCGGCTCCCA 57
QY 2344 AGTGCTGGGATT 2355
DB 56 AGTGCTGGGATT 45
RESULT 33
AA163475/C
ID AA163475 standard; DNA; 149 BP.
XX
XX AA163475;
AC
XX
DT 22-OCT-2001 (first entry)
XX
XX Human kidney related polynucleotide SEQ ID NO 790.
DE
XX
XX Human; kidney antigen; immunosuppressive; antiarthritic; antiheumatic;
KW antiproliferative; cytostatic; cardiact; vasotropic; cerebroprotective;
KW nocrotropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; anticonvulsant; antiparasitic;
KW gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; ds.
OS Homo sapiens.
XX
XX WO20015323-A2.
FN
XX
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001343.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
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PR 07-JUL-2000; 2000US-0216647P.
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PR 11-JUL-2000; 2000US-0217487P.
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PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.

Db 56 AGTCTCTGGATT 45

RESULT 34

ABK42381
ID ABK42381 standard; DNA; 308 BP.

XX ABK42381;

DT 21-MAY-2002 (first entry)

XX Genomic sequence #280 encoding novel human connective tissue polypeptide.

XX Human; connective tissue related disorder; cancer; gene therapy;

KW cytosstatic; gene; ds.

XX Homo sapiens.

OS WO200155343-A1.

XX PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001322.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

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PR 14-AUG-2000; 2000US-0225759P.

PR 16-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 23-AUG-2000; 2000US-0227182P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 06-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

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PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232402P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239933P.
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PR 20-OCT-2000; 2000US-0240960P.
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PR 17-NOV-2000; 2000US-0249297P.

PR 17-NOV-2000; 2000US-0249299P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251988P.
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PR 08-DEC-2000; 2000US-0251868P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-565190/63.
XX
XX Nucleic acid encoding novel connective tissue associated polypeptides,
XX used in diagnosing, preventing, treating or ameliorating a disorder such
XX as cancer or rheumatoid arthritis.
XX
XX Disclosure; SEQ ID NO 1268; 673pp; English.
XX
XX The present invention relates to the isolation of novel human connective
XX tissue related polypeptides (AUB6435-AUB6923) and the polynucleotide
XX (cDNA and genomic) sequences encoding them. The sequences of the
XX invention are useful in the diagnosis, treatment, prevention and/or
XX prognosis of diseases associated with connective tissue(s), including
XX cancer. The polynucleotide sequences of the invention are also useful in
XX gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the
XX novel human connective tissue related polypeptides. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 308 BP; 48 A; 97 C; 72 G; 91 T; 0 U; 0 Other;
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XX Query Match 3.0%; Score 72; DB 4; Length 308;
XX Best Local Similarity 100.0%; Pred. No. 6,6e-24;
XX Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 213 GCCAGATGCTCGATCTCTGACCTGATCGGCCACCTCGGCTCCCAAGTCT 272

QY 2350 GGGATTACAGGC 2361
Db 273 GGGATTACAGGC 284

RESULT 35
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ID ADB60537 standard; DNA; 308 BP.
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XX ADB60537;
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XX 04-DEC-2003 (first entry)
XX
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XX
XX cytosolic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;
XX antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;
XX antiinflammatory; antiallergic; antisthmatic; dermatological;
XX nephrotropic; virucide; fungicide; antibacterial; antiparasitic;
XX gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
XX systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;
XX cancer metastasis; neoplasia; leukemia; neurodegenerative disorder;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disease;

KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;
KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;
KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
KW gastrointestinal disorder; inflammatory bowel disease;
KW organ transplant rejection; immune system disorder; Bruton's disease;
KW X-linked lymphoproliferative syndrome;
KW B-cell lymphoproliferative disorder; HIV; AIDS; infection;
KW chromosome identification; chromosome mapping;
KW connective tissue related polynucleotide; gene; ds.
XX
XX Homo sapiens.
XX
XX US2003054375-A1.
XX
XX 20-MAR-2003.
XX
XX 07-MAR-2002; 2002US-00092154.
XX
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PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764847.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI, 2003-634869/60.
XX P-PSDB; ADB59434.
XX
XX New connective tissue-related polypeptides and polynucleotides, useful
XX for treating, preventing and/or prognosing e.g. disorders of connective
XX tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or
XX neoplasias.
XX
XX Disclosure; SEQ ID NO 1268; 248bp; English.
XX
XX
XX The invention describes an isolated nucleic acid molecule (I), which
XX comprises a sequence that is at least 95 % identical to a connective
XX tissue-related polynucleotide encoding connective tissue antigens (CTA).
XX The polypeptide or polynucleotide is useful for preventing, treating, or
XX ameliorating medical conditions in a mammal. The connective tissue
XX polypeptides, polynucleotides and antibodies are particularly useful for
XX treating, preventing and/or prognosing disorders of connective tissues
XX (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,
XX scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or
XX neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g.
XX Alzheimer's disease, or Parkinson's disease), cardiovascular diseases
XX (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass
XX complications), autoimmune diseases (e.g. systemic lupus erythematosus,
XX rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.
XX

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Query Match 3.0%; Score 72; DB 9; Length 308;
 Best Local Similarity 100.0%; Pred. No. 6.6e-24;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2290 GCCAGATGCTCTGATCTCTGACCTGTCGATCGCCACCTCGGCTCCCAAGTCT 2349
DB 213 GCCAGATGCTCTGATCTCTGACCTGTCGATCGCCACCTCGGCTCCCAAGTCT 272
QY 2350 GGGATTACAGGC 2361
DB 273 GGGATTACAGGC 284

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RESULT 36
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ID ABK42380 standard; DNA; 312 BP.
XX
XX AC ABK42380;
XX
XX 21-MAY-2002 (first entry)
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XX Genomic sequence #279 encoding novel human connective tissue polypeptide.
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XX Human; connective tissue related disorder; cancer; gene therapy;
XX
XX cytoskeletal; gene; de.
XX
XX Homo sapiens.
XX
XX WO200155343-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001322.
XX

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[illegible]

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-565190/63.
Nucleic acid encoding novel connective tissue associated polypeptides,
used in diagnosing, preventing, treating or ameliorating a disorder such
as cancer or rheumatoid arthritis.

XX PS Disclosure; SEQ ID NO 1267; 673bp; English.
XX CC The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful in
CC gene therapy. ABR42102-ABR42116 represent genomic sequences encoding the
CC novel human connective tissue related polypeptides. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ
SQ Sequence 312 BP; 49 A; 98 C; 72 G; 93 T; 0 U; 0 Other;
Query Match 3.0%; Score 72; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX AC ADB60536;
XX DT 04-DEC-2003 (first entry)
XX DE Connective tissue related genomic DNA #279.
XX KW cytoskeletal; neuroprotective; neurotropic; antiparkinsonian; cardiovascular;
KW antineurodegenerative; immunosuppressive; antirheumatic; antiarthritic;
KW antiinflammatory; antiallergic; antiasthmatic; dermatological;
KW nephrotropic; vitruvian; fungicide; antibacterial; antiparasitic;
KW gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;
KW cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;
KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;
KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;
KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
KW gastrointestinal disorder; inflammatory bowel disease;
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KW X-linked lymphoproliferative syndrome;
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KW chromosome identification; chromosome mapping;
KW connective tissue related polynucleotide; gene; ds.
XX OS Homo sapiens.
XX US2003054375-A1.
XX PD 20-MAR-2003.
XX PF 07-MAR-2002; 2002US-00092154.
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PR 08-NOV-2000; 2000US-0246609P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764847.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI; 2003-634869/60.
XX P-PSDB; ADB59434.
XX
PT New connective tissue-related polypeptides and polynucleotides, useful
PT for treating, preventing and/or prognosing e.g. disorders of connective
PT tissue (e.g. rheumatoid arthritis), cancers, cancer metastases and/or
PT neoplasias.
XX
PS Disclosure; SEQ ID NO 1267; 248bp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I), which

CC comprises a sequence that is at least 95 % identical to a connective
CC tissue-related polynucleotide encoding connective tissue antigens (CTA).
CC The polypeptide or polynucleotide is useful for preventing, treating, or
CC ameliorating medical conditions in a mammal. The connective tissue
CC polypeptides, polynucleotides and antibodies are particularly useful for
CC treating, preventing and/or prognosing disorders of connective tissues
CC (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,
CC scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or
CC neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g.
CC Alzheimer's disease, or Parkinson's disease), cardiovascular diseases
CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass
CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,
CC rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.
Query Match 3.0%; Score 72; DB 9; Length 312;
Best Local Similarity 100.0%; Pred. No. 6.6e-24; Indels 0; Gaps 0;
Matches 72; Conservative 0; Mismatches 0;
QY 2290 GCCAGATGCTCTGATCTCTGACCTGATCCGCCACCTGGCCCTCCAAAGTCT 2349
DB 217 GCCAGATGCTCTGATCTCTGACCTGATCCGCCACCTGGCCCTCCAAAGTCT 276
QY 2350 GGGATTACAGGC 2361
DB 277 GGGATTACAGGC 288
RESULT 38
AAK86628/c
ID AAK86628 standard; DNA, 264 BP.
XX
AC AAK86628;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41440.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytoskeletal; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PF 31-JAN-2000; 2000US-0179065P.
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PR 17-MAR-2000; 2000US-0190076P.
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PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
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PR 01-DEC-2000; 2000US-0250391P.
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PR 05-DEC-2000; 2000US-0256719P.
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PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HMDA-) HUMAN GENOME SCI INC.

PA Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
DR
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
PS
XX
XX Disclosure; SEQ ID NO 41440; 3071pp + Sequence Listing; English.

CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to prevent the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM62169
CC represent sequences used in the exemplification of the present invention

XX
SQ Sequence 264 BP; 74 A; 68 C; 81 G; 41 T; 0 U; 0 Other;

Query Match 3.0%; Score 71; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 2e-23;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 17-NOV-2000; 2000US-0249218P.
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PR 01-DEC-2000; 2000US-0250391P.
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PR 05-DEC-2000; 2000US-0251988P.
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PR 08-DEC-2000; 2000US-0251899P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI, 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure: SEQ ID NO 35963; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK67694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 264 BP; 41 A; 81 C; 68 G; 74 T; 0 U; 0 Other;
SQ
Query Match 3.0%; Score 71; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 2e-23;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2284 GTGTAGCCAGAGATGCTCGATCTCCGACCTCGTATCCGCCACCTCGGCTCCCA 2343
DB 194 GTGTAGCCAGAGATGCTCGATCTCCGACCTCGTATCCGCCACCTCGGCTCCCA 253
QY 2344 AGTGTGGGAT 2334
DB 254 AGTGTGGGAT 264
RESULT 40
AAK84063/C
ID AAK84063 standard; DNA, 264 BP.
XX AAK84063;
XX
XX 07-NOV-2001 (first entry)
DT

XX
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:38875.
XX
XX Human; immune; hematopoietic; immune/hematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
FN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
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PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
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PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
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PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249264P.
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PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.

PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Barash SC, Ruben SM;
XX WPI, 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX
PS Disclosure; SEQ ID NO 38875; 3071pp + Sequence listing; English.
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 264 BP; 74 A; 68 C; 81 G; 41 T; 0 U; 0 Other;
Query Match 3.0%; Score 71; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 2e-23;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 71 GTGTTAGCCAGATGCTCTGATCTCTGACCTCGGATCCGCCACTGCTCCCA 12
QY 2344 AGTGCTGGGAT 2354
DB 11 AGTGCTGGGAT 1

Search completed: August 4, 2006, 14:07:22
Job time : 1553 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 13:46:41 ; Search time 2548 Seconds
(without alignments)
11438.882 Million cell updates/sec

Title: US-09-966-724B-2

Perfect score: 2372

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size: 1

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Minimum DB seq length: 5

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Post-processing: Listing first 1000 summaries

Database: Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	13.8	327	9	US-10-822-254-1
2	276	11.6	327	9	US-10-822-254-5
3	276	11.6	327	9	US-10-822-254-7
4	225	9.5	327	9	US-10-822-254-9
5	215	9.1	296	10	US-10-895-393-16
6	176	7.4	176	6	US-10-211-088-144
7	167	7.0	313	6	US-10-007-926A-120
8	148	6.2	199	6	US-10-109-213-1
9	138	5.8	199	6	US-10-109-213-2
10	109	4.6	327	9	US-10-822-254-11
11	94	4.0	385	3	US-09-960-706-717
12	91	3.8	201	16	US-11-124-367A-27407
13	88	3.7	201	16	US-11-124-367A-27362
14	88	3.7	309	3	US-09-764-877-2621
15	88	3.7	309	3	US-10-242-515-2621
16	83	3.5	201	16	US-11-124-367A-27363
17	82	3.5	285	4	US-09-925-065A-472406

18	82	3.5	285	4	US-09-925-065A-472407	Sequence 472407, A
19	82	3.5	285	5	US-09-925-065A-472406	Sequence 472406, A
20	82	3.5	285	5	US-09-925-065A-472407	Sequence 472407, A
21	77	3.2	201	16	US-11-124-367A-27364	Sequence 27364, A
22	77	3.2	340	4	US-09-925-065A-567530	Sequence 567530, A
23	77	3.2	340	4	US-09-925-065A-567530	Sequence 567530, A
24	77	3.2	427	10	US-10-674-124A-17487	Sequence 17487, A
25	76	3.2	461	4	US-09-925-065A-231416	Sequence 231416, A
26	76	3.2	461	5	US-09-925-065A-231416	Sequence 231416, A
27	76	3.2	469	12	US-10-301-480-314882	Sequence 314882, A
28	76	3.2	469	12	US-10-301-480-328291	Sequence 328291, A
29	73	3.0	73	3	US-09-541-848-49	Sequence 84849, A
30	72	3.0	149	7	US-10-242-355-889	Sequence 889, A
31	72	3.0	308	6	US-09-764-847-1268	Sequence 1268, A
32	72	3.0	308	6	US-10-092-154-1268	Sequence 1268, A
33	72	3.0	312	3	US-09-764-847-1267	Sequence 1267, A
34	72	3.0	312	3	US-10-092-154-1267	Sequence 1267, A
35	69	2.9	181	7	US-10-074-024-601	Sequence 601, A
36	69	2.9	201	8	US-10-741-601-19428	Sequence 19428, A
37	69	2.9	201	9	US-10-741-600-53227	Sequence 53227, A
38	69	2.9	293	3	US-09-764-847-1418	Sequence 1418, A
39	69	2.9	293	3	US-09-764-891-7947	Sequence 7947, A
40	69	2.9	293	3	US-09-764-891-8222	Sequence 8222, A
41	69	2.9	293	3	US-09-764-891-8321	Sequence 8321, A
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43	69	2.9	353	3	US-09-803-719-47	Sequence 71947, A
44	69	2.9	353	10	US-10-779-543-13317	Sequence 13317, A
45	69	2.9	426	9	US-10-357-930-1824	Sequence 1824, A
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47	69	2.9	446	9	US-10-357-930-35795	Sequence 35795, A
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53	69	2.9	475	9	US-10-357-930-44596	Sequence 44596, A
54	69	2.9	68	9	US-10-758-307-74	Sequence 74, A
55	68	2.9	68	10	US-10-852-797-343	Sequence 343, A
56	68	2.9	463	3	US-09-814-353-14248	Sequence 14248, A
57	68	2.8	241	8	US-10-242-535A-44459	Sequence 44459, A
58	67	2.8	241	8	US-10-085-783A-44459	Sequence 44459, A
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69	65	2.7	365	9	US-10-674-124A-9622	Sequence 9622, A
70	65	2.7	399	9	US-10-674-124A-22908	Sequence 22908, A
71	65	2.7	487	3	US-09-918-995-6797	Sequence 6797, A
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77	64	2.7	212	3	US-09-814-353-15279	Sequence 15279, A
78	64	2.7	470	12	US-10-301-480-25456	Sequence 25456, A
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80	64	2.7	478	4	US-09-925-065A-161548	Sequence 161548, A
81	64	2.7	478	5	US-09-925-065A-161548	Sequence 161548, A
82	64	2.7	493	6	US-10-027-632-476121	Sequence 476121, A
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86	60	2.5	416	3	US-09-867-701-7338	Sequence 7338, A
87	60	2.5	476	4	US-09-925-065A-817783	Sequence 817783, A
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C 92	59	2.5	201	16	US-11-124-367A-1911	Sequence 1911, Ap	C 165	57	2.4	201	9	US-10-741-600-53223	Sequence 53223, A
C 93	59	2.5	201	16	US-11-124-367A-1913	Sequence 1913, Ap	C 166	57	2.4	201	10	US-10-995-561-79428	Sequence 79428, A
C 94	59	2.5	201	16	US-11-124-367A-1928	Sequence 1928, Ap	C 167	57	2.4	285	5	US-09-764-869-1569	Sequence 1569, Ap
C 95	59	2.5	201	16	US-11-124-367A-1930	Sequence 1930, Ap	C 168	57	2.4	285	6	US-10-091-504-1569	Sequence 1569, Ap
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C 97	59	2.5	201	16	US-11-124-367A-17825	Sequence 17825, A	C 170	57	2.4	287	6	US-09-796-692-8599	Sequence 8599, Ap
C 98	59	2.5	201	16	US-11-124-367A-18137	Sequence 18137, A	C 171	57	2.4	287	7	US-10-040-862-8599	Sequence 8599, Ap
C 99	59	2.5	201	16	US-11-124-367A-18139	Sequence 18139, A	C 172	57	2.4	287	6	US-10-057-475B-8599	Sequence 8599, Ap
C 100	59	2.5	374	3	US-09-814-353-14963	Sequence 14963, A	C 173	57	2.4	287	7	US-10-154-884B-8599	Sequence 8599, Ap
C 101	59	2.5	421	3	US-09-814-353-14897	Sequence 14897, A	C 174	57	2.4	287	3	US-10-764-324-8599	Sequence 8599, Ap
C 102	59	2.5	453	3	US-09-814-353-2239	Sequence 2239, Ap	C 175	57	2.4	315	3	US-10-764-877-2515	Sequence 2515, Ap
C 103	59	2.5	453	3	US-09-814-353-8579	Sequence 8579, Ap	C 176	57	2.4	315	7	US-10-242-515-2515	Sequence 2515, Ap
C 104	59	2.5	470	4	US-09-925-065A-733661	Sequence 733661, A	C 177	57	2.4	341	3	US-09-918-595-18053	Sequence 18053, A
C 105	59	2.5	470	4	US-09-925-065A-733661	Sequence 733661, A	C 178	57	2.4	346	3	US-09-796-692-8335	Sequence 8335, Ap
C 106	59	2.5	478	4	US-09-925-065A-733497	Sequence 733497, A	C 179	57	2.4	346	6	US-10-040-862-8335	Sequence 8335, Ap
C 107	59	2.5	478	4	US-09-925-065A-812339	Sequence 812339, A	C 180	57	2.4	346	7	US-10-057-475B-8335	Sequence 8335, Ap
C 108	59	2.5	478	4	US-09-925-065A-733497	Sequence 733497, A	C 181	57	2.4	346	7	US-10-154-884B-8335	Sequence 8335, Ap
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C 110	58	2.4	126	3	US-09-764-860-1020	Sequence 1020, Ap	C 183	57	2.4	415	3	US-09-814-353-3788	Sequence 3788, Ap
C 111	58	2.4	126	6	US-10-074-095-1020	Sequence 1020, Ap	C 184	57	2.4	424	3	US-09-814-353-10097	Sequence 10097, A
C 112	58	2.4	126	6	US-10-212-872-1020	Sequence 1020, Ap	C 185	57	2.4	424	6	US-10-674-124A-16064	Sequence 16064, A
C 113	58	2.4	169	3	US-09-860-670-168	Sequence 168, App	C 186	57	2.4	429	6	US-10-027-632-104325	Sequence 104325, A
C 114	58	2.4	169	7	US-10-227-646-168	Sequence 168, App	C 187	57	2.4	429	6	US-10-027-632-325337	Sequence 325337, A
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C 123	58	2.4	201	15	US-11-124-368A-7727	Sequence 7727, Ap	C 196	57	2.4	489	9	US-10-357-930-52421	Sequence 52421, A
C 124	58	2.4	201	15	US-11-124-368A-7814	Sequence 7814, Ap	C 197	57	2.4	490	5	US-09-925-065A-8656	Sequence 8656, Ap
C 125	58	2.4	201	15	US-11-124-368A-7904	Sequence 7904, Ap	C 198	57	2.4	490	5	US-09-925-065A-8656	Sequence 8656, Ap
C 126	58	2.4	201	15	US-11-124-368A-7939	Sequence 7939, Ap	C 199	57	2.4	490	12	US-10-301-480-103893	Sequence 103893, A
C 127	58	2.4	239	7	US-09-860-670-198	Sequence 198, App	C 200	57	2.4	490	12	US-10-301-480-723302	Sequence 723302, A
C 128	58	2.4	239	7	US-10-227-646-198	Sequence 198, App	C 201	56	2.4	145	3	US-09-860-670-192	Sequence 192, App
C 129	58	2.4	270	3	US-09-764-847-1216	Sequence 1216, Ap	C 202	56	2.4	145	7	US-10-227-646-192	Sequence 192, App
C 130	58	2.4	270	3	US-09-764-847-1217	Sequence 1217, Ap	C 203	56	2.4	201	8	US-10-741-601-19311	Sequence 19311, A
C 131	58	2.4	270	6	US-10-092-154-1216	Sequence 1216, Ap	C 204	56	2.4	201	8	US-10-741-601-23793	Sequence 23793, A
C 132	58	2.4	270	6	US-10-092-154-1217	Sequence 1217, Ap	C 205	56	2.4	201	9	US-10-741-600-44883	Sequence 24883, A
C 133	58	2.4	281	9	US-10-357-930-4635	Sequence 4635, Ap	C 206	56	2.4	201	9	US-10-741-600-53079	Sequence 53079, A
C 134	58	2.4	326	9	US-10-357-930-49979	Sequence 49979, A	C 207	56	2.4	201	9	US-10-741-600-64494	Sequence 64494, A
C 135	58	2.4	354	9	US-10-357-930-217	Sequence 217, App	C 208	56	2.4	201	10	US-10-995-561-31556	Sequence 31556, A
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C 138	58	2.4	399	10	US-10-779-543-11917	Sequence 11917, A	C 211	56	2.4	282	6	US-10-091-572-859	Sequence 859, App
C 139	58	2.4	407	9	US-10-357-930-9883	Sequence 9883, Ap	C 212	56	2.4	298	6	US-09-764-878-594	Sequence 394, App
C 140	58	2.4	407	9	US-10-357-930-13596	Sequence 13596, A	C 213	56	2.4	397	10	US-10-779-543-20099	Sequence 20099, A
C 141	58	2.4	412	3	US-09-814-353-1505	Sequence 1505, Ap	C 214	56	2.4	401	3	US-09-867-701-6438	Sequence 6438, Ap
C 142	58	2.4	412	3	US-09-814-353-7864	Sequence 7864, Ap	C 215	56	2.4	401	8	US-10-741-601-11011	Sequence 11011, A
C 143	58	2.4	422	9	US-10-357-930-18494	Sequence 18494, A	C 216	55	2.3	201	8	US-10-741-601-14888	Sequence 24888, A
C 144	58	2.4	422	9	US-10-357-930-34737	Sequence 34737, A	C 217	55	2.3	201	8	US-10-741-601-14888	Sequence 24888, A
C 145	58	2.4	427	9	US-10-357-930-31775	Sequence 31775, A	C 218	55	2.3	201	9	US-10-719-993-12947	Sequence 12947, A
C 146	58	2.4	430	9	US-10-674-124A-7055	Sequence 7055, Ap	C 219	55	2.3	201	9	US-10-719-993-12495	Sequence 12495, A
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C 148	58	2.4	431	9	US-10-357-930-1440	Sequence 1440, Ap	C 221	55	2.3	201	9	US-10-741-600-29821	Sequence 29821, A
C 149	58	2.4	446	9	US-10-357-930-1440	Sequence 1440, Ap	C 222	55	2.3	201	9	US-10-741-600-61808	Sequence 61808, A
C 150	58	2.4	450	9	US-10-357-930-10010	Sequence 10010, A	C 223	55	2.3	201	9	US-10-741-600-65605	Sequence 65605, A
C 151	58	2.4	460	9	US-10-357-930-1443	Sequence 1443, Ap	C 224	55	2.3	201	9	US-10-995-561-23484	Sequence 23484, A
C 152	58	2.4	460	9	US-10-357-930-31809	Sequence 31809, A	C 225	55	2.3	201	15	US-11-124-368A-20112	Sequence 20112, A
C 153	58	2.4	460	9	US-10-357-930-39888	Sequence 39888, A	C 226	55	2.3	201	15	US-11-124-368A-20186	Sequence 20186, A
C 154	58	2.4	467	9	US-10-357-930-30589	Sequence 30589, A	C 227	55	2.3	201	16	US-11-124-367A-15936	Sequence 15936, A
C 155	58	2.4	468	3	US-10-357-930-48305	Sequence 48305, A	C 228	55	2.3	201	16	US-11-124-367A-15753	Sequence 15753, A
C 156	57	2.4	188	3	US-09-764-860-602	Sequence 602, App	C 229	55	2.3	201	16	US-11-124-367A-15960	Sequence 15960, A
C 157	57	2.4	188	3	US-09-764-904-74	Sequence 74, Appl	C 230	55	2.3	201	16	US-11-124-367A-15970	Sequence 15970, A
C 158	57	2.4	188	6	US-10-091-548-74	Sequence 74, Appl	C 231	55	2.3	201	16	US-11-124-367A-15970	Sequence 15970, A
C 159	57	2.4	188	6	US-10-074-095-602	Sequence 602, App	C 232	55	2.3	201	16	US-11-124-367A-16023	Sequence 16023, A
C 160	57	2.4	188	7	US-10-212-872-602	Sequence 602, App	C 233	55	2.3	201	16	US-11-124-367A-16023	Sequence 16023, A
C 161	57	2.4	189	7	US-10-357-930-34943	Sequence 34943, A	C 234	55	2.3	201	16	US-11-124-367A-17231	Sequence 17231, A
C 162	57	2.4	193	3	US-09-764-877-2685	Sequence 2685, Ap	C 235	55	2.3	222	6	US-10-033-528-345	Sequence 345, App
C 163	57	2.4	193	7	US-10-242-515-2685	Sequence 2685, Ap	C 236	55	2.3	222	7	US-10-099-926-345	Sequence 345, App

C 227	55	2.3	222	10	US-10-961-527-345	Sequence 345, App	310	55	2.3	385	9	US-10-357-930-14860	Sequence 14860, A
C 228	55	2.3	228	3	US-09-860-670-208	Sequence 208, App	311	55	2.3	404	3	US-09-967-768A-43	Sequence 43, Appl
C 229	55	2.3	228	7	US-10-227-646-208	Sequence 208, App	312	55	2.3	404	10	US-10-843-61A-6188	Sequence 6188, Ap
C 240	55	2.3	247	7	US-09-860-670-200	Sequence 200, App	313	55	2.3	408	9	US-10-357-930-34623	Sequence 34623, A
C 241	55	2.3	247	3	US-10-227-646-200	Sequence 200, App	314	55	2.3	413	8	US-10-242-533A-37825	Sequence 37825, A
C 242	55	2.3	249	3	US-09-860-670-173	Sequence 173, App	315	55	2.3	413	8	US-10-085-783A-37825	Sequence 37825, A
C 243	55	2.3	249	7	US-10-227-646-173	Sequence 173, App	316	55	2.3	427	4	US-09-925-065A-732335	Sequence 732335, A
C 244	55	2.3	250	3	US-09-860-670-197	Sequence 197, App	317	55	2.3	427	5	US-09-925-065A-732335	Sequence 732335, A
C 245	55	2.3	250	7	US-10-227-646-197	Sequence 197, App	318	55	2.3	429	3	US-09-814-353-2660	Sequence 2560, Ap
C 246	55	2.3	258	3	US-09-984-429-629	Sequence 629, App	319	55	2.3	429	3	US-09-814-353-2660	Sequence 2560, Ap
C 247	55	2.3	264	3	US-09-764-891-8680	Sequence 8680, Ap	320	55	2.3	432	6	US-10-027-633-277790	Sequence 277790, Ap
C 248	55	2.3	267	7	US-09-860-670-196	Sequence 196, App	321	55	2.3	432	6	US-10-027-633-277791	Sequence 277791, Ap
C 249	55	2.3	267	7	US-10-227-646-196	Sequence 196, App	322	55	2.3	432	6	US-10-027-633-277792	Sequence 277792, Ap
C 250	55	2.3	276	3	US-09-860-670-202	Sequence 202, App	323	55	2.3	432	7	US-10-027-633-277790	Sequence 277790, Ap
C 251	55	2.3	276	7	US-10-227-646-202	Sequence 202, App	324	55	2.3	432	7	US-10-027-633-277791	Sequence 277791, Ap
C 252	55	2.3	279	3	US-09-860-670-180	Sequence 180, App	325	55	2.3	432	7	US-10-027-633-277792	Sequence 277792, Ap
C 253	55	2.3	279	7	US-10-227-646-180	Sequence 180, App	326	55	2.3	432	7	US-10-027-633-277792	Sequence 277792, Ap
C 254	55	2.3	282	3	US-09-764-891-9438	Sequence 9438, Ap	327	55	2.3	432	8	US-10-242-535A-17824	Sequence 37824, A
C 255	55	2.3	282	7	US-10-091-414-306	Sequence 306, App	328	55	2.3	432	8	US-10-085-783A-37824	Sequence 37824, A
C 256	55	2.3	282	10	US-10-984-180-3	Sequence 306, App	329	55	2.3	439	12	US-10-301-480-235599	Sequence 235599, A
C 257	55	2.3	283	3	US-09-860-670-219	Sequence 219, App	330	55	2.3	439	12	US-10-301-480-235600	Sequence 235600, A
C 258	55	2.3	283	7	US-10-227-646-219	Sequence 219, App	331	55	2.3	439	12	US-10-301-480-235601	Sequence 235601, A
C 259	55	2.3	287	6	US-10-115-278-6	Sequence 6, Appl	332	55	2.3	439	12	US-10-301-480-235602	Sequence 235602, A
C 260	55	2.3	287	9	US-10-762-966-6	Sequence 6, Appl	333	55	2.3	439	12	US-10-301-480-849008	Sequence 849008, A
C 261	55	2.3	287	10	US-10-673-575-7	Sequence 7, Appl	334	55	2.3	439	12	US-10-301-480-849010	Sequence 849010, A
C 262	55	2.3	288	7	US-10-229-058B-14	Sequence 14, Appl	335	55	2.3	439	12	US-10-301-480-849011	Sequence 849011, A
C 263	55	2.3	290	3	US-09-860-670-223	Sequence 223, App	336	55	2.3	441	3	US-09-764-891-6748	Sequence 6748, Ap
C 264	55	2.3	290	7	US-10-227-646-223	Sequence 223, App	337	55	2.3	441	3	US-09-764-891-6749	Sequence 6749, Ap
C 265	55	2.3	293	3	US-09-860-670-169	Sequence 169, App	338	55	2.3	441	6	US-10-091-572-598	Sequence 598, App
C 266	55	2.3	293	7	US-10-227-646-169	Sequence 169, App	339	55	2.3	441	6	US-10-091-572-599	Sequence 599, App
C 267	55	2.3	294	3	US-09-984-429-627	Sequence 627, App	340	55	2.3	441	9	US-10-357-930-5691	Sequence 5691, App
C 268	55	2.3	297	3	US-09-764-877-2183	Sequence 2183, Ap	341	55	2.3	442	3	US-09-918-995-11943	Sequence 11943, A
C 269	55	2.3	297	7	US-09-860-670-191	Sequence 191, App	342	55	2.3	443	4	US-09-925-065A-140617	Sequence 140617, A
C 270	55	2.3	297	7	US-10-227-646-191	Sequence 191, App	343	55	2.3	443	4	US-09-925-065A-140618	Sequence 140618, A
C 271	55	2.3	297	7	US-10-242-515-2183	Sequence 2183, Ap	344	55	2.3	443	4	US-09-925-065A-140619	Sequence 140619, A
C 272	55	2.3	299	3	US-09-860-670-226	Sequence 226, App	345	55	2.3	443	4	US-09-925-065A-140620	Sequence 140620, A
C 273	55	2.3	299	7	US-10-074-024-602	Sequence 602, App	346	55	2.3	443	5	US-09-925-065A-140620	Sequence 140620, A
C 274	55	2.3	300	3	US-10-227-646-226	Sequence 226, App	347	55	2.3	443	5	US-09-925-065A-140617	Sequence 140617, A
C 275	55	2.3	300	3	US-09-984-429-5611	Sequence 5611, App	348	55	2.3	443	5	US-09-925-065A-140618	Sequence 140618, A
C 276	55	2.3	300	3	US-09-984-429-678	Sequence 678, App	349	55	2.3	443	5	US-09-925-065A-140619	Sequence 140619, A
C 277	55	2.3	301	3	US-09-860-670-181	Sequence 181, App	350	55	2.3	443	6	US-10-027-632-277793	Sequence 277793, A
C 278	55	2.3	301	3	US-09-860-670-181	Sequence 181, App	351	55	2.3	443	6	US-10-027-632-277793	Sequence 277793, A
C 279	55	2.3	301	3	US-09-984-429-638	Sequence 638, App	352	55	2.3	447	4	US-09-925-065A-46720	Sequence 46720, A
C 280	55	2.3	301	7	US-10-227-646-181	Sequence 181, App	353	55	2.3	447	4	US-09-925-065A-46720	Sequence 46720, A
C 281	55	2.3	301	7	US-10-227-646-181	Sequence 181, App	354	55	2.3	447	10	US-10-779-543-17814	Sequence 17814, A
C 282	55	2.3	301	7	US-10-227-646-183	Sequence 183, App	355	55	2.3	447	10	US-10-301-480-147958	Sequence 147958, A
C 283	55	2.3	304	3	US-09-764-891-8441	Sequence 8441, Ap	356	55	2.3	447	12	US-10-301-480-761367	Sequence 761367, A
C 284	55	2.3	308	7	US-10-074-024-587	Sequence 587, App	357	55	2.3	449	9	US-10-357-930-5975	Sequence 38975, A
C 285	55	2.3	310	3	US-09-860-670-224	Sequence 224, App	358	55	2.3	449	9	US-10-357-930-5975	Sequence 38975, A
C 286	55	2.3	310	7	US-10-227-646-224	Sequence 224, App	359	55	2.3	449	3	US-09-814-353-12957	Sequence 12957, A
C 287	55	2.3	311	7	US-09-860-670-199	Sequence 199, App	360	55	2.3	459	4	US-09-925-065A-472633	Sequence 472633, A
C 288	55	2.3	311	7	US-10-227-646-199	Sequence 199, App	361	55	2.3	459	5	US-09-925-065A-472633	Sequence 472633, A
C 289	55	2.3	314	3	US-09-860-670-217	Sequence 217, App	362	55	2.3	460	4	US-09-925-065A-564331	Sequence 564331, A
C 290	55	2.3	314	3	US-09-764-891-9014	Sequence 9014, Ap	363	55	2.3	460	5	US-09-925-065A-564331	Sequence 564331, A
C 291	55	2.3	314	7	US-10-227-646-217	Sequence 217, App	364	55	2.3	463	3	US-09-925-065A-564331	Sequence 564331, A
C 292	55	2.3	316	7	US-09-984-429-618	Sequence 618, App	365	55	2.3	463	3	US-09-764-869-1978	Sequence 1978, Ap
C 293	55	2.3	316	7	US-10-074-024-607	Sequence 607, App	366	55	2.3	463	6	US-10-091-504-1978	Sequence 1978, Ap
C 294	55	2.3	322	3	US-09-764-887-506	Sequence 506, App	367	55	2.3	463	6	US-10-091-504-1978	Sequence 1978, Ap
C 295	55	2.3	322	3	US-09-764-891-5613	Sequence 5613, App	368	55	2.3	463	7	US-10-227-632-1979	Sequence 1979, Ap
C 296	55	2.3	322	3	US-09-984-429-679	Sequence 679, App	369	55	2.3	463	7	US-10-227-632-1979	Sequence 1979, Ap
C 297	55	2.3	322	6	US-10-073-961-506	Sequence 506, App	370	55	2.3	463	7	US-10-227-632-1979	Sequence 1979, Ap
C 298	55	2.3	322	7	US-10-074-024-585	Sequence 585, App	371	55	2.3	465	4	US-09-925-065A-947399	Sequence 947399, A
C 299	55	2.3	324	7	US-09-764-891-9012	Sequence 9012, App	372	55	2.3	465	5	US-09-925-065A-947399	Sequence 947399, A
C 300	55	2.3	332	3	US-09-764-891-8700	Sequence 8700, Ap	373	55	2.3	466	4	US-09-925-065A-508844	Sequence 508844, A
C 301	55	2.3	337	3	US-09-764-877-3785	Sequence 3785, App	374	55	2.3	466	4	US-09-925-065A-508845	Sequence 508845, A
C 302	55	2.3	337	7	US-10-242-515-3785	Sequence 3785, App	375	55	2.3	466	4	US-09-925-065A-508846	Sequence 508846, A
C 303	55	2.3	353	4	US-09-925-065A-689267	Sequence 689267, A	376	55	2.3	466	5	US-09-925-065A-508847	Sequence 508847, A
C 304	55	2.3	353	5	US-09-925-065A-689267	Sequence 689267, A	377	55	2.3	466	5	US-09-925-065A-508848	Sequence 508848, A
C 305	55	2.3	358	3	US-09-918-995-37710	Sequence 37710, A	378	55	2.3	466	5	US-09-925-065A-508849	Sequence 508849, A
C 306	55	2.3	370	3	US-09-984-429-521	Sequence 521, App	379	55	2.3	466	5	US-09-925-065A-508847	Sequence 508847, A
C 307	55	2.3	370	9	US-10-357-930-13481	Sequence 13481, A	380	55	2.3	466	6	US-10-027-632-114651	Sequence 114651, A
C 308	55	2.3	382	4	US-09-925-065A-506709	Sequence 506709, A	381	55	2.3	466	7	US-10-027-632-114651	Sequence 114651, A
C 309	55	2.3	382	5	US-09-925-065A-506709	Sequence 506709, A	382	55	2.3	467	4	US-09-925-065A-949560	Sequence 949560, A

383	55	2.3	467	5	US-09-925-065A-949560	Sequence 949560,	C 456	54	2.3	311	8	US-10-085-783A-30969	Sequence 30969, A
384	55	2.3	475	8	US-10-242-535A-44241	Sequence 44241, A	457	54	2.3	332	9	US-10-674-124A-23797	Sequence 23797, A
385	55	2.3	475	8	US-10-085-783A-44241	Sequence 44241, A	458	54	2.3	335	9	US-10-357-930-30785	Sequence 30785, A
386	55	2.3	479	9	US-10-674-124A-1220	Sequence 1220, Ap	459	54	2.3	375	5	US-10-357-930-39754	Sequence 39754, A
387	55	2.3	480	3	US-09-814-353-20881	Sequence 20881, A	460	54	2.3	386	8	US-10-242-535A-18717	Sequence 18717, A
388	55	2.3	482	4	US-09-925-065A-941604	Sequence 941604, A	461	54	2.3	388	8	US-10-085-783A-18717	Sequence 18717, A
389	55	2.3	482	5	US-09-925-065A-941604	Sequence 941604, A	462	54	2.3	407	9	US-10-357-930-12797	Sequence 12797, A
390	55	2.3	486	9	US-10-357-930-50010	Sequence 50010, A	463	54	2.3	411	3	US-09-954-456-1450	Sequence 1450, Ap
391	55	2.3	489	4	US-09-925-065A-935799	Sequence 935799, A	464	54	2.3	411	3	US-09-880-107-445	Sequence 445, App
392	55	2.3	489	5	US-09-925-065A-935799	Sequence 935799, A	465	54	2.3	411	10	US-10-843-641A-4477	Sequence 4477, App
393	55	2.3	494	4	US-09-925-065A-538062	Sequence 538062, A	466	54	2.3	412	9	US-09-918-995-16264	Sequence 16264, Ap
394	55	2.3	494	4	US-09-925-065A-558063	Sequence 558063, A	467	54	2.3	447	9	US-10-357-930-3628	Sequence 3628, Ap
395	55	2.3	494	4	US-09-925-065A-740820	Sequence 740820, A	468	54	2.3	453	4	US-09-925-065A-673493	Sequence 673493, A
396	55	2.3	494	5	US-09-925-065A-558062	Sequence 558062, A	469	54	2.3	453	5	US-09-925-065A-673493	Sequence 673493, A
397	55	2.3	494	5	US-09-925-065A-558063	Sequence 558063, A	470	54	2.3	458	9	US-10-357-930-33953	Sequence 33953, A
398	55	2.3	494	5	US-09-925-065A-740820	Sequence 740820, A	471	54	2.3	458	9	US-10-357-930-42827	Sequence 42827, A
399	55	2.3	496	10	US-10-450-763-1682	Sequence 1682, Ap	472	54	2.3	463	6	US-10-073-961-112	Sequence 112, App
400	55	2.3	497	3	US-09-918-995-14827	Sequence 14827, A	473	54	2.3	463	6	US-10-073-961-112	Sequence 112, App
401	54	2.3	101	3	US-09-764-887-454	Sequence 454, App	474	54	2.3	463	10	US-10-779-543-16254	Sequence 16254, A
402	54	2.3	101	3	US-09-764-847-2002	Sequence 2002, Ap	475	54	2.3	467	4	US-09-925-065A-618091	Sequence 618091, A
403	54	2.3	101	6	US-10-092-154-2002	Sequence 2002, Ap	476	54	2.3	467	5	US-09-925-065A-618091	Sequence 618091, A
404	54	2.3	101	6	US-10-073-961-454	Sequence 454, App	477	54	2.3	468	12	US-10-301-480-19675	Sequence 19675, A
405	54	2.3	158	3	US-09-860-670-167	Sequence 167, App	478	54	2.3	468	12	US-10-301-480-19676	Sequence 19676, A
406	54	2.3	158	7	US-10-227-646-167	Sequence 167, App	479	54	2.3	468	12	US-10-301-480-633084	Sequence 633084, A
407	54	2.3	201	8	US-10-741-601-11015	Sequence 11015, A	480	54	2.3	468	12	US-10-301-480-633085	Sequence 633085, A
408	54	2.3	201	8	US-10-741-601-15537	Sequence 15537, A	481	54	2.3	476	3	US-09-998-598-1168	Sequence 1168, Ap
409	54	2.3	201	8	US-10-741-601-15541	Sequence 15541, A	482	54	2.3	485	12	US-10-301-480-305380	Sequence 305380, A
410	54	2.3	201	8	US-10-741-601-15550	Sequence 15550, A	483	54	2.3	485	12	US-10-301-480-918789	Sequence 918789, A
411	54	2.3	201	8	US-10-741-601-23751	Sequence 23751, A	484	54	2.3	489	5	US-09-925-065A-219683	Sequence 219683, A
412	54	2.3	201	8	US-10-741-601-23753	Sequence 23753, A	485	54	2.3	489	5	US-09-925-065A-219683	Sequence 219683, A
413	54	2.3	201	9	US-10-719-993-12566	Sequence 12566, A	486	54	2.3	490	6	US-10-027-632-90218	Sequence 90218, A
414	54	2.3	201	9	US-10-719-993-14541	Sequence 14541, A	487	54	2.3	490	7	US-10-027-632-90219	Sequence 90219, A
415	54	2.3	201	9	US-10-719-993-14543	Sequence 14543, A	488	54	2.3	490	7	US-10-027-632-90218	Sequence 90218, A
416	54	2.3	201	9	US-10-719-993-52785	Sequence 52785, A	489	54	2.3	490	7	US-10-027-632-90219	Sequence 90219, A
417	54	2.3	201	9	US-10-741-600-26510	Sequence 26510, A	490	54	2.3	491	6	US-10-027-632-307366	Sequence 307366, A
418	54	2.3	201	9	US-10-741-600-44935	Sequence 44935, A	491	54	2.3	491	7	US-10-027-632-304188	Sequence 304188, A
419	54	2.3	201	9	US-10-741-600-44939	Sequence 44939, A	492	54	2.3	491	7	US-10-027-632-304188	Sequence 304188, A
420	54	2.3	201	9	US-10-741-600-44948	Sequence 44948, A	493	54	2.3	491	7	US-10-027-632-307366	Sequence 307366, A
421	54	2.3	201	9	US-10-741-600-59211	Sequence 59211, A	494	54	2.3	493	4	US-09-925-065A-915897	Sequence 915897, A
422	54	2.3	201	9	US-10-741-600-64416	Sequence 64416, A	495	54	2.3	493	5	US-09-925-065A-915897	Sequence 915897, A
423	54	2.3	201	9	US-10-741-600-64418	Sequence 64418, A	496	54	2.3	495	8	US-10-242-535A-8661	Sequence 8661, Ap
424	54	2.3	201	10	US-10-995-561-20705	Sequence 20705, A	497	54	2.3	495	8	US-10-085-783A-8661	Sequence 8661, Ap
425	54	2.3	201	10	US-10-995-561-23486	Sequence 23486, A	498	54	2.3	497	4	US-09-925-065A-902221	Sequence 902221, A
426	54	2.3	201	10	US-10-995-561-69440	Sequence 69440, A	499	54	2.3	497	5	US-09-925-065A-902221	Sequence 902221, A
427	54	2.3	201	10	US-10-995-561-71599	Sequence 71599, A	500	53	2.2	201	8	US-10-741-601-24706	Sequence 24706, A
428	54	2.3	201	10	US-10-995-561-72286	Sequence 72286, A	501	53	2.2	201	9	US-10-741-600-66219	Sequence 66219, A
429	54	2.3	201	10	US-10-995-561-72288	Sequence 72288, A	502	53	2.2	201	10	US-10-995-561-20773	Sequence 20773, A
430	54	2.3	201	10	US-10-995-561-73854	Sequence 73854, A	503	53	2.2	201	16	US-11-124-367A-153789	Sequence 153789, A
431	54	2.3	201	15	US-11-124-368A-12668	Sequence 12668, A	504	53	2.2	293	3	US-09-764-891-7770	Sequence 7770, Ap
432	54	2.3	201	15	US-11-124-368A-12669	Sequence 12669, A	505	53	2.2	293	3	US-09-764-891-7770	Sequence 7770, Ap
433	54	2.3	201	15	US-11-124-368A-12670	Sequence 12670, A	506	53	2.2	343	6	US-10-027-632-26505	Sequence 26505, A
434	54	2.3	201	15	US-11-124-368A-12671	Sequence 12671, A	507	53	2.2	343	6	US-10-027-632-26505	Sequence 26505, A
435	54	2.3	201	16	US-11-124-367A-15638	Sequence 15638, A	508	53	2.2	343	6	US-10-027-632-26505	Sequence 26505, A
436	54	2.3	201	16	US-11-124-367A-21732	Sequence 21732, A	509	53	2.2	394	7	US-10-027-632-26505	Sequence 26505, A
437	54	2.3	280	3	US-09-764-891-5523	Sequence 5523, App	510	53	2.2	394	7	US-10-357-930-81882	Sequence 81882, A
438	54	2.3	283	3	US-09-764-891-5523	Sequence 5523, App	511	53	2.2	394	7	US-10-357-930-81882	Sequence 81882, A
439	54	2.3	283	6	US-10-091-572-438	Sequence 438, App	512	53	2.2	414	4	US-09-925-065A-2830	Sequence 2830, Ap
440	54	2.3	303	3	US-09-764-860-776	Sequence 776, App	513	53	2.2	414	4	US-09-925-065A-2830	Sequence 2830, Ap
441	54	2.3	303	3	US-09-764-860-776	Sequence 776, App	514	53	2.2	414	4	US-09-925-065A-2830	Sequence 2830, Ap
442	54	2.3	303	3	US-09-764-860-776	Sequence 776, App	515	53	2.2	414	4	US-09-925-065A-2830	Sequence 2830, Ap
443	54	2.3	303	6	US-10-074-095-776	Sequence 776, App	516	53	2.2	414	4	US-09-925-065A-2830	Sequence 2830, Ap
444	54	2.3	303	7	US-10-212-872-776	Sequence 776, App	517	53	2.2	414	4	US-09-925-065A-2830	Sequence 2830, Ap
445	54	2.3	303	7	US-10-242-515-2535	Sequence 2535, Ap	518	53	2.2	446	4	US-09-925-065A-126479	Sequence 126479, A
446	54	2.3	303	7	US-10-242-515-2535	Sequence 2535, Ap	519	53	2.2	446	4	US-09-925-065A-126479	Sequence 126479, A
447	54	2.3	308	10	US-10-472-553-642	Sequence 642, App	520	53	2.2	465	4	US-09-925-065A-231973	Sequence 231973, A
448	54	2.3	309	3	US-09-764-877-2197	Sequence 2197, App	521	53	2.2	465	4	US-09-925-065A-231973	Sequence 231973, A
449	54	2.3	317	7	US-10-242-515-2197	Sequence 2197, App	522	53	2.2	465	5	US-09-925-065A-126479	Sequence 126479, A
450	54	2.3	317	8	US-10-242-535A-50968	Sequence 50968, A	523	53	2.2	465	5	US-09-925-065A-126479	Sequence 126479, A
451	54	2.3	317	8	US-10-085-783A-50968	Sequence 50968, A	524	53	2.2	465	5	US-09-925-065A-126479	Sequence 126479, A
452	54	2.3	324	3	US-09-764-891-5520	Sequence 5520, App	525	53	2.2	465	5	US-09-925-065A-231973	Sequence 231973, A
453	54	2.3	324	6	US-10-091-572-435	Sequence 435, App	526	53	2.2	465	5	US-09-925-065A-231973	Sequence 231973, A
454	54	2.3	326	9	US-10-357-930-9582	Sequence 9582, App	527	53	2.2	498	3	US-09-918-995-30641	Sequence 30641, A
455	54	2.3	341	8	US-10-242-535A-30969	Sequence 30969, A	528	53	2.2	500	10	US-10-779-543-20070	Sequence 20070, A

C 529	52	2.2	201	9	US-10-741-600-58922	Sequence 58922, A	602	51	2.2	362	4	US-09-925-065A-88288	Sequence 88288, A
C 530	52	2.2	201	10	US-10-995-561-52323	Sequence 52323, A	603	51	2.2	362	5	US-09-925-065A-88288	Sequence 88288, A
C 531	52	2.2	201	16	US-11-124-367A-17786	Sequence 17786, A	604	51	2.2	362	12	US-10-301-480-18929	Sequence 18929, A
C 532	52	2.2	238	7	US-10-242-355-875	Sequence 875, App	605	51	2.2	362	12	US-10-301-480-18929	Sequence 18929, A
C 533	52	2.2	389	4	US-09-925-065A-554407	Sequence 554407, A	606	51	2.2	364	10	US-10-972-024-406	Sequence 406, App
C 534	52	2.2	389	5	US-09-925-065A-554407	Sequence 554407, A	607	51	2.2	392	9	US-10-357-930-40676	Sequence 40676, A
C 535	52	2.2	395	10	US-10-779-543-10976	Sequence 10976, A	608	51	2.2	392	9	US-10-357-930-40676	Sequence 40676, A
C 536	52	2.2	407	3	US-09-867-701-6885	Sequence 6885, App	609	51	2.2	400	8	US-10-242-535A-8804	Sequence 8804, App
C 537	52	2.2	428	4	US-09-925-065A-819737	Sequence 819737, A	610	51	2.2	400	8	US-10-085-783A-8804	Sequence 8804, App
C 538	52	2.2	428	5	US-09-925-065A-819737	Sequence 819737, A	611	51	2.2	401	3	US-09-795-668-421	Sequence 421, App
C 539	52	2.2	451	9	US-10-674-124A-21367	Sequence 21367, A	612	51	2.2	401	3	US-09-795-668-421	Sequence 421, App
C 540	52	2.2	461	9	US-10-357-930-58379	Sequence 58379, A	613	51	2.2	401	3	US-09-795-668-421	Sequence 421, App
C 541	52	2.2	471	9	US-10-674-124A-3661	Sequence 3661, App	614	51	2.2	421	10	US-10-995-081-421	Sequence 421, App
C 542	52	2.2	474	9	US-10-674-124A-24199	Sequence 24199, A	615	51	2.2	421	3	US-09-918-995-35835	Sequence 35835, A
C 543	52	2.2	487	9	US-10-357-930-48292	Sequence 48292, A	616	51	2.2	424	9	US-10-357-930-48292	Sequence 48292, A
C 544	51	2.2	118	3	US-09-764-891-8324	Sequence 8324, App	617	51	2.2	451	10	US-10-756-149-152	Sequence 152, App
C 545	51	2.2	194	3	US-09-764-891-8324	Sequence 8324, App	618	51	2.2	461	3	US-09-867-701-6802	Sequence 6802, App
C 546	51	2.2	194	7	US-10-242-515-2426	Sequence 2426, App	619	51	2.2	479	9	US-10-674-124A-1118	Sequence 1118, App
C 547	51	2.2	201	8	US-10-741-601-24633	Sequence 24633, A	620	51	2.2	480	5	US-09-925-065A-32025	Sequence 32025, A
C 548	51	2.2	201	8	US-10-741-601-25926	Sequence 25926, A	621	51	2.2	480	5	US-09-925-065A-32025	Sequence 32025, A
C 549	51	2.2	201	8	US-10-741-601-25927	Sequence 25927, A	622	51	2.2	480	5	US-09-925-065A-32025	Sequence 32025, A
C 550	51	2.2	201	8	US-10-719-993-18970	Sequence 18970, A	623	51	2.2	480	6	US-10-027-632-137719	Sequence 137719, A
C 551	51	2.2	201	9	US-10-719-993-18976	Sequence 18976, A	624	51	2.2	480	7	US-10-027-632-137719	Sequence 137719, A
C 552	51	2.2	201	9	US-10-719-993-22269	Sequence 22269, A	625	51	2.2	482	4	US-10-301-480-133263	Sequence 133263, A
C 553	51	2.2	201	9	US-10-719-993-34818	Sequence 34818, A	626	51	2.2	482	4	US-09-925-065A-737314	Sequence 737314, A
C 554	51	2.2	201	9	US-10-719-993-35022	Sequence 35022, A	627	51	2.2	482	4	US-09-925-065A-741639	Sequence 741639, A
C 555	51	2.2	201	9	US-10-719-993-42762	Sequence 42762, A	628	51	2.2	482	4	US-09-925-065A-741640	Sequence 741640, A
C 556	51	2.2	201	9	US-10-719-993-50196	Sequence 50196, A	629	51	2.2	482	4	US-09-925-065A-817268	Sequence 817268, A
C 557	51	2.2	201	9	US-10-719-993-53042	Sequence 53042, A	630	51	2.2	482	5	US-09-925-065A-737314	Sequence 737314, A
C 558	51	2.2	201	9	US-10-741-600-38805	Sequence 38805, A	631	51	2.2	482	5	US-09-925-065A-741639	Sequence 741639, A
C 559	51	2.2	201	9	US-10-741-600-39631	Sequence 39631, A	632	51	2.2	482	5	US-09-925-065A-741640	Sequence 741640, A
C 560	51	2.2	201	9	US-10-741-600-42102	Sequence 42102, A	633	51	2.2	482	5	US-09-925-065A-817268	Sequence 817268, A
C 561	51	2.2	201	9	US-10-741-600-62096	Sequence 62096, A	634	51	2.2	484	5	US-10-357-930-57692	Sequence 57692, A
C 562	51	2.2	201	9	US-10-741-600-66146	Sequence 66146, A	635	51	2.2	489	3	US-09-918-995-578	Sequence 578, App
C 563	51	2.2	201	9	US-10-741-600-67344	Sequence 67344, A	636	51	2.2	489	4	US-09-925-065A-75000	Sequence 75000, A
C 564	51	2.2	201	9	US-10-741-600-68776	Sequence 68776, A	637	51	2.2	489	4	US-09-925-065A-75000	Sequence 75000, A
C 565	51	2.2	201	9	US-10-995-561-17457	Sequence 17457, A	638	51	2.2	489	5	US-09-925-065A-75001	Sequence 75001, A
C 566	51	2.2	201	10	US-10-995-561-17470	Sequence 17470, A	639	51	2.2	489	5	US-09-925-065A-75001	Sequence 75001, A
C 567	51	2.2	201	10	US-10-995-561-30272	Sequence 30272, A	640	51	2.2	489	12	US-10-301-480-176239	Sequence 176239, A
C 568	51	2.2	201	10	US-10-995-561-30741	Sequence 30741, A	641	51	2.2	489	12	US-10-301-480-176240	Sequence 176240, A
C 569	51	2.2	201	10	US-10-995-561-33927	Sequence 33927, A	642	51	2.2	489	12	US-10-301-480-789648	Sequence 789648, A
C 570	51	2.2	201	10	US-10-995-561-33927	Sequence 33929, A	643	51	2.2	489	12	US-10-301-480-789649	Sequence 789649, A
C 571	51	2.2	201	10	US-10-995-561-39465	Sequence 39465, A	644	51	2.2	490	7	US-10-074-024-154	Sequence 154, App
C 572	51	2.2	201	10	US-10-995-561-42456	Sequence 42456, A	645	51	2.2	491	4	US-09-925-065A-938715	Sequence 938715, A
C 573	51	2.2	201	10	US-10-995-561-46763	Sequence 46763, A	646	51	2.2	491	5	US-09-925-065A-938715	Sequence 938715, A
C 574	51	2.2	201	10	US-10-995-561-70504	Sequence 70504, A	647	51	2.2	491	5	US-10-450-763-8417	Sequence 8417, App
C 575	51	2.2	201	10	US-10-995-561-76757	Sequence 76757, A	648	51	2.2	491	7	US-10-131-827-7449	Sequence 7449, App
C 576	51	2.2	201	10	US-10-995-561-78840	Sequence 78840, A	649	51	2.2	50	16	US-11-222-526-147	Sequence 147, App
C 577	51	2.2	201	10	US-10-995-561-79439	Sequence 79439, A	650	51	2.2	105	3	US-09-764-891-7259	Sequence 7259, App
C 578	51	2.2	201	10	US-10-995-561-79444	Sequence 79444, A	651	51	2.2	148	7	US-10-074-024-589	Sequence 589, App
C 579	51	2.2	201	10	US-10-995-561-80595	Sequence 80595, A	652	51	2.2	201	8	US-10-741-601-19652	Sequence 19652, A
C 580	51	2.2	201	15	US-11-124-368A-9993	Sequence 9993, App	653	51	2.2	201	9	US-10-719-993-11378	Sequence 11378, A
C 581	51	2.2	201	15	US-11-124-368A-13844	Sequence 13844, A	654	51	2.2	201	9	US-10-719-993-11804	Sequence 11804, A
C 582	51	2.2	201	15	US-11-124-368A-13856	Sequence 13856, A	655	51	2.2	201	9	US-10-719-993-24883	Sequence 24883, A
C 583	51	2.2	201	15	US-11-124-367A-19570	Sequence 19570, A	656	51	2.2	201	9	US-10-741-600-46183	Sequence 46183, A
C 584	51	2.2	201	16	US-11-124-367A-19570	Sequence 19570, A	657	51	2.2	201	9	US-10-741-600-53651	Sequence 53651, A
C 585	51	2.2	201	16	US-11-124-367A-29640	Sequence 29640, A	658	51	2.2	201	9	US-10-741-600-53651	Sequence 53651, A
C 586	51	2.2	229	16	US-11-124-367A-32804	Sequence 32804, A	659	51	2.2	201	10	US-10-995-561-40948	Sequence 40948, A
C 587	51	2.2	229	7	US-09-860-670-225	Sequence 225, App	660	51	2.2	201	10	US-10-995-561-40948	Sequence 40948, A
C 588	51	2.2	254	3	US-09-764-864-1696	Sequence 1696, App	661	51	2.2	201	10	US-10-995-561-42844	Sequence 42844, A
C 589	51	2.2	292	3	US-09-764-864-1696	Sequence 1696, App	662	51	2.2	201	10	US-10-995-561-52962	Sequence 52962, A
C 590	51	2.2	292	3	US-09-764-864-1696	Sequence 1696, App	663	51	2.2	201	10	US-10-995-561-52962	Sequence 52962, A
C 591	51	2.2	292	3	US-09-764-864-1696	Sequence 1696, App	664	51	2.2	201	10	US-10-995-561-52962	Sequence 52962, A
C 592	51	2.2	292	6	US-10-092-154-1844	Sequence 1844, App	665	51	2.2	201	10	US-10-995-561-63220	Sequence 63220, A
C 593	51	2.2	300	8	US-10-092-154-1844	Sequence 1844, App	666	51	2.2	201	10	US-10-995-561-63220	Sequence 63220, A
C 594	51	2.2	300	10	US-10-779-543-3252	Sequence 3252, App	667	51	2.2	201	10	US-10-995-561-78577	Sequence 78577, A
C 595	51	2.2	310	8	US-10-242-535A-39440	Sequence 39440, A	668	51	2.2	201	15	US-11-124-368A-19746	Sequence 19746, A
C 596	51	2.2	310	8	US-10-085-783A-39440	Sequence 39440, A	669	51	2.2	201	15	US-11-124-367A-81952	Sequence 81952, A
C 597	51	2.2	326	3	US-09-764-891-6088	Sequence 6088, App	670	51	2.2	201	16	US-11-124-367A-81953	Sequence 81953, App
C 598	51	2.2	326	3	US-09-764-891-6090	Sequence 6090, App	671	51	2.2	201	16	US-11-124-367A-10993	Sequence 10993, A
C 599	51	2.2	329	7	US-09-764-877-3390	Sequence 3390, App	672	51	2.2	201	16	US-11-124-367A-15954	Sequence 15954, A
C 600	51	2.2	335	7	US-10-242-355-840	Sequence 840, App	673	51	2.2	201	16	US-11-124-367A-15955	Sequence 15955, A
C 601	51	2.2	342	3	US-09-867-701-8277	Sequence 8277, App	674	51	2.2	201	16	US-11-124-367A-28679	Sequence 28679, A

675	50	2.1	201	US-11-124-367A-31777	Sequence 31777, A	748	50	2.1	494	4	US-09-925-065A-869357	Sequence 869377, A
C 676	50	2.1	201	US-11-124-367A-33263	Sequence 33263, A	749	50	2.1	494	5	US-09-925-065A-869357	Sequence 869377, A
677	50	2.1	223	US-09-860-670-220	Sequence 220, App	C 750	50	2.1	499	4	US-09-925-065A-842223	Sequence 842223, A
678	50	2.1	223	US-10-227-546-220	Sequence 220, App	C 751	50	2.1	499	5	US-09-925-065A-842223	Sequence 842223, A
679	50	2.1	239	US-10-674-124A-21646	Sequence 21646, A	C 752	49	2.1	111	8	US-10-242-535A-38990	Sequence 38990, A
680	50	2.1	252	US-09-764-847-1033	Sequence 1033, App	C 753	49	2.1	111	8	US-10-085-783A-38990	Sequence 38990, A
681	50	2.1	252	US-10-092-154-1033	Sequence 1033, App	C 754	49	2.1	111	8	US-10-085-783A-38990	Sequence 38990, A
C 682	50	2.1	262	US-10-357-930-18436	Sequence 18436, A	755	49	2.1	201	8	US-10-741-601-21194	Sequence 21194, A
C 683	50	2.1	264	US-09-764-891-8746	Sequence 8746, App	756	49	2.1	201	9	US-10-719-993-7133	Sequence 7133, App
C 684	50	2.1	272	US-09-764-891-8746	Sequence 8746, App	C 757	49	2.1	201	9	US-10-719-993-7133	Sequence 7133, App
C 685	50	2.1	273	US-10-242-535A-55757	Sequence 55757, A	C 758	49	2.1	201	9	US-10-741-600-50959	Sequence 50959, A
C 686	50	2.1	273	US-10-085-783A-55757	Sequence 55757, A	C 759	49	2.1	201	9	US-10-741-600-50959	Sequence 50959, A
C 687	50	2.1	288	US-09-973-278-870	Sequence 870, App	760	49	2.1	201	9	US-10-741-600-50959	Sequence 50959, A
688	50	2.1	288	US-10-205-428-644	Sequence 929, App	C 761	49	2.1	201	10	US-10-995-561-26409	Sequence 26409, A
C 689	50	2.1	301	US-09-984-429-644	Sequence 644, App	C 762	49	2.1	201	15	US-11-124-367A-12667	Sequence 12667, A
C 690	50	2.1	317	US-09-764-891-7588	Sequence 7588, App	C 763	49	2.1	201	15	US-11-124-367A-12667	Sequence 12667, A
C 691	50	2.1	323	US-09-984-429-669	Sequence 669, App	764	49	2.1	201	16	US-11-124-367A-17933	Sequence 17933, A
C 692	50	2.1	337	US-10-357-930-48248	Sequence 48248, A	765	49	2.1	275	3	US-09-867-701-8897	Sequence 8897, App
C 693	50	2.1	361	US-09-803-719-115	Sequence 115, App	766	49	2.1	275	3	US-09-867-701-8897	Sequence 8897, App
C 694	50	2.1	361	US-10-779-543-13385	Sequence 13385, A	767	49	2.1	276	3	US-09-764-891-5817	Sequence 5817, App
C 695	50	2.1	364	US-09-803-719-110	Sequence 110, App	768	49	2.1	276	3	US-09-764-891-5817	Sequence 5817, App
C 696	50	2.1	364	US-10-779-543-13380	Sequence 13380, A	769	49	2.1	301	9	US-10-357-930-841	Sequence 841, App
C 697	50	2.1	366	US-10-242-535A-7668	Sequence 7668, App	770	49	2.1	317	3	US-09-871-161-109	Sequence 109, App
C 698	50	2.1	366	US-10-085-783A-7668	Sequence 7668, App	C 771	49	2.1	334	3	US-09-867-701-9936	Sequence 9936, App
C 699	50	2.1	377	US-10-357-930-10372	Sequence 10372, A	C 772	49	2.1	364	3	US-09-867-701-8282	Sequence 8282, App
C 700	50	2.1	378	US-10-027-632-142956	Sequence 142956, A	C 773	49	2.1	371	9	US-10-914-037-919	Sequence 919, App
C 701	50	2.1	378	US-10-027-632-142956	Sequence 142956, A	774	49	2.1	374	9	US-10-357-930-704	Sequence 704, App
C 702	50	2.1	378	US-10-357-930-9873	Sequence 9873, App	775	49	2.1	378	9	US-10-357-930-554	Sequence 554, App
C 703	50	2.1	378	US-10-357-930-19220	Sequence 19220, A	776	49	2.1	389	4	US-09-925-065A-492995	Sequence 42995, A
C 704	50	2.1	380	US-10-357-930-9718	Sequence 9718, App	777	49	2.1	389	4	US-09-925-065A-492995	Sequence 42995, A
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ALIGNMENTS

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; Publication No. US2005003783A1
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Ducu, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Runtin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of HdM2, Crystalline Forms Thereof and Metho
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-254-1

Query Match 13.8%; Score 327; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.6e-158;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 360 TCACAGATTCACGCTTCGGAACAAGACCCCTGTTAGACCAAGCCATTGCTTTGAAG 419
Db 1 TCACAGATTCACGCTTCGGAACAAGACCCCTGTTAGACCAAGCCATTGCTTTGAAG 60
QY 420 TTATTAAGTCTGTGGTGCAAAAAAGACCTTATCTATGAAAGGTTCTTTTAT 479
Db 61 TTATTAAGTCTGTGGTGCAAAAAAGACCTTATCTATGAAAGGTTCTTTTAT 120
QY 480 CTGGCCAGATATTTATGACTAAACGATATATGATGAGGAACAACATTTGATAT 539
Db 121 CTGGCCAGATATTTATGACTAAACGATATATGATGAGGAACAACATTTGATAT 180
QY 540 TGTTCAAATGATCTTTCAGAGATTTGTTGGCTGCACGCTTCTGTGAAGACAC 599
Db 181 TGTTCAAATGATCTTTCAGAGATTTGTTGGCTGCACGCTTCTGTGAAGACAC 240
QY 600 AGAAATATATATCCATGATCTACAGAACTTGGTACTGATCAATCGACGATATCG 659
Db 241 AGAAATATATATCCATGATCTACAGAACTTGGTACTGATCAATCGACGATATCG 300
QY 660 GACTCAGTACATCTGTGAGTGAAC 686
Db 301 GACTCAGTACATCTGTGAGTGAAC 327
```

```
RESULT 2
US-10-822-254-5
; Sequence 5, Application US/10822254
; Publication No. US2005003783A1
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Ducu, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Runtin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of HdM2, Crystalline Forms Thereof and Metho
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-254-5

Query Match 11.6%; Score 276; DB 9; Length 327;
Best Local Similarity 99.7%; Pred. No. 5.3e-132;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



```

? TITLE OF INVENTION: Expression
? FILE REFERENCE: 19025.012
? CURRENT APPLICATION NUMBER: US/160/895.3
? CURRENT FILING DATE: 2004-07-21
? PRIOR APPLICATION NUMBER: PCT/US04/0164
? PRIOR FILING DATE: 2004-01-21
? PRIOR APPLICATION NUMBER: 60/441,637
? PRIOR FILING DATE: 2003-01-21
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 16
? LENGTH: 236
? TYPE: DNA
? ORGANISM: Artificial
? FEATURE:
? OTHER INFORMATION: Synthetic Construct
US-10-895-393-16

```

Query Match	9.1%	Score 215;	DB 10;	Length 296;
Best Local Similarity	100.0%	Pred. No. 2.9e-100;		
Matches 215;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	9	CGAGCTTGAGTCTCTTCCTGGGGGCGCTGTGTGAGCCCTGTGTGTGCGAAAGATGAGCAAGAAG	68
Db	1	CGAGCTTGAGTCTCTTCCTGGGGGCGCTGTGTGAGCCCTGTGTGTGCGAAAGATGAGCAAGAAG	60
Oy	69	CCGAGCCCGAGGGGGGGGCGCGGACCCCTCTGACCGAGATCTCTGTGCGAGCCAGG	128
Db	61	CCGAGCCCGAGGGGGGGGCGCGGACCCCTCTGACCGAGATCTCTGTGCGAGCCAGG	120
Oy	129	AGCACCGTCCCTTCCTCCCGGATTAGTGGGTACGAGCGCCCAATGCCCTGTGCCCCGAGAGATGG	188
Db	121	AGCACCGTCCCTTCCTCCCGGATTAGTGGGTACGAGCGCCCAATGCCCTGTGCCCCGAGAGATGG	180
Oy	189	AATGATCCCGGAGGCCCGAGGGGCTCGTGCCTCCGC	223
Db	181	AATGATCCCGGAGGCCCGAGGGCTCTGTGCTTCCGC	215

```

RESULT 6
US-10-211-088-144
; Sequence 144; Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For Molecular B
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 144
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence encoding binding domain
US-10-211-088-144

```

Query Match	7.4%;	Score 176;	DB 6;	Length 176;
Best Local Similarity	100.0%;	Pred. No. 5.4e-80;		
Matches 176;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	435	GGTGCAAAAAGACACTTATCTATGAAAGGTTCTTTTATCTGGCAGTATTT	494
Db	1	GGTGCAAAAAGACACTTATCTATGAAAGGTTCTTTTATCTGGCAGTATTT	60

Oy	495	ATACGAAACGATTATATGATGAGAAGCAACAATATGTATTTGTTCAATGACCTT	554
Db	61	ATGACATTAACGATTATATGATGAGAAGCAACAATATGTATTTGTTCAAAAGACCTT	120
Oy	555	CTAGGAGATTGTTGGCGTCGCAAGCTCTCTGTGAAAGAAGCAGAGAAAATATA	610
Db	121	CTAGGAGATTGTTGGCGTCGCAAGCTTCTCTGTGAAAGAAGCAGAGAAAATATA	176

```

RESULT 7
US-10-007-926A-120
; Sequence 120. Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOUTIGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 5' terminal sequence, mouse double minute 2,
; OTHER INFORMATION: human homolog of, p53-binding protein (MDM2) gene.
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1278)
; OTHER INFORMATION: a, t, c or g
;
US-10-007-926A-120

```

Query Match	7.0%;	Score 167;	DB 7;	Length 319;
Best Local Similarity	100.0%;	Pred. No. 2.7e-75;		
Matches 167;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1773	ACTATTTTCCCGTGTGACCGGCTATAAGAGAAATATATATTCTAACATATAAACC	1833
Db	2	ACTTATTTTCCCTTACTTACCTGCTGTATAAGAGAAATATATATTTCTAACATATAAACC	61
QY	1833	TAGGAATTAGCAACCTGAATTTATTCACATATATCAAAAGTGAGAAATGCGCTCAATT	1893
Db	62	TAGGATTTTAGCAACCTGAATTTATTCACATATATPAAAGTGGAGAAATGCGCTCAATT	121
QY	1893	CACATAGATTTCTTCTCTTTAGTATPAATATGACCACTTTGGTAGGG	1939
Db	122	CACATAGATTTCTTCTCTTTAGTATPAATATGACCTTCTTTGGTAGGG	168

```

RESULT 8
US-10-109-213-1
; Sequence 1, Application US/10109213
; Publication No. US20020168670A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/10/109,213
; CURRENT FILING DATE: 2002-03-27

```

```

; PRIOR APPLICATION NUMBER: US/09/200.355
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 199
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-109-213-1

Query Match
Best Local Similarity 77.9%; Score 148; DB 6; Length 199;
Matches 155; Conservative 43; Mismatches 1; Indels 0; Gaps 0;

QY 244 GAAACCTGGGAGCTTGGAGGACCCCGGACTCCAGCGGAAACCCCGAGTGTAGGA 303
DB 1 GAAACCTGGGAGCTTGGAGGACCCCGGACTCCAGCGGAAACCCCGAGTGTAGGA 60
QY 304 GCAGGCAATGTGCATATACCAATGTCTGTACTGTAGTGTGTGTACCACTGCAC 363
DB 61 GCAGGCAATGTGCATATACCAATGTCTGTACTGTAGTGTGTGTACCACTGCAC 120
QY 364 AGATTCCAGCTTCGGAACAAGAGACCCGCTTGAACCAAGCCATTGCTTTGAAGTTAT 423
DB 121 AGAATCCAGCTTCGGAACAAGAGACCCGCTTGAACCAAGCCATTGCTTTGAAGTTAT 180
QY 424 TAAAGTCTTGTGTGCACA 442
DB 181 TAAAGTCTTGTGTGCACA 199

RESULT 9
US-10-109-213-2
; Sequence 2, Application US/10109213
; Publication No. US20020168670A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/10/109,213
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/200,355
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-109-213-2

Query Match
Best Local Similarity 5.8%; Score 138; DB 6; Length 199;
Matches 102; Conservative 36; Mismatches 0; Indels 0; Gaps 0;

QY 305 CAGGCAATGTGCATATACCAATGTCTGTACTGTAGTGTGTGTGTACCACTGCAC 364
DB 62 CAGGCAATGTGCATATACCAATGTCTGTACTGTAGTGTGTGTGTACCACTGCAC 121
QY 365 GATTTCAGCTTCGGAACAAGAGACCCGCTTGAACCAAGCCATTGCTTTGAAGTTAT 424
DB 122 GATTTCAGCTTCGGAACAAGAGACCCGCTTGAACCAAGCCATTGCTTTGAAGTTAT 181
QY 425 AAAAGTCTTGTGTGCACA 442
DB 182 AAAAGTCTTGTGTGCACA 199

RESULT 10
US-10-822-254-11
; Sequence 11, Application US/10822254
; Publication No. US20050037383A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Duca, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Rumin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Meth
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-254-11

Query Match
Best Local Similarity 4.6%; Score 109; DB 9; Length 327;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 578 AGCTTCTCTGTGAAGAAGCAGAGAAATATATACCATCTACAGAACTGTGTACT 637
DB 219 AGCTTCTCTGTGAAGAAGCAGAGAAATATATACCATCTACAGAACTGTGTACT 278
QY 638 AGTCATCAGCAGATCATCTCGACTCAGTACATCTGTAGTGAAC 686
DB 279 AGTCATCAGCAGATCATCTCGACTCAGTACATCTGTAGTGAAC 327

RESULT 11
US-09-960-706-717
; Sequence 717, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplae
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 717
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 N20967
US-09-960-706-717

Query Match
Best Local Similarity 4.0%; Score 94; DB 3; Length 385;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTACACCGTGTAGCCAGAGATGTTGATCTCTGACCTCGTGTATCCGCCACCTC 2333
DB 13 GGGTTACACCGTGTAGCCAGAGATGTTGATCTCTGACCTCGTGTATCCGCCACCTC 72
QY 2334 GGCTCCCAAGTGTGGATTACAGCATGAC 2367
```

Db 73 GGCTCCCAAGTGTGGATTACAGGATGAGC 106

RESULT 12
US-11-124-367A-27407/c
; Sequence 27407, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:

APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CU001519.ORD
CURRENT FILING DATE: 2005-05-09
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US/11/124,367A
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27407
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-27407

Query Match
Best Local Similarity 3.8%; Score 91; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 9,1e-36;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2282 CCGTGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACTTCGGCTTCC 2341
Db 100 CCGTGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACTTCGGCTTCC 41

Qy 2342 AAAGTGTGGATTACAGGATGAGCCACCG 2372
Db 40 AAAGTGTGGATTACAGGATGAGCCACCG 10

RESULT 13
US-11-124-367A-27362/c
; Sequence 27362, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:

APPLICANT: Hongjin Huang
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CU001519.ORD
CURRENT FILING DATE: 2005-05-09
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US/11/124,367A
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27362
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-27362

Query Match 3.7%; Score 88; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 3,3e-34;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2285 TGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACTTCGGCTTCCAAA 2344
Db 100 TGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACTTCGGCTTCCAAA 41
Qy 2345 GTGCTGGATTACAGGATGAGCCACCG 2372
Db 40 GTGCTGGATTACAGGATGAGCCACCG 13

RESULT 14
US-09-764-877-2621

; Sequence 2621, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2621
LENGTH: 309
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-2621

Query Match 3.7%; Score 88; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 3,4e-34;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTACCGTGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACTTC 2333
Db 200 GGGTTACCGTGTAGCCAGATGTCGATCTCTGACCTCGTATCCGCCACTTC 259

Qy 2334 GGCTCCCAAGTGTGGATTACAGGC 2361
Db 260 GGCTCCCAAGTGTGGATTACAGGC 287

RESULT 15
US-10-242-515-2621

; Sequence 2621, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005C1
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US/10/242,515
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 4031

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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2621
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-2621
```

```
Query Match          3.7%; Score 88; DB 7; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.4e-34;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2274 GGGTTTACCGTGTGATGACGAGATGATCTCTGACCTCGATCCGCCACCTC 2333
          |||
DB      200 GGGTTTACCGTGTGATGACGAGATGATCTCTGACCTCGATCCGCCACCTC 259
```

```
QY      2334 GGGCTTCCCAAGTGTGGATTTACAGGC 2361
          |||
DB      260 GGGCTTCCCAAGTGTGGATTTACAGGC 287
```

RESULT 16

```
US-11-124-367A-27363/C
; Sequence 27363, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27363
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-27363
```

```
Query Match          3.5%; Score 83; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.3e-31;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2290 GCCAGATGTTCTGATCTCTGACCTCGATTCGCCACCTCGGCTCCCAAGTGCT 2349
          |||
DB      100 GCCAGATGTTCTGATCTCTGACCTCGATTCGCCACCTCGGCTCCCAAGTGCT 41
```

```
QY      2350 GGGATTACAGGATGAGCCACCG 2372
          |||
DB      40 GGGATTACAGGATGAGCCACCG 18
```

RESULT 17

```
US-09-925-065A-472406/C
; Sequence 472406, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
```

```
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 472406
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-472406
```

```
Query Match          3.5%; Score 82; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.5e-31;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2280 CACCGTTAGCCAGATGATCTCGATCTCTGACCTCGTATCCGCCACCTCGGCTC 2339
          |||
DB      231 CACCGTTAGCCAGATGATCTCGATCTCTGACCTCGTATCCGCCACCTCGGCTC 172
```

```
QY      2340 CCAAGTGCTGGATTACAGGC 2361
          |||
DB      171 CCAAGTGCTGGATTACAGGC 150
```

RESULT 18

```
US-09-925-065A-472407/C
; Sequence 472407, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 472407
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-472407
```

```
Query Match          3.5%; Score 82; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.5e-31;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2280 CACCGTTAGCCAGATGATCTCGATCTCTGACCTCGTATCCGCCACCTCGGCTC 2339
          |||
DB      231 CACCGTTAGCCAGATGATCTCGATCTCTGACCTCGTATCCGCCACCTCGGCTC 172
```

```
QY      2340 CCAAGTGCTGGATTACAGGC 2361
          |||
DB      171 CCAAGTGCTGGATTACAGGC 150
```

RESULT 19

```
US-09-925-065A-472406/C
; Sequence 472406, Application US/09925065A
```



```
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 472406
/ LENGTH: 285
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-472406

Query Match      3.5%; Score 82; DB 5; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.5e-31;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2280 CACCGTTAGCCAGATGCTCGATCTCCGACCTCGATCCGCCACCTCGGCTC 2339
Db      231  CACCGTTAGCCAGATGCTCGATCTCCGACCTCGATCTCCGCCACCTCGGCTC 172
Qy      2340 CCAAAGTCTGGGATTACAGGC 2361
Db      171  CCAAAGTCTGGGATTACAGGC 150

RESULT 20
US-09-925-065A-472407/c
/ Sequence 472407, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT FILING DATE: US/09/925,065A
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 472407
/ LENGTH: 285
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-472407

Query Match      3.5%; Score 82; DB 5; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.5e-31;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2280 CACCGTTAGCCAGATGCTCGATCTCCGACCTCGATCCGCCACCTCGGCTC 2339
Db      231  CACCGTTAGCCAGATGCTCGATCTCCGACCTCGATCTCCGCCACCTCGGCTC 172
```

```
Db      231  CACCGTTAGCCAGATGCTCGATCTCCGACCTCGATCCGCCACCTCGGCTC 172
Qy      2340 CCAAAGTCTGGGATTACAGGC 2361
Db      171  CCAAAGTCTGGGATTACAGGC 150

RESULT 21
US-11-124-367A-27364/c
/ Sequence 27364, Application US/11124367A
/ Publication No. US20060024700A1
/ GENERAL INFORMATION:
/ APPLICANT: Michele Cargill
/ APPLICANT: Hongjin Huang
/ TITLE OF INVENTION: Genetic Polymorphisms Associated with
/ FILE REFERENCE: CL001519.ORD
/ CURRENT FILING DATE: US/11/124,367A
/ PRIOR APPLICATION NUMBER: US 60/568,846
/ PRIOR FILING DATE: 2004-05-07
/ PRIOR APPLICATION NUMBER: US 60/582,609
/ PRIOR FILING DATE: 2004-06-25
/ PRIOR APPLICATION NUMBER: US 60/599,554
/ PRIOR FILING DATE: 2004-08-09
/ NUMBER OF SEQ ID NOS: 34460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27364
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-124-367A-27364

Query Match      3.2%; Score 77; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.7e-28;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2296 ATGGCTGATCTCTGACCTCGATCGGCGCCACCTCGGCTCCAAAGTCTGGATT 2355
Db      100  ATGGCTGATCTCTGACCTCGATCGGCGCCACCTCGGCTCCAAAGTCTGGATT 41
Qy      2356 ACAGGCGATGAGCCACCG 2372
Db      40  ACAGGCGATGAGCCACCG 24

RESULT 22
US-09-925-065A-567530
/ Sequence 567530, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT FILING DATE: US/09/925,065A
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 567530
/ LENGTH: 340
/ TYPE: DNA
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```

; ORGANISM: Homo sapiens
US-09-925-065A-567530

Query Match
Best Local Similarity 100.0%; Score 77; DB 4; Length 340;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGCTCTGATCTCTGACCTGCGGACCTGCGGCTCCCAAA 2344
DB 55 TGTAGCCAGATGCTCTGATCTCTGACCTGCGGACCTGCGGCTCCCAAA 114
QY 2345 GTGCTGGATTACAGGC 2361
DB 115 GTGCTGGATTACAGGC 131

RESULT 23
US-09-925-065A-567530
; Sequence 567530, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 567530
; LENGTH: 340
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-567530

Query Match
Best Local Similarity 100.0%; Score 77; DB 5; Length 340;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGCTCTGATCTCTGACCTGCGGACCTGCGGCTCCCAAA 2344
DB 55 TGTAGCCAGATGCTCTGATCTCTGACCTGCGGACCTGCGGCTCCCAAA 114
QY 2345 GTGCTGGATTACAGGC 2361
DB 115 GTGCTGGATTACAGGC 131

RESULT 24
US-10-674-124A-17487
; Sequence 17487, Application US/10674124A
; Publication No. US20040197979A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidekoshi
; APPLICANT: TAMAYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATTELLITE
; FILE REFERENCE: ORIN-003CTP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
```

```

; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 17487
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: chr11.fa.07frz.71465096
; FEATURE:
; OTHER INFORMATION: Located on chromosome 11
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; FEATURE:
; OTHER INFORMATION: sequence : 57058295
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 247203
US-10-674-124A-17487

Query Match
Best Local Similarity 100.0%; Score 77; DB 9; Length 427;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGCTCTGATCTCTGACCTGCGGACCTGCGGCTCCCAAA 2344
DB 255 TGTAGCCAGATGCTCTGATCTCTGACCTGCGGACCTGCGGCTCCCAAA 314
QY 2345 GTGCTGGATTACAGGC 2361
DB 315 GTGCTGGATTACAGGC 331

RESULT 25
US-09-925-065A-231416/c
; Sequence 231416, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231416
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-231416

Query Match
Best Local Similarity 100.0%; Score 76; DB 4; Length 461;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGATGCTCTGATCTCTGACCTGCGGACCTGCGGCTCCCAAA 2345
```

```
Db      245 GTTAGCCAGATGCTCTGATCTCTGACCTGTGATCCGCCCACTCGGCTCCCAAG 186
      |||
OY      2346 TGCTGGATTACAGGC 2361
      |||
Db      185 TGCTGGATTACAGGC 170
```

RESULT 26

```
US-09-925-065A-231416/c
; Sequence 231416, Application US/09925065A
; Publication No. US2005028172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231416
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-231416
```

Query Match 3.2%; Score 76; DB 5; Length 461;

Best Local Similarity 100.0%; Pred. No. 6.1e-28; Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY      2286 GTTAGCCAGATGCTCTGATCTCTGACCTGTGATCCGCCCACTCGGCTCCCAAG 2345
      |||
Db      245 GTTAGCCAGATGCTCTGATCTCTGACCTGTGATCCGCCCACTCGGCTCCCAAG 186
```

```
OY      2346 TGCTGGATTACAGGC 2361
      |||
Db      185 TGCTGGATTACAGGC 170
```

RESULT 27

```
US-10-301-480-314882/c
; Sequence 314882, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314882
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-314882
```

Query Match 3.2%; Score 76; DB 12; Length 469;

Best Local Similarity 100.0%; Pred. No. 6.1e-28; Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY      2286 GTTAGCCAGATGCTCTGATCTCTGACCTGTGATCCGCCCACTCGGCTCCCAAG 2345
      |||
Db      245 GTTAGCCAGATGCTCTGATCTCTGACCTGTGATCCGCCCACTCGGCTCCCAAG 186
      |||
OY      2346 TGCTGGATTACAGGC 2361
      |||
Db      185 TGCTGGATTACAGGC 170
```

RESULT 28

```
US-10-301-480-928291/c
; Sequence 928291, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 928291
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-928291
```

Query Match 3.2%; Score 76; DB 12; Length 469;

Best Local Similarity 100.0%; Pred. No. 6.1e-28; Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY      2286 GTTAGCCAGATGCTCTGATCTCTGACCTGTGATCCGCCCACTCGGCTCCCAAG 2345
      |||
Db      245 GTTAGCCAGATGCTCTGATCTCTGACCTGTGATCCGCCCACTCGGCTCCCAAG 186
```

```
OY      2346 TGCTGGATTACAGGC 2361
      |||
Db      185 TGCTGGATTACAGGC 170
```

RESULT 29

```
US-09-541-848-49/c
; Sequence 49, Application US/09541848
; Publication No. US20030119765A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, Jiandong
; APPLICANT: AGRAWAL, Sudhir
; APPLICANT: ZHANG, Ruiwen
; TITLE OF INVENTION: MD-M2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 29924/98057C
; CURRENT APPLICATION NUMBER: US/09/541,848
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 09/383,507
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/073,567
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 08/916,834
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentm Ver. 2.0
; SEQ ID NO 49
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
```


; SEQ ID NO 1267
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1267

Query Match 3.0%; Score 72; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290 GCCAGATGCTGATCTCTGACCTGATCCGCCACCTGGCCTCCCAAGTCT 2349
Db 217 GCCAGATGCTGATCTCTGACCTGATCCGCCACCTGGCCTCCCAAGTCT 276

Qy 2350 GGGATTACAGGC 2361
Db 277 GGGATTACAGGC 288

RESULT 34

US-10-092-154-1267
; Sequence 1267, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1267
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1267

Query Match 3.0%; Score 72; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290 GCCAGATGCTGATCTCTGACCTGATCCGCCACCTGGCCTCCCAAGTCT 2349
Db 217 GCCAGATGCTGATCTCTGACCTGATCCGCCACCTGGCCTCCCAAGTCT 276

Qy 2350 GGGATTACAGGC 2361
Db 277 GGGATTACAGGC 288

RESULT 35

US-10-074-024-601/c
; Sequence 601, Application US/10074024
; Publication No. US20030232975A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC001C1
; CURRENT APPLICATION NUMBER: US/10/074,024
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 879
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 601
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-074-024-601

Query Match 2.9%; Score 69; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGAGACAGGGTTTACCGTTAGCCAGATGCTGATCTCTGACCTGCT 2319
Db 129 TTTTAGTAGAGACAGGGTTTACCGTTAGCCAGATGCTGATCTCTGACCTGCT 70
Qy 2320 GATCCGCC 2328
Db 69 GATCCGCC 61

RESULT 36

US-10-741-601-19428/c
; Sequence 19428, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19428
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-19428

Query Match 2.9%; Score 69; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGAGACAGGGTTTACCGTTAGCCAGATGCTGATCTCTGACCTGCT 2319
Db 186 TTTTAGTAGAGACAGGGTTTACCGTTAGCCAGATGCTGATCTCTGACCTGCT 127

Qy 2320 GATCCGCC 2328
Db 126 GATCCGCC 118

RESULT 37

US-10-741-600-53227/c
; Sequence 53227, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53227
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-53227

Query Match 2.9%; Score 69; DB 9; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGAGACAGGGTTTACCGTTAGCCAGATGCTGATCTCTGACCTGCT 2319
Db 186 TTTTAGTAGAGACAGGGTTTACCGTTAGCCAGATGCTGATCTCTGACCTGCT 127

Qy 2320 GATCCGCC 2328
Db 126 GATCCGCC 118

```
RESULT 38
US-09-764-847-1418/c
; Sequence 1418, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1418
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1418

Query Match
Best Local Similarity 100.0%; Score 69; DB 3; Length 293;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 2319
DB 115 TTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 56
QY 2320 GATCCGCC 2328
DB 55 GATCCGCC 47

RESULT 39
US-09-764-891-7947
; Sequence 7947, Application US/09764891
; Publication No. US2003007808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7947
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7947

Query Match
Best Local Similarity 100.0%; Score 69; DB 3; Length 293;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 2319
DB 179 TTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 238
QY 2320 GATCCGCC 2328
DB 239 GATCCGCC 247

RESULT 40
US-09-764-891-8222
; Sequence 8222, Application US/09764891
; Publication No. US2003007808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
```

```
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8222
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8222

Query Match
Best Local Similarity 100.0%; Score 69; DB 3; Length 293;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 2319
DB 179 TTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 238
QY 2320 GATCCGCC 2328
DB 239 GATCCGCC 247
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Search completed: August 4, 2006, 14:32:15
Job time : 2567 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 20:43:09 ; Search time 499 Seconds
(without alignments)
7528.771 Million cell updates/sec

Title: US-09-966-724B-2

Perfect score: 2372

Sequence: 1 GCACCGCGCAGAGCTTGCTG.....ATTACAGCATGACGACCG 2372

Scoring table: OLIGO_NUC

Searched: 2193277 seqs, 791917567 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3365896

Minimum DB seq length: 5

Maximum DB seq length: 500

Post-processing: Listing first 1000 summaries

Database: Published Applications NA New:*

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- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEM_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCV_NEM_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEM_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	157	6.6	364	US-11-266-748A-60150	Sequence 60150, A
3	55	2.3	428	US-11-266-748A-57794	Sequence 57794, A
4	50	2.1	50	US-10-511-937-283	Sequence 283, App
5	50	2.1	474	US-11-266-748A-60447	Sequence 60447, A
6	44	1.9	500	US-11-266-748A-21382	Sequence 21382, A
7	43	1.8	438	US-11-266-748A-50804	Sequence 50804, A
8	43	1.8	444	US-11-266-748A-21936	Sequence 21936, A
9	43	1.8	444	US-11-266-748A-31940	Sequence 31940, A
10	42	1.8	463	US-11-266-748A-38062	Sequence 38062, A
11	42	1.8	463	US-11-266-748A-46391	Sequence 46391, A
12	40	1.7	349	US-11-327-124A-215	Sequence 215, App
13	39	1.6	245	US-11-266-748A-217154	Sequence 217154, App
14	39	1.6	359	US-11-266-748A-414670	Sequence 414670, A
15	38	1.6	455	US-11-266-748A-61942	Sequence 61942, A
16	38	1.6	464	US-11-266-748A-61449	Sequence 61449, A
17	38	1.6	486	US-11-266-748A-217171	Sequence 217171, A
18	38	1.6	486	US-11-266-748A-23850	Sequence 23850, A
19	37	1.6	224	US-11-266-748A-170884	Sequence 170884, A
20	37	1.6	355	US-11-301-554-749	Sequence 749, App
21	37	1.6	425	US-11-266-748A-208969	Sequence 208969, A
22	37	1.6	437	US-11-266-748A-50353	Sequence 50353, A
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24	37	1.6	461	US-11-266-748A-235428	Sequence 235428, A

25	36	1.5	50	US-10-554-711-12	Sequence 12, Appl
26	36	1.5	50	US-10-554-711-17	Sequence 17, Appl
27	36	1.5	50	US-10-554-711-24	Sequence 24, Appl
28	36	1.5	50	US-10-554-711-26	Sequence 26, Appl
29	36	1.5	50	US-10-554-711-27	Sequence 27, Appl
30	36	1.5	50	US-10-554-711-29	Sequence 29, Appl
31	36	1.5	50	US-10-554-711-30	Sequence 30, Appl
32	36	1.5	213	US-11-266-748A-40751	Sequence 40751, A
33	36	1.5	335	US-11-266-748A-35463	Sequence 35463, A
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36	36	1.5	462	US-11-266-748A-48475	Sequence 48475, A
37	36	1.5	474	US-11-266-748A-60828	Sequence 60828, A
38	35	1.5	50	US-10-554-711-13	Sequence 13, Appl
39	35	1.5	50	US-10-554-711-25	Sequence 25, Appl
40	35	1.5	50	US-10-554-711-32	Sequence 32, Appl
41	35	1.5	50	US-10-554-711-33	Sequence 33, Appl
42	35	1.5	432	US-11-195-344-1	Sequence 1, Appl
43	35	1.5	432	US-11-195-344-205	Sequence 205, App
44	35	1.5	452	US-11-195-344-257	Sequence 257, App
45	35	1.5	454	US-11-266-748A-208180	Sequence 208180, App
46	34	1.4	241	US-11-266-748A-658	Sequence 658, App
47	34	1.4	403	US-10-488-619-441	Sequence 441, App
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53	33	1.4	281	US-11-266-748A-390684	Sequence 390684, A
54	33	1.4	401	US-11-266-748A-215385	Sequence 215385, A
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56	33	1.4	444	US-11-266-748A-352411	Sequence 352411, A
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81	32	1.3	498	US-11-266-748A-212638	Sequence 212638, A
82	32	1.3	499	US-11-266-748A-326022	Sequence 326022, A
83	32	1.3	499	US-11-266-748A-350940	Sequence 350940, A
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87	31	1.3	295	US-11-266-748A-391453	Sequence 391453, A
88	31	1.3	295	US-11-266-748A-482171	Sequence 482171, A
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115	29	1.2	414	6	US-10-533-365-220	Sequence 220, App	c 188	27	1.1	464	8	US-11-266-748A-60549	Sequence 60549, App
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166	27	1.1	386	8	US-11-266-748A-215391	Sequence 215391, A	c 239	26	1.1	469	8	US-11-266-748A-209125	Sequence 209125, A
167	27	1.1	387	6	US-10-533-365-218	Sequence 218, App1	c 240	26	1.1	469	8	US-11-266-748A-37651	Sequence 37651, A
168	27	1.1	392	6	US-10-488-619-66	Sequence 66, App1	c 241	26	1.1	480	8	US-11-266-748A-40254	Sequence 40254, A
169	27	1.1	393	8	US-11-266-748A-57891	Sequence 57891, A	c 242	26	1.1	480	8	US-11-266-748A-40254	Sequence 40254, A
170	27	1.1	413	8	US-11-266-748A-15579	Sequence 15579, A	c 243	26	1.1	480	8	US-11-266-748A-40254	Sequence 40254, A

C 244	26	1.1	480	8	US-11-266-748A-214608	Sequence 214608,	C 317	24	1.0	315	8	US-11-266-748A-11209	Sequence 11209, A
C 245	26	1.1	481	8	US-11-301-554-583	Sequence 583, App	C 318	24	1.0	354	8	US-11-266-748A-32890	Sequence 32890, A
C 246	26	1.1	483	8	US-11-266-748A-53226	Sequence 53226, A	C 319	24	1.0	354	8	US-11-266-748A-32890	Sequence 32890, A
C 247	26	1.1	485	8	US-11-266-748A-61092	Sequence 61092, A	C 320	24	1.0	359	8	US-11-266-748A-321752	Sequence 321752, A
C 248	26	1.1	488	8	US-11-266-748A-257204	Sequence 257204, A	C 321	24	1.0	359	8	US-11-266-748A-326084	Sequence 326084, A
C 249	26	1.1	488	8	US-11-266-748A-317721	Sequence 317721, A	C 322	24	1.0	366	8	US-11-266-748A-375648	Sequence 375648, A
C 250	26	1.1	492	8	US-11-266-748A-59023	Sequence 59023, A	C 323	24	1.0	366	8	US-11-266-748A-389587	Sequence 389587, A
C 251	25	1.1	50	6	US-10-554-711-18	Sequence 18, App1	C 324	24	1.0	366	8	US-11-266-748A-459027	Sequence 459027, A
C 252	25	1.1	305	8	US-11-266-748A-373558	Sequence 373558, A	C 325	24	1.0	368	8	US-11-266-748A-256439	Sequence 256439, A
C 253	25	1.1	305	8	US-11-266-748A-456937	Sequence 456937, A	C 326	24	1.0	368	8	US-11-266-748A-316956	Sequence 316956, A
C 254	25	1.1	309	8	US-11-266-748A-377566	Sequence 377566, A	C 327	24	1.0	368	8	US-11-266-748A-49389	Sequence 49389, A
C 255	25	1.1	309	8	US-11-266-748A-460945	Sequence 460945, A	C 328	24	1.0	368	8	US-11-266-748A-209067	Sequence 209067, A
C 256	25	1.1	336	8	US-11-266-748A-217030	Sequence 217030, A	C 329	24	1.0	386	8	US-11-266-748A-33850	Sequence 33850, A
C 257	25	1.1	352	8	US-11-266-748A-207996	Sequence 207996, A	C 330	24	1.0	388	8	US-11-266-748A-373716	Sequence 373716, A
C 258	25	1.1	352	8	US-11-266-748A-233364	Sequence 233364, A	C 331	24	1.0	388	8	US-11-266-748A-457095	Sequence 457095, A
C 259	25	1.1	364	8	US-11-266-748A-268758	Sequence 268758, A	C 332	24	1.0	390	8	US-11-266-748A-38687	Sequence 38687, A
C 260	25	1.1	364	8	US-11-266-748A-339275	Sequence 339275, A	C 333	24	1.0	391	6	US-10-511-937-553	Sequence 583, App
C 261	25	1.1	371	8	US-11-266-748A-255259	Sequence 255259, A	C 334	24	1.0	393	8	US-11-266-748A-40029	Sequence 40029, A
C 262	25	1.1	371	8	US-11-266-748A-315776	Sequence 315776, A	C 335	24	1.0	393	8	US-11-266-748A-212048	Sequence 212048, A
C 263	25	1.1	398	8	US-11-266-748A-35620	Sequence 35620, A	C 336	24	1.0	403	8	US-10-473-173-485	Sequence 485, App
C 264	25	1.1	398	8	US-11-266-748A-40097	Sequence 40097, A	C 337	24	1.0	403	8	US-11-266-748A-59681	Sequence 59681, A
C 265	25	1.1	402	8	US-11-266-748A-40889	Sequence 40889, A	C 338	24	1.0	403	8	US-11-266-748A-161338	Sequence 161338, A
C 266	25	1.1	402	8	US-11-266-748A-269588	Sequence 269588, A	C 339	24	1.0	403	8	US-11-266-748A-413378	Sequence 413378, A
C 267	25	1.1	402	8	US-11-266-748A-354482	Sequence 354482, A	C 340	24	1.0	403	8	US-11-266-748A-215384	Sequence 215384, A
C 268	25	1.1	402	8	US-11-266-748A-437861	Sequence 437861, A	C 341	24	1.0	403	8	US-11-266-748A-337569	Sequence 337569, A
C 269	25	1.1	406	8	US-11-266-748A-172552	Sequence 172552, A	C 342	24	1.0	410	7	US-11-195-344-267	Sequence 267, App
C 270	25	1.1	410	8	US-11-266-748A-36090	Sequence 36090, A	C 343	24	1.0	410	8	US-11-266-748A-211886	Sequence 211886, A
C 271	25	1.1	411	8	US-11-266-748A-217712	Sequence 217712, A	C 344	24	1.0	410	8	US-11-266-748A-35434	Sequence 35434, A
C 272	25	1.1	412	6	US-10-473-173-202	Sequence 202, App	C 345	24	1.0	413	8	US-11-266-748A-37722	Sequence 37722, A
C 273	25	1.1	414	8	US-11-266-748A-210930	Sequence 210930, A	C 346	24	1.0	414	8	US-11-266-748A-208881	Sequence 208881, A
C 274	25	1.1	418	8	US-11-266-748A-234788	Sequence 234788, A	C 347	24	1.0	416	8	US-11-266-748A-233784	Sequence 233784, A
C 275	25	1.1	420	8	US-11-266-748A-217826	Sequence 217826, A	C 348	24	1.0	416	8	US-11-266-748A-265384	Sequence 265384, A
C 276	25	1.1	420	8	US-11-266-748A-207818	Sequence 207818, A	C 349	24	1.0	416	8	US-11-266-748A-272825	Sequence 272825, A
C 277	25	1.1	421	8	US-11-266-748A-233233	Sequence 233233, A	C 350	24	1.0	416	8	US-11-266-748A-280522	Sequence 280522, A
C 278	25	1.1	427	8	US-11-266-748A-60396	Sequence 60396, A	C 351	24	1.0	416	8	US-11-266-748A-325901	Sequence 325901, A
C 279	25	1.1	434	8	US-11-266-748A-139922	Sequence 139922, A	C 352	24	1.0	416	8	US-11-266-748A-333342	Sequence 333342, A
C 280	25	1.1	438	6	US-10-802-875-15	Sequence 15, App1	C 353	24	1.0	417	8	US-11-266-748A-60896	Sequence 60896, A
C 281	25	1.1	438	6	US-10-812-797-15	Sequence 15, App1	C 354	24	1.0	426	8	US-11-266-748A-427459	Sequence 427459, A
C 282	25	1.1	439	8	US-11-266-748A-266508	Sequence 266508, A	C 355	24	1.0	435	8	US-11-266-748A-10313	Sequence 10313, A
C 283	25	1.1	439	8	US-11-266-748A-280430	Sequence 280430, A	C 356	24	1.0	435	8	US-11-266-748A-156124	Sequence 156124, A
C 284	25	1.1	439	8	US-11-266-748A-327025	Sequence 327025, A	C 357	24	1.0	439	8	US-11-266-748A-57856	Sequence 57856, A
C 285	25	1.1	454	8	US-11-266-748A-61325	Sequence 61325, A	C 358	24	1.0	439	8	US-11-266-748A-208475	Sequence 208475, A
C 286	25	1.1	454	8	US-11-266-748A-218434	Sequence 218434, A	C 359	24	1.0	442	8	US-11-266-748A-212715	Sequence 212715, A
C 287	25	1.1	454	8	US-11-266-748A-218434	Sequence 218434, A	C 360	24	1.0	442	8	US-11-266-748A-214635	Sequence 214635, A
C 288	25	1.1	460	8	US-11-266-748A-319080	Sequence 319080, A	C 361	24	1.0	442	8	US-11-266-748A-236067	Sequence 236067, A
C 289	25	1.1	464	8	US-11-266-748A-61850	Sequence 61850, A	C 362	24	1.0	442	8	US-11-266-748A-237167	Sequence 237167, A
C 290	25	1.1	471	8	US-11-266-748A-428919	Sequence 428919, A	C 363	24	1.0	446	8	US-11-266-748A-61962	Sequence 61962, A
C 291	25	1.1	472	8	US-11-266-748A-208501	Sequence 208501, A	C 364	24	1.0	446	8	US-11-266-748A-220128	Sequence 220128, A
C 292	25	1.1	481	8	US-11-266-748A-233640	Sequence 233640, A	C 365	24	1.0	446	8	US-11-266-748A-339797	Sequence 339797, A
C 293	25	1.1	481	8	US-11-266-748A-12285	Sequence 12285, A	C 366	24	1.0	454	6	US-10-488-619-608	Sequence 608, App
C 294	25	1.1	499	8	US-11-266-748A-208770	Sequence 208770, A	C 367	24	1.0	455	8	US-11-266-748A-60597	Sequence 60597, A
C 295	25	1.1	500	8	US-11-266-748A-176746	Sequence 176746, A	C 368	24	1.0	457	8	US-11-266-748A-215260	Sequence 215260, A
C 296	24	1.0	44	7	US-11-320-440-35	Sequence 35, App1	C 369	24	1.0	461	8	US-11-266-748A-211845	Sequence 211845, A
C 297	24	1.0	50	6	US-10-554-711-31	Sequence 31, App1	C 370	24	1.0	463	8	US-11-266-748A-219111	Sequence 219111, A
C 298	24	1.0	50	6	US-10-554-711-31	Sequence 31, App1	C 371	24	1.0	463	8	US-11-266-748A-239351	Sequence 239351, A
C 299	24	1.0	132	8	US-11-266-748A-86962	Sequence 86962, A	C 372	24	1.0	469	8	US-11-266-748A-54081	Sequence 54081, A
C 300	24	1.0	132	8	US-11-266-748A-139773	Sequence 139773, A	C 373	24	1.0	469	8	US-11-266-748A-216763	Sequence 216763, A
C 301	24	1.0	134	8	US-11-266-748A-480210	Sequence 480210, A	C 374	24	1.0	473	8	US-11-266-748A-58875	Sequence 58875, A
C 302	24	1.0	142	8	US-11-266-748A-174239	Sequence 174239, A	C 375	24	1.0	475	8	US-11-266-748A-270974	Sequence 270974, A
C 303	24	1.0	142	8	US-11-266-748A-245972	Sequence 245972, A	C 376	24	1.0	475	8	US-11-266-748A-331491	Sequence 331491, A
C 304	24	1.0	161	8	US-11-266-748A-9507	Sequence 9507, App	C 377	24	1.0	479	8	US-11-266-748A-365110	Sequence 365110, A
C 305	24	1.0	161	8	US-11-266-748A-9507	Sequence 9507, App	C 378	24	1.0	479	8	US-11-266-748A-449089	Sequence 449089, A
C 306	24	1.0	175	8	US-11-266-748A-530	Sequence 530, App	C 379	24	1.0	481	8	US-11-266-748A-61447	Sequence 61447, A
C 307	24	1.0	197	8	US-11-266-748A-104081	Sequence 104081, A	C 380	24	1.0	484	8	US-11-266-748A-50263	Sequence 50263, A
C 308	24	1.0	211	8	US-11-266-748A-156892	Sequence 156892, A	C 381	24	1.0	484	8	US-11-266-748A-58429	Sequence 58429, A
C 309	24	1.0	211	8	US-11-266-748A-103706	Sequence 103706, A	C 382	24	1.0	496	8	US-11-266-748A-35661	Sequence 35661, A
C 310	24	1.0	238	8	US-11-266-748A-7811	Sequence 7811, App	C 383	24	1.0	497	8	US-11-266-748A-429915	Sequence 429915, A
C 311	24	1.0	246	8	US-11-266-748A-171099	Sequence 171099, A	C 384	24	1.0	500	8	US-11-266-748A-211962	Sequence 211962, A
C 312	24	1.0	246	8	US-11-266-748A-245260	Sequence 245260, A	C 385	24	1.0	500	8	US-11-266-748A-235493	Sequence 235493, A
C 313	24	1.0	278	8	US-11-266-748A-271418	Sequence 271418, A	C 386	24	1.0	23	6	US-10-511-937-1854	Sequence 1854, App
C 314	24	1.0	278	8	US-11-266-748A-31935	Sequence 31935, A	C 387	23	1.0	23	7	US-11-320-440-123	Sequence 123, App
C 315	24	1.0	295	8	US-11-266-748A-378979	Sequence 378979, A	C 388	23	1.0	212	8	US-11-266-748A-391857	Sequence 391857, A
C 316	24	1.0	295	8	US-11-266-748A-462358	Sequence 462358, A	C 389	23	1.0	212	8	US-11-266-748A-482575	Sequence 482575, A

390	23	1.0	267	7	US-11-195-344-245	Sequence 245, App	463	23	1.0	489	8	US-11-266-748A-208092	Sequence 208092,
391	23	1.0	300	8	US-11-266-748A-179736	Sequence 179736,	C 464	23	1.0	489	8	US-11-266-748A-233446	Sequence 233446,
392	23	1.0	330	8	US-11-266-748A-210257	Sequence 210257,	C 465	23	1.0	492	8	US-11-266-748A-40655	Sequence 40655, A
C 393	23	1.0	330	8	US-11-266-748A-234503	Sequence 234503,	C 466	23	1.0	494	8	US-11-266-748A-216594	Sequence 216594
C 394	23	1.0	332	8	US-11-266-748A-103943	Sequence 103943,	C 467	23	1.0	495	8	US-11-266-748A-16531	Sequence 16531, A
C 395	23	1.0	332	8	US-11-266-748A-156754	Sequence 156754,	C 468	23	1.0	499	7	US-11-327-124A-95	Sequence 95, App1
C 396	23	1.0	363	8	US-11-266-748A-208511	Sequence 208511,	C 469	23	1.0	500	8	US-11-266-748A-60541	Sequence 60541, A
C 397	23	1.0	363	8	US-11-266-748A-215102	Sequence 215102,	C 470	23	1.0	500	8	US-11-266-748A-207879	Sequence 207879
C 398	23	1.0	363	8	US-11-266-748A-237416	Sequence 237416,	C 471	23	1.0	500	8	US-11-266-748A-208052	Sequence 208052,
C 399	23	1.0	364	8	US-11-266-748A-50167	Sequence 50167, A	C 472	23	1.0	500	8	US-11-266-748A-208463	Sequence 208463,
C 400	23	1.0	374	8	US-11-266-748A-34252	Sequence 34252, A	C 473	23	1.0	500	8	US-11-266-748A-233269	Sequence 233269,
C 401	23	1.0	380	8	US-11-266-748A-59771	Sequence 59771, A	C 474	23	1.0	500	8	US-11-266-748A-233409	Sequence 233409,
C 402	23	1.0	381	8	US-11-266-748A-272697	Sequence 272697,	C 475	23	1.0	500	8	US-11-266-748A-233624	Sequence 233624,
C 403	23	1.0	381	8	US-11-266-748A-333214	Sequence 333214,	C 476	23	1.0	500	8	US-11-266-748A-419449	Sequence 419449,
C 404	23	1.0	386	8	US-11-301-554-1620	Sequence 1620, Ap	C 477	22	0.9	22	7	US-11-320-440-299	Sequence 299, App
C 405	23	1.0	393	8	US-11-266-748A-57906	Sequence 57906, A	C 478	22	0.9	60	7	US-11-320-440-167	Sequence 167, App
C 406	23	1.0	400	8	US-11-266-748A-59300	Sequence 59300, A	C 479	22	0.9	135	8	US-11-266-748A-375337	Sequence 375337,
C 407	23	1.0	400	8	US-11-266-748A-212986	Sequence 212986,	C 480	22	0.9	135	8	US-11-266-748A-458716	Sequence 458716,
C 408	23	1.0	400	8	US-11-266-748A-220108	Sequence 220108,	C 481	22	0.9	172	8	US-11-266-748A-302215	Sequence 302215,
C 409	23	1.0	400	8	US-11-266-748A-236231	Sequence 236231,	C 482	22	0.9	225	8	US-11-266-748A-272757	Sequence 272757,
C 410	23	1.0	407	8	US-11-266-748A-61956	Sequence 61956, A	C 483	22	0.9	225	8	US-11-266-748A-333274	Sequence 333274,
C 411	23	1.0	416	8	US-11-301-554-971	Sequence 971, App	C 484	22	0.9	260	8	US-11-301-554-1208	Sequence 1208, Ap
C 412	23	1.0	417	8	US-11-266-748A-360521	Sequence 360521,	C 485	22	0.9	265	8	US-11-266-748A-370073	Sequence 370073,
C 413	23	1.0	417	8	US-11-266-748A-443500	Sequence 443500,	C 486	22	0.9	265	8	US-11-266-748A-453452	Sequence 453452,
C 414	23	1.0	419	8	US-11-266-748A-60664	Sequence 60664, A	C 487	22	0.9	284	8	US-11-266-748A-213261	Sequence 213261,
C 415	23	1.0	419	8	US-11-266-748A-218587	Sequence 218587,	C 488	22	0.9	284	8	US-11-266-748A-236372	Sequence 236372,
C 416	23	1.0	425	8	US-11-266-748A-120605	Sequence 120605,	C 489	22	0.9	300	8	US-11-266-748A-102107	Sequence 102107,
C 417	23	1.0	427	8	US-11-266-748A-211069	Sequence 211069,	C 490	22	0.9	300	8	US-11-266-748A-154918	Sequence 154918,
C 418	23	1.0	429	8	US-11-266-748A-220153	Sequence 220153,	C 491	22	0.9	318	8	US-11-266-748A-613	Sequence 613, App
C 419	23	1.0	429	8	US-11-266-748A-239811	Sequence 239811,	C 492	22	0.9	336	8	US-11-266-748A-268902	Sequence 268902,
C 420	23	1.0	431	8	US-11-266-748A-217928	Sequence 217928,	C 493	22	0.9	336	8	US-11-266-748A-329419	Sequence 329419,
C 421	23	1.0	431	8	US-11-266-748A-238843	Sequence 238843,	C 494	22	0.9	355	8	US-11-266-748A-7890	Sequence 7890, Ap
C 422	23	1.0	437	8	US-11-266-748A-354318	Sequence 354318,	C 495	22	0.9	361	8	US-11-266-748A-167980	Sequence 167980,
C 423	23	1.0	437	8	US-11-266-748A-375697	Sequence 375697	C 496	22	0.9	361	8	US-11-266-748A-244571	Sequence 244571,
C 424	23	1.0	438	8	US-11-266-748A-218338	Sequence 218338,	C 497	22	0.9	363	8	US-11-266-748A-48657	Sequence 48657, A
C 425	23	1.0	440	8	US-11-266-748A-53038	Sequence 53038, A	C 498	22	0.9	365	8	US-11-266-748A-209002	Sequence 209002,
C 426	23	1.0	440	8	US-11-266-748A-216880	Sequence 216880,	C 499	22	0.9	371	8	US-11-266-748A-23819	Sequence 23819,
C 427	23	1.0	444	8	US-11-266-748A-338432	Sequence 338432,	C 500	22	0.9	371	8	US-11-266-748A-413510	Sequence 413510,
C 428	23	1.0	448	8	US-11-301-554-1607	Sequence 1607, Ap	C 501	22	0.9	381	8	US-11-266-748A-60593	Sequence 60593, A
C 429	23	1.0	450	8	US-11-266-748A-57914	Sequence 57914, A	C 502	22	0.9	389	8	US-11-266-748A-39554	Sequence 39554, A
C 430	23	1.0	451	8	US-11-266-748A-46898	Sequence 46898, A	C 503	22	0.9	397	8	US-11-266-748A-171009	Sequence 171009,
C 431	23	1.0	451	8	US-11-266-748A-209124	Sequence 209124,	C 504	22	0.9	405	8	US-11-266-748A-61347	Sequence 61347, A
C 432	23	1.0	451	8	US-11-266-748A-233877	Sequence 233877,	C 505	22	0.9	405	8	US-11-266-748A-21886	Sequence 21886,
C 433	23	1.0	451	8	US-11-266-748A-360272	Sequence 360272,	C 506	22	0.9	408	8	US-11-266-748A-237859	Sequence 237859,
C 434	23	1.0	451	8	US-11-266-748A-443651	Sequence 443651,	C 507	22	0.9	408	8	US-11-266-748A-369660	Sequence 369660,
C 435	23	1.0	452	8	US-11-266-748A-213717	Sequence 213717,	C 508	22	0.9	408	8	US-11-266-748A-453039	Sequence 453039,
C 436	23	1.0	454	8	US-11-266-748A-44582	Sequence 44582, A	C 509	22	0.9	411	8	US-11-266-748A-216547	Sequence 216547,
C 437	23	1.0	456	8	US-11-266-748A-60299	Sequence 60299, A	C 510	22	0.9	411	8	US-11-266-748A-238449	Sequence 238449,
C 438	23	1.0	466	8	US-11-266-748A-60462	Sequence 60462, A	C 511	22	0.9	412	8	US-11-266-748A-380640	Sequence 380640,
C 439	23	1.0	467	8	US-11-266-748A-217887	Sequence 217887,	C 512	22	0.9	412	8	US-11-266-748A-464019	Sequence 464019,
C 440	23	1.0	467	8	US-11-266-748A-338808	Sequence 338808,	C 513	22	0.9	414	8	US-11-266-748A-212041	Sequence 212041,
C 441	23	1.0	468	8	US-11-266-748A-59570	Sequence 59570, A	C 514	22	0.9	420	8	US-11-266-748A-254171	Sequence 254171,
C 442	23	1.0	469	6	US-10-473-173-361	Sequence 361, App	C 515	22	0.9	420	8	US-11-266-748A-314688	Sequence 314688,
C 443	23	1.0	470	8	US-11-266-748A-59873	Sequence 59873, A	C 516	22	0.9	428	8	US-11-266-748A-61350	Sequence 61350, A
C 444	23	1.0	470	8	US-11-266-748A-213428	Sequence 213428,	C 517	22	0.9	429	8	US-11-266-748A-378315	Sequence 378315,
C 445	23	1.0	470	8	US-11-266-748A-236469	Sequence 236469,	C 518	22	0.9	429	8	US-11-266-748A-461694	Sequence 461694,
C 446	23	1.0	471	8	US-11-266-748A-61484	Sequence 61484, A	C 519	22	0.9	434	8	US-11-266-748A-34911	Sequence 34911, A
C 447	23	1.0	474	8	US-11-266-748A-11235	Sequence 11235, A	C 520	22	0.9	436	8	US-11-266-748A-214830	Sequence 214830,
C 448	23	1.0	474	8	US-11-266-748A-212855	Sequence 212855,	C 521	22	0.9	436	8	US-11-266-748A-237270	Sequence 237270,
C 449	23	1.0	476	8	US-11-266-748A-41684	Sequence 41684, A	C 522	22	0.9	438	8	US-11-266-748A-212852	Sequence 212852,
C 450	23	1.0	477	8	US-11-266-748A-60467	Sequence 60467, A	C 523	22	0.9	438	8	US-11-266-748A-236034	Sequence 236034,
C 451	23	1.0	477	8	US-11-266-748A-58545	Sequence 58545, A	C 524	22	0.9	439	8	US-11-266-748A-49127	Sequence 49127, A
C 452	23	1.0	477	8	US-11-266-748A-213476	Sequence 213476,	C 525	22	0.9	441	8	US-11-266-748A-57813	Sequence 57813, A
C 453	23	1.0	480	8	US-11-266-748A-272042	Sequence 272042,	C 526	22	0.9	443	8	US-11-266-748A-208605	Sequence 208605,
C 454	23	1.0	480	8	US-11-266-748A-332559	Sequence 332559,	C 527	22	0.9	447	8	US-11-266-748A-332521	Sequence 332521,
C 455	23	1.0	483	8	US-11-266-748A-59884	Sequence 59884, A	C 528	22	0.9	449	8	US-11-266-748A-267609	Sequence 267609,
C 456	23	1.0	483	8	US-11-266-748A-210893	Sequence 210893,	C 529	22	0.9	453	8	US-11-266-748A-12513	Sequence 12513, A
C 457	23	1.0	483	8	US-11-266-748A-212889	Sequence 212889,	C 530	22	0.9	453	8	US-11-266-748A-219446	Sequence 219446,
C 458	23	1.0	483	8	US-11-266-748A-215092	Sequence 215092,	C 531	22	0.9	458	8	US-11-266-748A-208989	Sequence 208989,
C 459	23	1.0	483	8	US-11-266-748A-236148	Sequence 236148,	C 532	22	0.9	459	8	US-11-266-748A-62059	Sequence 62059, A
C 460	23	1.0	483	8	US-11-266-748A-237410	Sequence 237410,	C 533	22	0.9	462	8	US-11-266-748A-62059	Sequence 62059, A
C 461	23	1.0	485	8	US-11-266-748A-179215	Sequence 179215,	C 534	22	0.9	463	8	US-11-266-748A-60625	Sequence 60625, A
C 462	23	1.0	489	8	US-11-266-748A-40457	Sequence 40457, A	C 535	22	0.9	463	8	US-11-266-748A-218404	Sequence 218404,

682	21	0.9	452	8	US-11-266-748A-58156	Sequence 58156, A	755	20	0.8	155	8	US-11-266-748A-14335	Sequence 14335, A
683	21	0.9	452	8	US-11-266-748A-215546	Sequence 215546, A	756	20	0.8	168	6	US-10-560-723-6	Sequence 6, Appl1
684	21	0.9	452	8	US-11-266-748A-237673	Sequence 237673, A	757	20	0.8	181	8	US-11-266-748A-413160	Sequence 413160, A
685	21	0.9	453	8	US-11-266-748A-61448	Sequence 61448, A	758	20	0.8	242	8	US-11-266-748A-52183	Sequence 52183, A
686	21	0.9	453	8	US-11-266-748A-208816	Sequence 208816, A	759	20	0.8	242	8	US-11-266-748A-210353	Sequence 210353, A
687	21	0.9	453	8	US-11-266-748A-208816	Sequence 208816, A	760	20	0.8	242	8	US-11-266-748A-234555	Sequence 224555, A
688	21	0.9	454	8	US-11-266-748A-215084	Sequence 215084, A	761	20	0.8	261	8	US-11-266-748A-392019	Sequence 322019, A
689	21	0.9	454	8	US-11-266-748A-237406	Sequence 237406, A	762	20	0.8	261	8	US-11-266-748A-482737	Sequence 482737, A
690	21	0.9	455	8	US-11-266-748A-210455	Sequence 210455, A	763	20	0.8	281	8	US-11-266-748A-77886	Sequence 77886, A
691	21	0.9	455	8	US-11-266-748A-234607	Sequence 234607, A	764	20	0.8	281	8	US-11-266-748A-110035	Sequence 110035, A
692	21	0.9	456	8	US-11-266-748A-40742	Sequence 40742, A	765	20	0.8	284	8	US-11-266-748A-1130697	Sequence 130697, A
693	21	0.9	456	8	US-11-266-748A-62020	Sequence 62020, A	766	20	0.8	284	8	US-11-266-748A-4139	Sequence 4139, Ap
694	21	0.9	456	8	US-11-266-748A-211887	Sequence 211887, A	767	20	0.8	288	6	US-10-526-905-7	Sequence 7, Appl1
695	21	0.9	456	8	US-11-266-748A-235435	Sequence 235435, A	768	20	0.8	309	8	US-11-266-748A-85132	Sequence 85132, A
696	21	0.9	456	8	US-11-266-748A-256213	Sequence 256213, A	769	20	0.8	318	8	US-11-266-748A-138519	Sequence 138519, A
697	21	0.9	456	8	US-11-266-748A-316730	Sequence 316730, A	770	20	0.8	318	8	US-11-266-748A-363257	Sequence 363257, A
698	21	0.9	461	7	US-11-195-344-17	Sequence 17, Appl	771	20	0.8	318	8	US-11-266-748A-446636	Sequence 446636, A
699	21	0.9	461	7	US-11-195-344-108	Sequence 108, Appl	772	20	0.8	318	8	US-11-266-748A-446636	Sequence 446636, A
700	21	0.9	461	7	US-11-195-344-272	Sequence 272, App	773	20	0.8	320	8	US-11-266-748A-303072	Sequence 303072, A
701	21	0.9	461	8	US-11-266-748A-49220	Sequence 49220, A	774	20	0.8	320	8	US-11-266-748A-272981	Sequence 272981, A
702	21	0.9	461	8	US-11-266-748A-209580	Sequence 209580, A	775	20	0.8	333	8	US-11-266-748A-333498	Sequence 333498, A
703	21	0.9	461	8	US-11-266-748A-234096	Sequence 234096, A	776	20	0.8	333	8	US-11-266-748A-333498	Sequence 333498, A
704	21	0.9	462	8	US-11-266-748A-45276	Sequence 45276, A	777	20	0.8	336	8	US-11-266-748A-207413	Sequence 207413, A
705	21	0.9	462	8	US-11-266-748A-91028	Sequence 91028, A	778	20	0.8	337	8	US-11-266-748A-270772	Sequence 270772, A
706	21	0.9	462	8	US-11-266-748A-143839	Sequence 143839, A	779	20	0.8	337	8	US-11-266-748A-31289	Sequence 31289, A
707	21	0.9	462	8	US-11-266-748A-211027	Sequence 211027, A	780	20	0.8	339	8	US-11-266-748A-375213	Sequence 375213, A
708	21	0.9	462	8	US-11-266-748A-234821	Sequence 234821, A	781	20	0.8	339	8	US-11-266-748A-458592	Sequence 458592, A
709	21	0.9	463	8	US-11-266-748A-60091	Sequence 60091, A	782	20	0.8	351	8	US-11-266-748A-61486	Sequence 61486, A
710	21	0.9	466	8	US-11-266-748A-61737	Sequence 61737, A	783	20	0.8	351	8	US-11-266-748A-212640	Sequence 212640, A
711	21	0.9	470	8	US-11-266-748A-211390	Sequence 211390, A	784	20	0.8	351	8	US-11-266-748A-212640	Sequence 212640, A
712	21	0.9	470	8	US-11-266-748A-235074	Sequence 235074, A	785	20	0.8	356	8	US-11-266-748A-229453	Sequence 229453, A
713	21	0.9	473	8	US-11-266-748A-61739	Sequence 61739, A	786	20	0.8	363	8	US-11-266-748A-61094	Sequence 61094, A
714	21	0.9	476	8	US-11-266-748A-207937	Sequence 207937, A	787	20	0.8	367	8	US-11-266-748A-229439	Sequence 229439, A
715	21	0.9	480	8	US-11-266-748A-207937	Sequence 207937, A	788	20	0.8	367	8	US-11-266-748A-411192	Sequence 411192, A
716	21	0.9	480	8	US-11-266-748A-233318	Sequence 233318, A	789	20	0.8	371	8	US-11-266-748A-271588	Sequence 271588, A
717	21	0.9	482	8	US-11-266-748A-57917	Sequence 57917, A	790	20	0.8	371	8	US-11-266-748A-331105	Sequence 332105, A
718	21	0.9	482	8	US-11-266-748A-219449	Sequence 219449, A	791	20	0.8	373	8	US-11-266-748A-219449	Sequence 218349, A
719	21	0.9	487	8	US-11-266-748A-217935	Sequence 217935, A	792	20	0.8	373	8	US-11-266-748A-233047	Sequence 239047, A
720	21	0.9	488	8	US-11-266-748A-62190	Sequence 62190, A	793	20	0.8	374	6	US-10-501-187-56	Sequence 36, Appl1
721	21	0.9	488	8	US-11-266-748A-215403	Sequence 215403, A	794	20	0.8	375	8	US-11-266-748A-85138	Sequence 85138, A
722	21	0.9	493	7	US-11-195-344-214	Sequence 214, App	795	20	0.8	375	8	US-11-266-748A-137949	Sequence 137949, A
723	21	0.9	493	8	US-11-266-748A-213681	Sequence 213681, A	796	20	0.8	376	8	US-11-266-748A-377782	Sequence 377782, A
724	21	0.9	493	8	US-11-266-748A-236690	Sequence 236690, A	797	20	0.8	376	8	US-11-266-748A-461161	Sequence 461161, A
725	21	0.9	494	8	US-11-266-748A-60592	Sequence 60592, A	798	20	0.8	378	8	US-11-266-748A-215174	Sequence 215174, A
726	21	0.9	494	8	US-11-266-748A-218593	Sequence 218593, A	799	20	0.8	378	8	US-11-266-748A-413182	Sequence 413182, A
727	21	0.9	494	8	US-11-266-748A-239152	Sequence 239152, A	800	20	0.8	387	8	US-11-266-748A-59659	Sequence 59659, A
728	21	0.9	496	8	US-11-266-748A-265398	Sequence 265398, A	801	20	0.8	388	8	US-11-266-748A-37297	Sequence 37297, A
729	21	0.9	496	8	US-11-266-748A-325915	Sequence 325915, A	802	20	0.8	389	8	US-11-266-748A-207727	Sequence 207727, A
730	21	0.9	497	8	US-11-266-748A-61476	Sequence 61476, A	803	20	0.8	391	6	US-10-488-619-963	Sequence 963, App
731	21	0.9	497	8	US-11-266-748A-257593	Sequence 257593, A	804	20	0.8	393	7	US-11-327-124A-62	Sequence 62, Appl1
732	21	0.9	497	8	US-11-266-748A-318110	Sequence 318110, A	805	20	0.8	398	8	US-11-266-748A-348611	Sequence 348611, A
733	21	0.9	498	8	US-11-266-748A-62043	Sequence 62043, A	806	20	0.8	398	8	US-11-266-748A-431990	Sequence 431990, A
734	21	0.9	498	8	US-11-266-748A-213378	Sequence 213378, A	807	20	0.8	400	8	US-11-266-748A-17053	Sequence 17053, A
735	21	0.9	498	8	US-11-266-748A-236756	Sequence 236756, A	808	20	0.8	400	8	US-11-266-748A-219375	Sequence 219375, A
736	21	0.9	499	8	US-11-266-748A-44731	Sequence 44731, A	809	20	0.8	402	8	US-11-266-748A-216060	Sequence 216060, A
737	21	0.9	499	8	US-11-266-748A-214623	Sequence 214623, A	810	20	0.8	402	8	US-11-266-748A-234683	Sequence 234683, A
738	21	0.9	499	8	US-11-266-748A-237159	Sequence 237159, A	811	20	0.8	403	8	US-11-266-748A-33199	Sequence 33199, A
739	21	0.9	500	8	US-11-266-748A-51338	Sequence 51338, A	812	20	0.8	403	8	US-11-266-748A-171421	Sequence 171421, A
740	20	0.8	20	6	US-10-511-937-946	Sequence 946, App	813	20	0.8	403	8	US-11-266-748A-231990	Sequence 231990, A
741	20	0.8	20	6	US-10-511-937-1277	Sequence 1277, Ap	814	20	0.8	404	8	US-11-266-748A-245334	Sequence 245334, A
742	20	0.8	20	6	US-10-511-937-2102	Sequence 2102, Ap	815	20	0.8	404	8	US-11-266-748A-35020	Sequence 35020, A
743	20	0.8	20	6	US-10-553-298-47	Sequence 47, Appl	816	20	0.8	411	8	US-11-266-748A-45659	Sequence 45659, A
744	20	0.8	20	6	US-11-283-528-27	Sequence 27, Appl	817	20	0.8	411	8	US-11-266-748A-214506	Sequence 214506, A
745	20	0.8	20	8	US-11-245-514-24	Sequence 24, Appl	818	20	0.8	411	8	US-11-266-748A-218387	Sequence 218387, A
746	20	0.8	27	8	US-11-245-514-24	Sequence 24, Appl	819	20	0.8	414	8	US-11-266-748A-60310	Sequence 60310, A
747	20	0.8	27	8	US-11-245-514-28	Sequence 28, Appl	820	20	0.8	414	8	US-11-266-748A-218730	Sequence 218730, A
748	20	0.8	40	6	US-10-519-505-92	Sequence 92, Appl	821	20	0.8	421	8	US-11-266-748A-58999	Sequence 58999, A
749	20	0.8	41	8	US-11-245-514-25	Sequence 25, Appl	822	20	0.8	425	8	US-11-266-748A-214638	Sequence 214638, A
750	20	0.8	50	6	US-10-554-711-6	Sequence 26, Appl	823	20	0.8	425	8	US-11-266-748A-362522	Sequence 362522, A
751	20	0.8	87	8	US-11-245-444-1	Sequence 6, Appl1	824	20	0.8	425	8	US-11-266-748A-362522	Sequence 362522, A
752	20	0.8	140	8	US-11-266-748A-772644	Sequence 372644, A	825	20	0.8	425	8	US-11-266-748A-445501	Sequence 445501, A
753	20	0.8	140	8	US-11-266-748A-456023	Sequence 456023, A	826	20	0.8	427	6	US-10-488-619-386	Sequence 386, App
754	20	0.8	152	8	US-11-266-748A-426810	Sequence 426810, A	827	20	0.8	437	8	US-11-266-748A-53099	Sequence 53099, A

828	20	0.8	437	8	US-11-266-748A-208928	Sequence 208928,	C 901	20	0.8	488	8	US-11-266-748A-236692	Sequence 236692,
C 829	20	0.8	437	8	US-11-266-748A-233797	Sequence 233797,	C 902	20	0.8	489	8	US-11-266-748A-274625	Sequence 274625,
830	20	0.8	437	8	US-11-266-748A-391218	Sequence 391218,	C 903	20	0.8	489	8	US-11-266-748A-458004	Sequence 458004,
C 831	20	0.8	437	8	US-11-266-748A-481936	Sequence 481936,	C 904	20	0.8	492	8	US-11-266-748A-60174	Sequence 60174, A
832	20	0.8	440	8	US-11-266-748A-355999	Sequence 355999,	C 905	20	0.8	492	8	US-11-266-748A-212861	Sequence 212861,
C 833	20	0.8	440	8	US-11-266-748A-449378	Sequence 449378,	C 906	20	0.8	492	8	US-11-266-748A-219589	Sequence 219589,
834	20	0.8	441	8	US-11-266-748A-296556	Sequence 296556,	C 907	20	0.8	492	8	US-11-266-748A-336154	Sequence 336154,
C 835	20	0.8	441	8	US-11-266-748A-362920	Sequence 362920,	C 908	20	0.8	492	8	US-11-266-748A-339513	Sequence 339513,
C 836	20	0.8	441	8	US-11-266-748A-446299	Sequence 446299,	C 909	20	0.8	494	8	US-11-266-748A-35589	Sequence 35589, A
837	20	0.8	443	8	US-11-266-748A-212655	Sequence 212655,	C 910	20	0.8	498	8	US-11-266-748A-207358	Sequence 207358,
C 838	20	0.8	443	8	US-11-266-748A-213892	Sequence 213892,	C 911	20	0.8	499	8	US-11-266-748A-61673	Sequence 61673, A
C 839	20	0.8	444	8	US-11-266-748A-428278	Sequence 428278,	C 912	20	0.8	500	7	US-11-266-748A-370941	Sequence 215, App
C 840	20	0.8	444	8	US-11-266-748A-61445	Sequence 61445, A	C 913	20	0.8	500	8	US-11-266-748A-370941	Sequence 270941,
C 841	20	0.8	445	8	US-11-266-748A-272294	Sequence 272294,	C 914	20	0.8	500	8	US-11-266-748A-331458	Sequence 331458,
C 842	20	0.8	445	8	US-11-266-748A-332811	Sequence 332811,	C 915	20	0.8	500	8	US-10-519-505-7	Sequence 331458,
843	20	0.8	446	8	US-11-266-748A-609925	Sequence 609925, A	C 916	19	0.8	19	6	US-10-519-505-7	Sequence 7, App1
C 844	20	0.8	446	8	US-11-266-748A-212755	Sequence 212755,	C 917	19	0.8	140	8	US-11-255-980-15	Sequence 133, App
C 845	20	0.8	446	8	US-11-266-748A-236087	Sequence 236087,	C 918	19	0.8	158	8	US-11-266-748A-480664	Sequence 389946,
C 846	20	0.8	447	8	US-11-266-748A-57863	Sequence 57863, A	C 919	19	0.8	158	8	US-11-266-748A-480664	Sequence 480664,
C 847	20	0.8	449	8	US-11-266-748A-40567	Sequence 40567, A	C 920	19	0.8	161	8	US-11-266-748A-307521	Sequence 307521,
C 848	20	0.8	449	8	US-11-266-748A-218195	Sequence 218195,	C 921	19	0.8	174	8	US-11-266-748A-426711	Sequence 426711,
C 849	20	0.8	449	8	US-11-266-748A-238992	Sequence 238992,	C 922	19	0.8	196	8	US-11-266-748A-372237	Sequence 372237,
C 850	20	0.8	454	8	US-11-266-748A-60712	Sequence 60712, A	C 923	19	0.8	196	8	US-11-266-748A-332754	Sequence 332754,
C 851	20	0.8	456	8	US-11-266-748A-254834	Sequence 254834,	C 924	19	0.8	198	8	US-11-266-748A-373425	Sequence 373425,
C 852	20	0.8	456	8	US-11-266-748A-280429	Sequence 280429,	C 925	19	0.8	198	8	US-11-266-748A-456804	Sequence 456804,
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C 856	20	0.8	457	8	US-11-266-748A-273416	Sequence 273416,	C 929	19	0.8	238	8	US-11-266-748A-153511	Sequence 153511,
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C 858	20	0.8	460	8	US-11-266-748A-13005	Sequence 13005, A	C 931	19	0.8	254	8	US-11-266-748A-307203	Sequence 307203,
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C 876	20	0.8	466	8	US-11-266-748A-333649	Sequence 333649,	C 949	19	0.8	292	8	US-11-266-748A-332932	Sequence 332932,
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C 889	20	0.8	475	8	US-11-266-748A-372123	Sequence 372123,	C 962	19	0.8	338	8	US-11-266-748A-11537	Sequence 11537, A
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C 899	20	0.8	488	6	US-10-473-173-332	Sequence 332, App	C 972	19	0.8	348	8	US-11-266-748A-330755	Sequence 330755,
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c 996 19 0.8 406 8 US-11-266-748A-39534 Sequence 39534, A
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c 998 19 0.8 408 8 US-11-266-748A-445374 Sequence 445374,
c 999 19 0.8 413 7 US-11-327-124A-134 Sequence 134, App
1000 19 0.8 415 8 US-11-266-748A-218054 Sequence 218054,
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ALIGNMENTS

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RESULT 1
US-11-266-748A-7936
; Sequence 7936, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7936
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-7936
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Best Local Similarity 100.0%; Pred. No. 5.4e-57;
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Db 220 GATCAAAAGGACCTTGTACAGAGCCTTACAGAGAAACCTTCATCTTACATTGGTT 279
Qy 771 TCTAGACCATCTACCTCATCTTACAGAGAGCAATTAGAGACAG 816
Db 280 TCTAGACCATCTACCTCATCTTACAGAGAGCAATTAGAGACAG 325
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RESULT 2
US-11-266-748A-60150
; Sequence 60150, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60150
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-60150
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Db 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCATTTGCTTTGAAGTTATTTAAAGTCT 120
Qy 432 GTTGTGCAAAAAGACACTTATTAATCTTGAAGAGG 468
Db 121 GTTGTGCAAAAAGACACTTATTAATCTTGAAGAGG 157
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RESULT 3
US-11-266-748A-57794
; Sequence 57794, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 57794
LENGTH: 428
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-57794
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Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 183 GGGTTTCAACCGTTAGCCAGGATGCTCTGATCTCTGATCCGATCCGCC 237
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US-10-511-937-283
Sequence 283, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
PRIOR FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 283
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-283
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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GACAACCAATTCAAATGATTTGCTAACTATTTCCTAGTTGACCTGT 50
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Sequence 60447, Application US/11266748A
Publication No. US2006013463A1
GENERAL INFORMATION:
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
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PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 60447
LENGTH: 474
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-60447
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Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Sequence 213882, Application US/11266748A
Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213882
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; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-213882

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Best Local Similarity 100.0%; Pred. No. 4.8e-08;
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RESULT 7
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; Sequence 50804, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50804
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (375)..(383)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (385)..(402)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (404)..(429)
```

```
; OTHER INFORMATION: n is a, c, g, or t
; US-11-266-748A-50804

Query Match          1.8%; Score 43; DB 8; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2319 TGATCCGCCACCTCGGCTCCCAAGTGTGGATTACAGGC 2361
Db      52 TGATCCGCCACCTCGGCTCCCAAGTGTGGATTACAGGC 94

RESULT 8
; US-11-266-748A-219366/C
; Sequence 219366, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 219366
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-219366

Query Match          1.8%; Score 43; DB 8; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2330 CTTGGGCTCCCAAGTGTGGATTACAGCATGAGCCACCG 2372
Db      143 CTTGGGCTCCCAAGTGTGGATTACAGCATGAGCCACCG 101

RESULT 9
; US-11-266-748A-239401
; Sequence 239401, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
```

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; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 239401
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-239401

```

```

Query Match      1.8%; Score 43; DB 8; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      2330 CCTCGACCTCCCAAGTGTGGAGATTACGAGATGAGCCAGC 2372
Db      302 CCTCGACCTCCCAAGTGTGGAGATTACGAGATGAGCCAGC 344

```

```

RESULT 10
US-11-266-748A-380602
; Sequence 380602, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 380602
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-380602

```

```

Query Match      1.8%; Score 42; DB 8; Length 463;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      2275 GGTTCACCGTGTAGCCAGATGCTCGATCTCTGACCT 2316

```

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Db      11 GGTTCACCGTGTAGCCAGATGCTCGATCTCTGACCT 52

```

```

RESULT 11
US-11-266-748A-463981/C
; Sequence 463981, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 463981
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-463981

```

```

Query Match      1.8%; Score 42; DB 8; Length 463;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2275 GGTTCACCGTGTAGCCAGATGCTCGATCTCTGACCT 2316
Db      453 GGTTCACCGTGTAGCCAGATGCTCGATCTCTGACCT 412

```

```

RESULT 12
US-11-327-124A-215
; Sequence 215, Application US/11327124A
; Publication No. US20060166242A1
; GENERAL INFORMATION:
; APPLICANT: Fennell, Craig
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: MARKERS OF PRE-TERM LABOR
; FILE REFERENCE: 14096.1004USU1
; CURRENT APPLICATION NUMBER: US/11/327,124A
; PRIOR FILING DATE: 2006-01-06
; PRIOR APPLICATION NUMBER: US 60/641,875
; PRIOR FILING DATE: 2005-01-06
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 215
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-327-124A-215

```

```

Query Match      1.7%; Score 40; DB 7; Length 349;
Best Local Similarity 100.0%; Pred. No. 2e-06;

```

```
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2285 TGTAGCCAGATGTCTCGATCTCTGACCTCGTATCC 2324
DB 54 TGTAGCCAGATGTCTCGATCTCTGACCTCGTATCC 93

RESULT 13
US-11-266-748A-217154
; Sequence 217154, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 217154
; LENGTH: 245
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-217154

Query Match 1.6%; Score 39; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2334 GGCCTCCCAAGTGTGGATTACGAGCATGAGCCACCG 2372
DB 74 GGCCTCCCAAGTGTGGATTACGAGCATGAGCCACCG 112

RESULT 14
US-11-266-748A-414670
; Sequence 414670, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 414670
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-414670

Query Match 1.6%; Score 38; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2293 AGGATGCTTCGATCTCTGACCTCGTATCCGCCACCC 2331
DB 314 AGGATGCTTCGATCTCTGACCTCGTATCCGCCACCC 352

RESULT 15
US-11-266-748A-61942/c
; Sequence 61942, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61942
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-61942

Query Match 1.6%; Score 38; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGTGGATTACAGCATGAGCCACC 2372
DB 270 GCCTCCCAAGTGTGGATTACAGCATGAGCCACC 233

RESULT 16
US-11-266-748A-61449
Sequence 61449, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 61449
LENGTH: 464
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-61449

Query Match 1.6%; Score 38; DB 8; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGTGGATTACAGCATGAGCCACC 2372
DB 243 GCCTCCCAAGTGTGGATTACAGCATGAGCCACC 280

RESULT 17
US-11-266-748A-217171
Sequence 217171, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 217171
LENGTH: 486
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-217171

Query Match 1.6%; Score 38; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GCCTCCCAAGTGTGGATTACAGCATGAGCCACC 2371
DB 339 GCCTCCCAAGTGTGGATTACAGCATGAGCCACC 376

RESULT 18
US-11-266-748A-238530/c
Sequence 238530, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 238530
LENGTH: 486
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-238530

Query Match 1.6%; Score 38; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GCCTCCCAAGTGTGGATTACAGCATGAGCCACC 2371
DB 148 GCCTCCCAAGTGTGGATTACAGCATGAGCCACC 111

RESULT 19

```
US-11-266-748A-170884/c
; Sequence 170884, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 170884
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-170884

Query Match      1.6%; Score 37; DB 8; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
US-11-266-748A-170884/c
; Sequence 208969, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 208969
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-170884/c

Query Match      1.6%; Score 37; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
NAME/KEY: misc_feature
LOCATION: (24)..(24)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-208969
```

```
Query Match          1.6%; Score 37; DB 8; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2325 GCCCAGCTGGGCTCCCAAGTGTGGATTACAGGC 2361
Db      392 GCCCAGCTGGGCTCCCAAGTGTGGATTACAGGC 356
```

```
RESULT 22
US-11-266-748A-50353/C
Sequence 50353, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 50353
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-50353
```

```
Query Match          1.6%; Score 37; DB 8; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2335 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 2371
Db      344 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 308
```

```
RESULT 23
US-11-266-748A-211874
Sequence 211874, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
```

```
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 211874
LENGTH: 461
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-211874
```

```
Query Match          1.6%; Score 37; DB 8; Length 461;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2325 GCCCAGCTGGGCTCCCAAGTGTGGATTACAGGC 2361
Db      69 GCCCAGCTGGGCTCCCAAGTGTGGATTACAGGC 105
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```
RESULT 24
US-11-266-748A-235428/C
Sequence 235428, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 235428
LENGTH: 461
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-235428
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Query Match          1.6%; Score 37; DB 8; Length 461;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2325 GCCCACTGGGCTCCCAAGTGTGGATTACAGGC 2361
DB 393 GCCCACTGGGCTCCCAAGTGTGGATTACAGGC 357

RESULT 25
US-10-554-711-12/c
; Sequence 12, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-12

Query Match 1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGAGTGTCTCGATCTC 2309
DB 36 GGGTTTACCGTGTAGCCAGAGTGTCTCGATCTC 1

RESULT 26
US-10-554-711-17/c
; Sequence 17, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-17

Query Match 1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGAGTGTCTCGATCTC 2309
DB 36 GGGTTTACCGTGTAGCCAGAGTGTCTCGATCTC 1

RESULT 27
US-10-554-711-24/c
; Sequence 24, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-24

Query Match 1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGAGTGTCTCGATCTC 2309
DB 36 GGGTTTACCGTGTAGCCAGAGTGTCTCGATCTC 1

RESULT 28
US-10-554-711-26/c
; Sequence 26, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-26

Query Match 1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGAGTGTCTCGATCTC 2309
DB 36 GGGTTTACCGTGTAGCCAGAGTGTCTCGATCTC 1

RESULT 29
US-10-554-711-27/c
; Sequence 27, Application US/10554711
; Publication No. US20060115806A1

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; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-27

Query Match          1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 2309
DB 36 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 1

RESULT 30
US-10-554-711-29/c
; Sequence 29, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-29

Query Match          1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 2309
DB 36 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 1

RESULT 31
US-10-554-711-30/c
; Sequence 30, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
```

```
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-30

Query Match          1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 2309
DB 36 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 1

RESULT 32
US-11-266-748A-40751
; Sequence 40751, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40751
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-40751

Query Match          1.5%; Score 36; DB 8; Length 213;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGTCCTCGATCTCCAGCTCGTG 2320
DB 6 TGTAGCCAGGATGTCCTCGATCTCCAGCTCGTG 1

RESULT 33
US-11-266-748A-354643
```



```
/ Sequence 48475, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptome Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ CURRENT FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 48475
/ LENGTH: 462
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-11-266-748A-48475

Query Match          1.5%; Score 36; DB 8; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2325 GCCCAGCTGGGCTCCCAAGTGTGGATTACAGG 2360
Db      387 GCCCAGCTGGGCTCCCAAGTGTGGATTACAGG 352

RESULT 37
US-11-266-748A-60828/c
/ Sequence 60828, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptome Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ CURRENT FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
```

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/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 60828
/ LENGTH: 474
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (363)..(363)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (440)..(440)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (453)..(453)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (461)..(461)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (474)..(474)
/ OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-60828

Query Match          1.5%; Score 36; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2325 GCCCAGCTGGGCTCCCAAGTGTGGATTACAGG 2360
Db      201 GCCCAGCTGGGCTCCCAAGTGTGGATTACAGG 166

RESULT 38
US-10-554-711-13/c
/ Sequence 13, Application US/10554711
/ Publication No. US20060115806A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Georgia Research Foundation
/ APPLICANT: McDonald, John F.
/ TITLE OF INVENTION: Global Analysis of Transposable Elements
/ FILE REFERENCE: 21099.0075P1
/ CURRENT APPLICATION NUMBER: US/10/554,711
/ CURRENT FILING DATE: 2005-10-28
/ PRIOR APPLICATION NUMBER: 60/466,798
/ PRIOR FILING DATE: 2003-04-29
/ NUMBER OF SEQ ID NOS: 778
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-711-13
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Query Match          1.5%; Score 35; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2294 GGATGCTCGATCTCTGACCTGTGATCCGCC 2328
Db      36 GGATGCTCGATCTCTGACCTGTGATCCGCC 2

RESULT 39
US-10-554-711-25/c
```

```
; Sequence 25, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John P.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-25
```

```
Query Match 1.5%; Score 35; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2294 GGATGCTCGATCTCCTGACCTCGTGTCCGCC 2328
Db 36 GGATGCTCGATCTCCTGACCTCGTGTCCGCC 2
```

```
RESULT 40
US-10-554-711-32/C
; Sequence 32, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John P.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-32
```

```
Query Match 1.5%; Score 35; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2274 GGGTTTCACCGTGTAGCCAGATGTCGATCT 2308
Db 35 GGGTTTCACCGTGTAGCCAGATGTCGATCT 1
```

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Search completed: August 4, 2006, 20:56:33
Job time : 501 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 13:41:44 ; Search time 11265 Seconds
(without alignments)
11774.581 Million cell updates/sec

Title: US-09-966-724B-2
Perfect score: 2372
Sequence: 1 GCACCGCGCGAGCTTGCTG.....ATTACAGCATGAGCCACCG 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 2795965780 residues
Word size : 1

Total number of hits satisfying chosen parameters: 36196904

Minimum DB seq length: 5
Maximum DB seq length: 500

Post-processing: listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	ID	Description
1	384	16.2	400	8	CN409877 170004182
2	377	15.9	377	7	BF155177 QV0-BT084
3	367	15.5	482	10	R80343 R80343
4	320	13.5	427	1	AA214617 zt88h09.s
5	289	12.2	300	4	BK482386 DKFZp686H
6	234	9.9	486	7	AW070956 xa31h03.x
7	231	9.7	393	1	AL704062 DKFZp686N
8	219	9.2	476	7	BE676440 CT000980
9	200	8.9	265	8	CT000980 CT000980
10	211	8.4	399	10	H79860 yu78f12.r1
11	199	8.4	414	7	BF089387 PM2-HT092
12	193	8.1	221	7	BF30973 QV1-HT041
13	167	7.0	319	10	H13638 y107c11.r1
14	167	7.0	469	7	BE935243 MR0-MT012
15	166	7.0	415	1	AI281316 qk39d01.x
16	166	7.0	421	1	AI336475 qo61d06.x
17	166	7.0	423	1	AA937920 of72e04.s
18	166	7.0	423	1	AI346140 qp43e08.x
19	166	7.0	437	1	AI274906 q149a03.x

C 20	148	6.2	148	7	AM999946 MR0-BN007
C 21	140	5.9	335	1	AI339173 q899a02.x
C 22	138	5.8	233	2	BF746144 R11-RN025
C 23	129	5.4	253	7	BF336925 CM2-CT500
C 24	125	5.3	345	7	BE765314 IL2-NT010
C 25	119	5.0	227	7	BF081983 PM1-AN009
C 26	115	4.8	415	1	AI246037 qk44h12.x
C 27	108	4.6	366	1	AA568852 mm27a12.b
C 28	106	4.5	456	10	R80235 y196d02.s1
C 29	98	4.1	489	12	CC000590 UP_479-4N
C 30	94	4.0	385	10	N20967 yx57c04.s1
C 31	94	4.0	437	7	BE019522 hb57c10.y
C 32	92	3.9	147	2	BF949018 MR3-NN022
C 33	92	3.9	147	2	BF949018 MR3-NN022
C 34	88	3.7	151	10	FP35659 HSPD32490 H
C 35	88	3.7	298	2	BG956827 IL3-CT067
C 36	88	3.7	303	10	DM419606 HHAGE0193
C 37	88	3.7	309	11	AQ094950 HS 3028.A
C 38	88	3.7	454	11	AO153405 HS_2234.B
C 39	88	3.7	474	1	AL048925 DKFZp434K
C 40	87	3.7	330	3	BQ351361 QV0-HT036
C 41	87	3.7	433	2	BM127662 y698b10.y
C 42	87	3.7	439	10	N27353 yw52e08.s1
C 43	87	3.7	440	2	BM127350 i698b10.x
C 44	87	3.7	445	9	DA257128 DA257128
C 45	87	3.7	479	9	DA517190 DA517190
C 46	87	3.7	497	5	CK906249 i698b10.y
C 47	85	3.6	319	2	BG546523 602574272
C 48	83	3.5	187	4	BX955194 DKFZp781A
C 49	83	3.5	385	10	T47739 yb16904.s1
C 50	81	3.4	354	10	DM466069 HHAGE0073
C 51	81	3.4	449	4	CA434763 UI-H-D10
C 52	80	3.4	422	11	AQ058627 CIT-HSP-2
C 53	78	3.3	276	10	DM428120 HHAGE0278
C 54	78	3.3	355	2	BG152682 naf58h12.
C 55	78	3.3	408	11	AQ020826 RPTC11-58
C 56	78	3.3	435	7	BE042649 ho24c10.x
C 57	78	3.3	438	3	BUS92584 i076d08.x
C 58	78	3.3	452	2	BF911530 IL0-UT010
C 59	77	3.2	210	1	AA593359 nm07905.s
C 60	77	3.2	262	1	AA365165 ESTV5866
C 61	77	3.2	293	1	AA558227 nl34e07.s
C 62	77	3.2	315	1	AA557854 nl64e02.s
C 63	77	3.2	389	14	AG197480 Pan t1rog1
C 64	77	3.2	389	11	AI312149 ta79b12.x
C 65	77	3.2	398	11	AQ584608 RPTC-11-4
C 66	77	3.2	412	1	AA810037 od11g04.s
C 67	77	3.2	485	9	DB061436 DB061436
C 68	76	3.2	385	1	AJ346318 SHR-00001
C 69	76	3.2	454	4	BK455662 DKFZp781J
C 70	75	3.2	308	2	BI060016 IL3-UT011
C 71	75	3.2	377	11	AQ005848 CIT-HSP-2
C 72	74	3.1	410	10	DM419014 HHAGE0017
C 73	74	3.1	486	10	H29303 ym60a07.s1
C 74	73	3.1	326	1	AA480772 ne86d10.s
C 75	72	3.0	263	3	BM692874 UI-E-CK1-
C 76	72	3.0	263	3	BM692874 UI-E-CK1-
C 77	72	3.0	318	8	CV421900 RC4-HT093
C 78	72	3.0	417	1	AI313166 q8B1f06.x
C 79	71	3.0	128	1	AA687987 nt55f03.s
C 80	71	3.0	140	1	AA604326 no83g12.s
C 81	71	3.0	392	2	BF958161 RC5-NN106
C 82	71	3.0	452	11	AQ512849 HS 5141.B
C 83	70	3.0	297	10	DM421384 HHAGE0211
C 84	70	3.0	324	11	DM417557 HHAGE0182
C 85	70	3.0	305	11	AQ040371 CIT-HSP-2
C 86	70	3.0	375	1	AT251021 GR49h06.x
C 87	70	3.0	377	9	DR033642 5000BCT03
C 88	70	3.0	379	2	BG004281 RC6-GN007
C 89	69	2.9	244	4	BK491664 DKFZp781O
C 90	69	2.9	257	2	BG989387 MR2-HT116
C 91	69	2.9	297	10	DM421619 HHAGE0213
C 92	69	2.9	303	1	AI216799 qm31h07.x

C 93	69	2.9	337	2	BF888015	BF888015 QV3-TN016	C 166	64	2.7	440	7	AW962713	AW962713 EST374786
C 94	69	2.9	390	10	DM430222	DM430222 HHAGE0029	167	64	2.7	455	11	AZ755765	AZ755765 ev05h02.r
C 95	69	2.9	431	10	N55273	N55273 YV46604.s1	168	64	2.7	471	9	DB146705	DB146705 DB146705
C 96	69	2.9	432	5	CD676551	CD676551 h002d09.y	169	64	2.7	483	11	AQ798614	AQ798614 HS_2238.B
C 97	69	2.9	472	8	CV402640	CV402640 RC0-BN03	170	64	2.7	495	11	AQ264829	AQ264829 CTBT1-EI-
C 98	69	2.9	482	9	DA309759	DA309759 DA309759	171	63	2.7	150	2	BQ494854	BQ494854 602540860
C 99	68	2.9	183	2	BF869171	BF869171 IL5-ET010	C 172	63	2.7	297	3	BQ277822	BQ277822 AGENCOURT
C 100	68	2.9	203	2	BG959152	BG959152 PM4-CT080	C 173	63	2.7	271	10	DM421639	DM421639 HHAGE0213
C 101	68	2.9	220	1	AA336362	AA336362 EST41153	C 174	63	2.7	327	7	BE243593	BE243593 TCBAPI009
C 102	68	2.9	240	1	AA378821	AA378821 EST911724	C 175	63	2.7	388	2	BF756894	BF756894 RC5-CT059
C 103	68	2.9	240	1	AA378822	AA378822 EST911725	C 176	63	2.7	459	9	DB254923	DB254923 DB254923
C 104	68	2.9	304	1	AL434706	AL434706 CT139E09.x	C 177	63	2.7	481	7	AW966181	AW966181 RCPT-11-3
C 105	68	2.9	328	3	BU940536	BU940536 AGENCOURT	C 178	63	2.7	495	11	AQ531096	AQ531096 RCPT-11-3
C 106	68	2.9	345	7	BE063133	BE063133 CM2-BT026	C 179	62	2.6	247	7	DB314361	DB314361 DB314361
C 107	68	2.9	345	11	AQ057469	AQ057469 CT1-HSP-2	C 180	62	2.6	314	11	AQ373185	AQ373185 Pan trogl
C 108	68	2.9	353	4	BK486268	BK486268 DKFZP6860	C 181	62	2.6	318	14	AG195739	AG195739 Pan trogl
C 109	68	2.9	361	11	AQ618132	AQ618132 HS_5168.B	C 182	62	2.6	347	7	AA346575	AA346575 EST52751
C 110	68	2.9	365	11	AQ134844	AQ134844 HS_3053_A	C 183	62	2.6	353	7	AW938400	AW938400 PM4-DT005
C 111	68	2.9	390	3	BQ354048	BQ354048 CM1-HT087	C 184	62	2.6	360	4	EX491893	EX491893 DKFZP781H
C 112	68	2.9	400	2	BG980008	BG980008 PM3-CN010	C 185	62	2.6	384	1	AA554319	AA554319 n103c07.s
C 113	68	2.9	407	9	DB275663	DB275663 DB275663	C 186	62	2.6	408	3	BU953774	BU953774 AGENCOURT
C 114	68	2.9	414	4	BK486484	BK486484 DKFZP686A	C 187	62	2.6	422	3	BQ330072	BQ330072 CM3-ET004
C 115	68	2.9	415	2	BF767457	BF767457 CM1-CN006	C 188	62	2.6	474	11	AQ630172	AQ630172 RCPT-11-4
C 116	68	2.9	436	3	BM831927	BM831927 K-EST0106	C 189	62	2.6	477	11	AQ452719	AQ452719 HS_5116.B
C 117	68	2.9	445	11	AQ108678	AQ108678 CT1-HSP-2	C 190	61	2.6	494	11	AQ588120	AQ588120 CTBT1-EI-
C 118	68	2.9	455	3	BQ082740	BQ082740 K-EST0144	C 191	61	2.6	247	1	AA744650	AA744650 ny79f09.s
C 119	68	2.9	465	2	BF844783	BF844783 RC5-ET0103	C 192	61	2.6	253	10	F00290	AA383838 EST97300
C 120	68	2.9	473	2	BE854162	BE854162 MR2-BN009	C 193	61	2.6	269	9	AA593267	AA593267 m08c09.s
C 121	68	2.9	481	4	BS506031	BS506031 DKFZP686N	C 194	61	2.6	390	5	CD722773	CD722773 o113h09.y
C 122	67	2.8	255	7	AW954446	AW954446 EST366516	C 195	61	2.6	434	9	DB296503	DB296503 DB296503
C 123	67	2.8	313	10	DM415408	DM415408 HHAGE0161	C 196	61	2.6	452	1	AA629932	AA629932 ae64a05.s
C 124	67	2.8	459	11	B14696	B14696 342114.TV.C	C 197	60	2.5	252	1	AU185811	AU185811 AU185811
C 125	67	2.8	484	1	AT339440	AT339440 CT02909.x	C 198	60	2.5	304	1	AU185811	CN272355 170006000
C 126	66	2.8	394	11	AQ044082	AQ044082 CT1-HSP-2	C 199	60	2.5	309	8	CN272355	CN272355
C 127	66	2.8	412	7	BE044986	BE044986 hnz5d03.x	C 200	60	2.5	314	4	CD103782	CD103782 AGENCOURT
C 128	66	2.8	414	9	DB343255	DB343255 DB343255	C 201	60	2.5	343	14	AG197866	AG197866 Pan trogl
C 129	66	2.8	423	5	CD242224	CD242224 AGENCOURT	C 202	60	2.5	354	1	AA084715	AA084715 zn06b02.s
C 130	66	2.8	463	1	AT141675	AT141675 ct08c06.x	C 203	60	2.5	373	1	AV703682	AV703682 AV703682
C 131	65	2.7	170	11	BS7010	BS7010 CT1-HSP-200	C 204	60	2.5	390	11	AQ386889	AQ386889 RCPT11-15
C 132	65	2.7	241	10	DM439608	DM439608 HHAGE0383	C 205	60	2.5	403	1	AA587662	AA587662 nj42c04.s
C 133	65	2.7	298	2	BF858756	BF858756 RC5-F7019	C 206	60	2.5	405	1	AT860020	AT860020 wnz2h07.x
C 134	65	2.7	321	7	AW804281	AW804281 QV0-UM009	C 207	60	2.5	407	11	AQ206933	AQ206933 HS_3238_B
C 135	65	2.7	344	1	AA837058	AA837058 od18c04.s	C 208	60	2.5	416	1	AA827981	AA827981 cd70d10.s
C 136	65	2.7	383	7	AW954447	AW954447 EST366517	C 209	60	2.5	420	1	AL709504	AL709504 DKFZP686F
C 137	65	2.7	410	1	AA161083	AA161083 zc62g12.s	C 210	60	2.5	450	1	AA581903	AA581903 nm32a12.s
C 138	65	2.7	413	2	BM313771	BM313771 ih06d04.x	C 211	60	2.5	456	2	BM311624	BM311624 ig59h06.x
C 139	65	2.7	425	2	BG292263	BG292263 602386711	C 212	60	2.5	462	7	AA469989	AA469989 xz27c02.x
C 140	65	2.7	433	4	BX509522	BX509522 DKFZP686N	C 213	60	2.5	487	11	AQ372508	AQ372508 RCPT11-15
C 141	65	2.7	438	11	AQ547205	AQ547205 RCPT-11-3	C 214	60	2.5	488	9	DB342571	DB342571 zv47a11.y
C 142	65	2.7	439	10	N66945	N66945 z848d11.s1	C 215	60	2.5	488	9	DB342571	DB342571 DB342571
C 143	65	2.7	441	9	DB321305	DB321305 DB321305	C 216	59	2.5	170	10	DM456209	DM456209 HHAGE0529
C 144	65	2.7	454	1	AT299050	AT299050 qm14d12.x	C 217	59	2.5	207	10	BF850953	BF850953 MR4-EN007
C 145	65	2.7	456	11	AQ938658	AQ938658 NL1-CP9C	C 218	59	2.5	235	2	DR980073	DR980073 SM015618
C 146	65	2.7	458	1	AA583808	AA583808 nm1h10.s	C 219	59	2.5	276	7	BE973738	BE973738 601680730
C 147	65	2.7	464	10	T55236	T55236 yH47b02.s1	C 220	59	2.5	283	10	DM426195	DM426195 HHAGE0223
C 148	65	2.7	478	2	BF875257	BF875257 QV3-ET009	C 221	59	2.5	294	10	DM422638	DM422638 HHAGE0229
C 149	65	2.7	485	10	H73389	H73389 yJ04h05.r1	C 222	59	2.5	313	3	BU954898	BU954898 AGENCOURT
C 150	65	2.7	487	11	AQ485557	AQ485557 RCPT-11-2	C 223	59	2.5	316	1	AT358501	AT358501 Gw40a10.x
C 151	65	2.7	490	7	AM504669	AM504669 UI-HF-BN0	C 224	59	2.5	364	10	DY067428	DY067428 000802BAP
C 152	65	2.7	496	7	AM272758	AM272758 xu22f01.x	C 225	59	2.5	366	10	DY154827	DY154827 000802BAP
C 153	65	2.7	500	9	DN949487	DN949487 1r70a06.k	C 226	59	2.5	392	2	DB321502	DB321502 DB321502
C 154	64	2.7	225	1	AA332624	AA332624 EST36596	C 227	59	2.5	409	7	AM193609	AM193609 xml8c02.x
C 155	64	2.7	226	2	BT101084	BT101084 MR2-BN009	C 228	59	2.5	412	1	AL699049	AL699049 DKFZP686N
C 156	64	2.7	305	3	BM677090	BM677090 UI-E-E01-	C 229	59	2.5	416	7	BE207545	BE207545 ba75a03.x
C 157	64	2.7	324	7	AM474160	AM474160 yJ11f12.x	C 230	59	2.5	484	2	BF724372	BF724372 bx04b06.y
C 158	64	2.7	349	11	AQ104631	AQ104631 HS_3049_B	C 231	58	2.4	195	10	DM450956	DM450956 BQ311958
C 159	64	2.7	366	9	DA084230	DA084230 DA084230	C 232	58	2.4	217	3	BQ358234	BQ358234 QV2-HT049
C 160	64	2.7	372	11	AQ481144	AQ481144 RCPT-11-2	C 233	58	2.4	236	10	DM441895	DM441895 HHAGE0396
C 161	64	2.7	391	11	AV732611	AV732611 AV732611	C 234	58	2.4	256	10	DM441897	DM441897 HHAGE0396
C 162	64	2.7	399	11	AQ220113	AQ220113 HS_3248.B	C 235	58	2.4	263	10	DB297724	DB297724 HSPD00760.H
C 163	64	2.7	412	1	AA613232	AA613232 nol9e05.s	C 237	58	2.4	264	10	DM432914	DM432914 HHAGE0316
C 164	64	2.7	421	5	CD668665	CD668665 EST3386.h	C 238	58	2.4	264	10	DM432914	DM432914 HHAGE0316

C 229	58	2.4	300	10	DM420646	DM420646 HHAGE0203	312	57	2.4	399	1	A1446638	A1446638 tjl1b09.x
C 240	58	2.4	310	7	BF217299	BF217299 601885644	313	57	2.4	402	1	AA437161	AA437161 zv61b10.x
C 241	58	2.4	325	1	AA569193	AA569193 nm30e07.s	314	57	2.4	403	11	A0030471	A0030471
C 242	58	2.4	341	10	DM408799	DM408799 HHAGE0095	315	57	2.4	408	2	BC272300	BC272300 nah67a09-
C 243	58	2.4	351	1	AA640034	AA640034 mp39g04.s	316	57	2.4	408	2	BM784814	BM784814 K-EST0063
C 244	58	2.4	355	2	BC993458	BC993458 CM3-HT117	317	57	2.4	408	3	BQ358368	BQ358368 RC0-HT093
C 245	58	2.4	359	1	AA346454	AA346454 EST52610	318	57	2.4	410	2	BF926380	BF926380 RC6-NT015
C 246	58	2.4	359	2	BI018146	BI018146 CM1-MT024	319	57	2.4	417	7	AV732919	AV732919 AV732919
C 247	58	2.4	361	5	H69640	H69640 YF91E07.r1	320	57	2.4	420	7	BE832569	BE832569 CM3-MT011
C 248	58	2.4	371	10	CK000820	CK000820 AGENCOURT	321	57	2.4	431	3	BM766764	BM766764 K-EST0048
C 249	58	2.4	374	1	AA714632	AA714632 nx91a01.s	322	57	2.4	437	1	AA670468	AA670468 e937b08.s
C 250	58	2.4	376	11	AA056586	AA056586 CIT-HSP-2	323	57	2.4	437	11	AA0685482	AA0685482 HS-5528_B
C 251	58	2.4	380	2	BF802384	BF802384 CM0-CIT009	324	57	2.4	438	1	AA134347	AA134347 zo23f09.s
C 252	58	2.4	387	11	BS8274	BS8274 CIT-HSP-201	325	57	2.4	442	4	EX952239	EX952239 DKFZP781C
C 253	58	2.4	393	11	AA129757	AA129757 HS-2253_A	326	57	2.4	443	1	A1291124	A1291124 qml5612.x
C 254	58	2.4	394	2	BI439766	BI439766 jcl7f11.x	327	57	2.4	449	2	BC236735	BC236735 nai47f01.
C 255	58	2.4	407	11	AA044609	AA044609 CIT-HSP-2	328	57	2.4	449	10	R97934	R97934 y460h09.s1
C 256	58	2.4	408	11	AA052575	AA052575 HS-5207_A	329	57	2.4	449	13	C2453628	C2453628 MCF735G19
C 257	58	2.4	423	1	AA079688	AA079688 zm21b04.s	330	57	2.4	450	4	CA950254	CA950254 1r89b10.x
C 258	58	2.4	434	1	AA001029	AA001029 ze46b12.x	331	57	2.4	451	2	BF832548	BF832548 PM3-HT090
C 259	58	2.4	436	1	AI016000	AI016000 ou95g03.x	332	57	2.4	452	5	CD369526	CD369526 UI-H-FTI-
C 260	58	2.4	441	1	AI674873	AI674873 wc77f09.x	333	57	2.4	453	4	EX952224	EX952224 DKFZP781A
C 261	58	2.4	445	7	BE072475	BE072475 QV3-BT053	334	57	2.4	455	4	BM821684	BM821684 K-EST0090
C 262	58	2.4	445	11	AA0224580	AA0224580 HS-2012_A	335	57	2.4	455	7	AA467340	AA467340 he09e09.x
C 263	58	2.4	451	7	AA070037	AA070037 xt28b12.x	336	57	2.4	457	9	DB300351	DB300351 DB300351
C 264	58	2.4	460	2	BI019428	BI019428 CM3-MT019	337	57	2.4	458	5	CK429370	CK429370 o135g02.y
C 265	58	2.4	469	7	AM081048	AM081048 xc39g08.x	338	57	2.4	458	11	B99780	B99780 CIT-HSP-228
C 266	58	2.4	476	9	DB362271	DB362271 DB362271	339	57	2.4	461	1	AA513293	AA513293 nh85b05.s
C 267	58	2.4	483	3	BU581466	BU581466 in37b11.y	340	57	2.4	461	11	AA0188539	AA0188539 HS-3228_B
C 268	58	2.4	485	1	AA601253	AA601253 no14h05.s	341	57	2.4	462	9	DA320912	DA320912 DA320912
C 269	58	2.4	486	11	AA027185	AA027185 CITB1-B1-	342	57	2.4	466	9	DB215542	DB215542 DB215542
C 270	58	2.4	488	1	BQ478120	BQ478120 i8k1a01.x	343	57	2.4	466	11	AA041292	AA041292 RPTC-11-1
C 271	58	2.4	490	9	DB375094	DB375094 DB375094	344	57	2.4	467	3	BU570301	BU570301 AGENCOURT
C 272	58	2.4	500	11	B37212	B37212 HS-1043-A1-	345	57	2.4	472	2	BF825343	BF825343 wh94a08.x
C 273	57	2.4	135	2	BI029483	BI029483 IL5-MT026	346	57	2.4	472	2	BF825343	BF825343 RC4-HN003
C 274	57	2.4	138	10	N45188	N45188 yv25h02.r1	347	57	2.4	476	2	BF831846	BF831846 PM3-HT090
C 275	57	2.4	175	3	BQ337417	BQ337417 CM3-MT034	348	57	2.4	478	1	AA173374	AA173374 zp32d02.x
C 276	57	2.4	194	7	AM649378	AM649378 IL3-CT001	349	57	2.4	481	1	A1291268	A1291268 GMT16e04.x
C 277	57	2.4	194	7	AM649378	AM649378 IL3-CT001	350	57	2.4	481	1	AA309254	AA309254 EST180368
C 278	57	2.4	201	10	DM449760	DM449760 HHAGE0474	351	57	2.4	485	5	CD724032	CD724032 o129e06.y
C 279	57	2.4	220	2	AM903004	AM903004 CM2-NN102	352	57	2.4	487	3	BM831357	BM831357 K-EST0105
C 280	57	2.4	230	2	BF942942	BF942942 QV0-NN114	353	57	2.4	487	3	BO083578	BO083578 K-EST0146
C 281	57	2.4	261	2	BF988583	BF988583 CM3-GN019	354	57	2.4	490	9	DB208237	DB208237 DB208237
C 282	57	2.4	269	2	BI019457	BI019457 CM3-MT019	355	57	2.4	491	3	BM988774	BM988774 UI-H-DIO-
C 283	57	2.4	272	4	BK479592	BK479592 DKFZP686B	356	57	2.4	491	3	BP418287	BP418287 BP418287
C 284	57	2.4	274	10	F32894	F32894 HSPD5590 H	357	57	2.4	492	7	BB872393	BB872393 601448655
C 285	57	2.4	282	7	AM236342	AM236342 xn73c09.x	358	57	2.4	494	1	AU147696	AU147696 AU147696
C 286	57	2.4	285	2	BI030892	BI030892 IL5-MT026	359	57	2.4	166	11	A2516814	A2516814 ARRLSP4H
C 287	57	2.4	292	4	BK501252	BK501252 DKFZP779M	360	57	2.4	222	5	CD240664	CD240664
C 288	57	2.4	295	7	BE167863	BE167863 CM2-HT051	361	57	2.4	226	3	BQ335219	BQ335219 IL5-MT026
C 289	57	2.4	301	8	CR772766	CR772766 DKFZP46BD	362	57	2.4	316	11	B34242	B34242 HS-1024-A2-
C 290	57	2.4	303	2	BI029244	BI029244 IL5-MT026	363	57	2.4	322	10	H39713	H39713 y052h07.r1
C 291	57	2.4	305	11	AA0631069	AA0631069 RPTC-11-4	364	57	2.4	325	10	H44095	H44095 y073d03.r1
C 292	57	2.4	320	2	BF896589	BF896589 QV1-MT022	365	57	2.4	328	3	BO342707	BO342707 CM2-NN114
C 293	57	2.4	321	7	AM440976	AM440976 he06f06.x	366	57	2.4	340	7	AA264959	AA264959 XG58d11.x
C 294	57	2.4	322	7	BO344638	BO344638 RC6-NT015	367	57	2.4	353	5	CD767839	CD767839 AGENCOURT
C 295	57	2.4	342	4	CA946468	CA946468 ni106f01.x	368	57	2.4	355	14	D0638728	D0638728 CluIf1-HI
C 296	57	2.4	347	5	CD369571	CD369571 UI-H-FTI-	369	57	2.4	401	1	AA503473	AA503473 ng21h12.s
C 297	57	2.4	347	5	CD369571	CD369571 UI-H-FTI-	370	57	2.4	409	11	AA0216392	AA0216392 HS-2189_A
C 298	57	2.4	350	2	BF899983	BF899983 CM3-MT019	371	57	2.4	410	12	CG891563	CG891563 YGME243A3
C 299	57	2.4	353	2	BI086493	BI086493 602849765	372	57	2.4	423	11	B70666	B70666 CIT-HSP-206
C 300	57	2.4	357	2	BI086493	BI086493 602849765	373	57	2.4	427	7	AM512667	AM512667 xmo2c05.x
C 301	57	2.4	359	7	BE933711	BE933711 QV4-HT089	374	57	2.4	428	10	R54885	R54885 y174g04.r1
C 302	57	2.4	361	10	DM464911	DM464911 HHAGE0061	375	57	2.4	437	10	T91187	T91187 yd50d11.s1
C 303	57	2.4	362	1	AI537556	AI537556 tp10a09.x	376	57	2.4	445	11	AA0521948	AA0521948 HS-5063_B
C 304	57	2.4	363	4	CA434669	CA434669 UI-H-DIO-	377	57	2.4	452	1	AA773584	AA773584 av61d08.s
C 305	57	2.4	368	7	AV764526	AV764526 AV764526	378	57	2.4	455	7	AV742337	AV742337 AV742337
C 306	57	2.4	373	7	AM794809	AM794809 RC6-UM001	379	57	2.4	460	8	CV319379	CV319379 CM2-NN114
C 307	57	2.4	391	11	AA0265134	AA0265134 CIT-HSP-2	380	57	2.4	460	11	AA0894333	AA0894333 HS-3175_A
C 308	57	2.4	391	11	BM756707	BM756707 K-EST0035	381	57	2.4	465	3	BU567202	BU567202 AGENCOURT
C 309	57	2.4	396	2	BI027138	BI027138 QV1-MT013	382	57	2.4	467	7	AV742309	AV742309 AV742309
C 310	57	2.4	397	2	BI019410	BI019410 CM3-MT019	383	57	2.4	474	1	AA584458	AA584458 no05g09.s
C 311	57	2.4	397	2	BI019410	BI019410 CM3-MT019	384	57	2.4	474	1	AA584458	AA584458 no05g09.s

C 385	56	2.4	477	7	AV741609	458	55	2.3	325	1	AA557945
C 386	56	2.4	479	3	BP387566	459	55	2.3	330	10	R38154
C 387	56	2.4	479	11	AQ225492	460	55	2.3	332	4	CB308854
C 388	56	2.4	483	3	BU727763	461	55	2.3	334	4	BK493558
C 389	56	2.4	497	11	B56584	462	55	2.3	335	4	BA678436
C 390	55	2.3	107	2	BF874937	463	55	2.3	336	9	DB299114
C 391	55	2.3	174	7	AM834106	464	55	2.3	337	11	AZ319869
C 392	55	2.3	164	10	DM457213	465	55	2.3	338	10	T07451
C 393	55	2.3	185	10	DM453655	466	55	2.3	339	10	F26152
C 394	55	2.3	188	10	DM453224	467	55	2.3	339	10	F26152
C 395	55	2.3	192	11	AQ419192	468	55	2.3	339	11	B45031
C 396	55	2.3	195	10	DM450918	469	55	2.3	340	10	DM409176
C 397	55	2.3	197	2	BF872215	470	55	2.3	342	1	AA376763
C 398	55	2.3	197	2	BF872217	471	55	2.3	343	3	BU726254
C 399	55	2.3	206	7	AV740060	472	55	2.3	344	11	AZ319531
C 400	55	2.3	212	10	DM447503	473	55	2.3	345	9	DM519248
C 401	55	2.3	220	1	A1536555	474	55	2.3	345	9	DM372995
C 402	55	2.3	222	7	AV738722	475	55	2.3	346	2	BF763771
C 403	55	2.3	222	10	DM445354	476	55	2.3	346	3	BU564460
C 404	55	2.3	222	10	DM445355	477	55	2.3	351	2	B1044658
C 405	55	2.3	226	1	A160954	478	55	2.3	352	4	BX485943
C 406	55	2.3	230	7	BE142249	479	55	2.3	352	11	AO628938
C 407	55	2.3	233	10	DM442711	480	55	2.3	354	1	A1287651
C 408	55	2.3	238	1	AA493852	481	55	2.3	354	3	BU963331
C 409	55	2.3	241	11	BH010820	482	55	2.3	354	10	DM466089
C 410	55	2.3	242	2	BF827737	483	55	2.3	355	11	AOQ27777
C 411	55	2.3	244	11	BH010819	484	55	2.3	355	11	AOQ13393
C 412	55	2.3	245	7	BE172686	485	55	2.3	357	11	AA586562
C 413	55	2.3	246	4	BK475938	486	55	2.3	357	11	B48798
C 414	55	2.3	250	2	B1016461	487	55	2.3	357	7	BF091721
C 415	55	2.3	251	3	BU736283	488	55	2.3	359	3	BQ082389
C 416	55	2.3	251	10	DM436888	489	55	2.3	360	9	DB372857
C 417	55	2.3	254	7	BE378770	490	55	2.3	360	10	R81455
C 418	55	2.3	260	1	AA747777	491	55	2.3	360	11	B91708
C 419	55	2.3	263	11	AQ345131	492	55	2.3	362	14	AG266053
C 420	55	2.3	272	8	CN270383	493	55	2.3	364	11	AQ585080
C 421	55	2.3	273	7	AM074398	494	55	2.3	365	10	F03097
C 422	55	2.3	282	9	DA647277	495	55	2.3	370	11	AM194071
C 423	55	2.3	284	10	DM425885	496	55	2.3	370	11	AOQ99378
C 424	55	2.3	286	10	DM425276	497	55	2.3	372	11	AOQ39592
C 425	55	2.3	287	1	AA927092	498	55	2.3	373	7	AA810318
C 426	55	2.3	289	10	DM424376	499	55	2.3	373	7	AV761584
C 427	55	2.3	290	10	DM423986	500	55	2.3	375	1	A1053672
C 428	55	2.3	292	9	DB306239	501	55	2.3	377	7	AV760937
C 429	55	2.3	293	10	DM423001	502	55	2.3	379	3	BQ268741
C 430	55	2.3	294	1	AA100372	503	55	2.3	380	1	AA553436
C 431	55	2.3	295	10	DM422027	504	55	2.3	380	11	AOQ95276
C 432	55	2.3	295	10	DM422278	505	55	2.3	381	2	BG272215
C 433	55	2.3	295	10	DM422350	506	55	2.3	383	2	BF771291
C 434	55	2.3	301	10	DM420342	507	55	2.3	383	7	AM769399
C 435	55	2.3	302	3	BQ372743	508	55	2.3	384	1	A1446182
C 436	55	2.3	302	11	AQ066068	509	55	2.3	385	3	BM710678
C 437	55	2.3	305	3	BQ441427	510	55	2.3	389	1	A1266576
C 438	55	2.3	306	1	AA332991	511	55	2.3	392	11	AQ205664
C 439	55	2.3	307	1	AA559290	512	55	2.3	395	7	BE834614
C 440	55	2.3	307	10	DM417194	513	55	2.3	395	11	AO893103
C 441	55	2.3	308	1	AA605274	514	55	2.3	396	11	AA252263
C 442	55	2.3	308	4	BK507755	515	55	2.3	396	4	BK494090
C 443	55	2.3	309	8	CN411432	516	55	2.3	398	4	BK494090
C 444	55	2.3	310	1	AA653964	517	55	2.3	398	14	AG198961
C 445	55	2.3	310	14	AG191703	518	55	2.3	399	1	AA101626
C 446	55	2.3	311	4	BO429929	519	55	2.3	400	3	BO315479
C 447	55	2.3	311	4	CB228842	520	55	2.3	401	4	BX489082
C 448	55	2.3	314	4	AA806602	521	55	2.3	401	9	DB374494
C 449	55	2.3	314	2	B1012428	522	55	2.3	402	1	AA348311
C 450	55	2.3	318	7	A1349874	523	55	2.3	403	1	AA302963
C 451	55	2.3	318	7	AM474152	524	55	2.3	404	1	AA233519
C 452	55	2.3	320	1	AA365694	525	55	2.3	404	7	AV729449
C 453	55	2.3	320	3	BU535916	526	55	2.3	404	10	N71724
C 454	55	2.3	320	3	BU565821	527	55	2.3	404	11	AQ052661
C 455	55	2.3	322	10	DM412850	528	55	2.3	407	1	A1610159
C 456	55	2.3	322	10	CB230995	529	55	2.3	407	1	AQ463801
C 457	55	2.3	323	4	CB230995	530	55	2.3	408	11	AA557945

AA557945 n117b07.s
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AA678436 ah01d01.s
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BK485943 DKF2P686G
AO628938 RPTC1-11-4
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AOQ13393 HS 3038.B
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BO082829 K-BST0098
DB372857 DB372857
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AO585080 RPTC1-11-4
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AM194071 x184f12.x
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AOQ39592 CIT-HSP-2
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AV761584 AV761584
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AV760937 AV760937
BQ268741 ik19h01.s
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AOQ95276 HS 3037.A
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BF771291 RC2-IT004
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A1446182 ti95b01.x
BM710678 UI-E-DX0-
A1266576 gm31d09.x
AQ205664 HS_3236_B
AA810370 mx15e08.s
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AA48311 EST154743
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C 678	54	2.3	365	10	T69648	T69648 ycc4c07.r1	C 751	54	2.3	476	11	AO552314	AO552314 RPT-11-3
C 679	54	2.3	367	10	AV647080	AV647080 AV647080	C 752	54	2.3	480	11	AO547395	AO547395 RPT-11-4
C 680	54	2.3	369	9	DB373898	DB373898 DB373898	C 753	54	2.3	483	1	AA223258	AA223258 zc08b04.s
C 681	54	2.3	369	11	AQ043567	AQ043567 CIT-HSP-2	C 754	54	2.3	484	11	AZ916651	AZ916651 up-387-BB
C 682	54	2.3	370	7	BF476591	BF476591 naa57b12.	C 755	54	2.3	484	10	N25042	N25042 yw4D05.s1
C 683	54	2.3	372	2	BF827410	BF827410 RC3-HN002	C 756	54	2.3	485	10	N25965	N25965 yx87h06.s1
C 684	54	2.3	374	9	DB373537	DB373537 DB373537	C 757	54	2.3	493	7	AM833903	AM833903 QVO-TT000
C 685	54	2.3	377	11	AQ758459	AQ758459 HS-3085.B	C 758	54	2.3	495	8	CR557033	CR557033 DKF2P459A
C 686	54	2.3	385	10	R02223	R02223 y48rC05.s1	C 759	54	2.3	500	3	BM994083	BM994083 UI-H-DT0-
C 687	54	2.3	386	7	AM504326	AM504326 UI-HF-BN0	C 760	53	2.2	135	10	DM460741	DM460741 UI-E-DX0-
C 688	54	2.3	387	9	DB378639	DB378639 DB378639	C 761	53	2.2	158	2	E1053776	E1053776 CM3-GN033
C 689	54	2.3	389	11	AQ505005	AQ505005 RPT-11-2	C 762	53	2.2	177	2	BF848555	BF848555 IL5-BN08
C 690	54	2.3	390	10	T54503	T54503 yb06g07.s1	C 763	53	2.2	179	10	DM454711	DM454711 HHAGE0514
C 691	54	2.3	393	9	DB376634	DB376634 DB376634	C 764	53	2.2	200	7	AM502694	AM502694 UI-HF-BR0
C 692	54	2.3	398	2	BF780054	BF780054 MR4-DT007	C 765	53	2.2	247	1	AA594701	AA594701 nc01g11.s
C 693	54	2.3	398	9	DB373538	DB373538 DB373538	C 766	53	2.2	252	3	BT736279	BT736279 UI-E-DX0-
C 694	54	2.3	399	11	AQ755575	AQ755575 HS-2210-B	C 767	53	2.2	254	1	AA910118	AA910118 oe28f11.s
C 695	54	2.3	401	2	BF839225	BF839225 MR1-HT106	C 768	53	2.2	259	10	DM434273	DM434273 HHAGE0330
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C 697	54	2.3	403	1	A1827259	A1827259 w109h12.x	C 770	53	2.2	287	1	AA984829	AA984829 am93f09.s
C 698	54	2.3	404	10	H04758	H04758 yj51d01.s1	C 771	53	2.2	300	1	AU100425	AU100425 AU100425
C 699	54	2.3	406	1	A193634	A193634 LH3907.x	C 772	53	2.2	301	5	CD689775	CD689775 EST6298.h
C 700	54	2.3	406	2	BF875930	BF875930 CM0-ET016	C 773	53	2.2	326	10	R83585	R83585 yP16a06.r1
C 701	54	2.3	410	1	AA113861	AA113861 zn65h04.s	C 774	53	2.2	328	1	A1446464	A1446464 tJ19f02.x
C 702	54	2.3	410	1	AA579249	AA579249 nf28e01.s	C 775	53	2.2	331	1	AA856969	AA856969 oe03e09.s
C 703	54	2.3	410	9	DB341290	DB341290 DB341290	C 776	53	2.2	358	1	AA635433	AA635433 nc72b01.s
C 704	54	2.3	411	1	AA218727	AA218727 zq97g08.s	C 777	53	2.2	358	1	AU156018	AU156018 AU156018
C 705	54	2.3	411	7	BE139567	BE139567 xt20b06.x	C 778	53	2.2	373	11	AZ755935	AZ755935 ew04b11.r
C 706	54	2.3	411	11	AQ371385	AQ371385 HS-5043.A	C 779	53	2.2	374	11	B37346	B37346 HS-1043-A2-
C 707	54	2.3	412	1	AV651452	AV651452 AV651452	C 780	53	2.2	377	11	AQ102230	AQ102230 HS-3029.A
C 708	54	2.3	412	10	R82210	R82210 yj17g08.s1	C 781	53	2.2	379	11	AQ199759	AQ199759 RPT11-47
C 709	54	2.3	414	1	AA533138	AA533138 nj46h04.s	C 782	53	2.2	385	3	BO358965	BO358965 PM0-HT131
C 710	54	2.3	415	1	A1934307	A1934307 wo01c06.x	C 783	53	2.2	389	1	AA204655	AA204655 zq81b01.r
C 711	54	2.3	416	10	R71624	R71624 y513b05.s1	C 784	53	2.2	391	1	AA151807	AA151807 z139g02.r
C 712	54	2.3	417	1	AA67819	AA67819 EST78964	C 785	53	2.2	392	8	CR559619	CR559619 DKF2P459A
C 713	54	2.3	422	1	A1720141	A1720141 as78b08.x	C 786	53	2.2	403	11	AQ146678	AQ146678 HS-2242.A
C 714	54	2.3	422	7	AA407220	AA407220 UI-HF-BM0	C 787	53	2.2	404	10	T15407	T15407 IB1095 Infa
C 715	54	2.3	424	10	T94866	T94866 ye32e03.s1	C 788	53	2.2	406	9	DA085752	DA085752 DA085752
C 716	54	2.3	426	1	A1921673	A1921673 wo28f02.x	C 789	53	2.2	408	9	DA819736	DA819736 DA819736
C 717	54	2.3	426	7	AA172727	AA172727 xJ02f07.x	C 790	53	2.2	416	11	B31253	B31253 HS-1007-A2-
C 718	54	2.3	426	9	DB324377	DB324377 DB324377	C 791	53	2.2	417	9	DB251574	DB251574 DB251574
C 719	54	2.3	428	11	CZ462377	CZ462377 MCF752e21	C 792	53	2.2	420	1	AA508091	AA508091 ng93c05.s
C 720	54	2.3	428	11	AQ457142	AQ457142 HS-5162.A	C 793	53	2.2	420	10	T71998	T71998 ye07e06.r1
C 721	54	2.3	429	5	CF137335	CF137335 UI-HF-BN0	C 794	53	2.2	423	11	AQ231927	AQ231927 HS-3243.B
C 722	54	2.3	430	11	AQ583324	AQ583324 RPT-11-4	C 795	53	2.2	424	11	AQ264587	AQ264587 CITBT-EI-
C 723	54	2.3	435	11	AQ020131	AQ020131 CIT-HSP-2	C 796	53	2.2	430	9	BF893985	BF893985 QV1-MT016
C 724	54	2.3	436	10	T53329	T53329 ya88b05.s1	C 797	53	2.2	439	7	AA469462	AA469462 hc84g01.x
C 725	54	2.3	437	5	CF138927	CF138927 UI-HF-BN0	C 798	53	2.2	443	9	DB196263	DB196263 DB196263
C 726	54	2.3	437	7	AV759362	AV759362 AV759362	C 799	53	2.2	444	11	AQ547510	AQ547510 RPT-11-4
C 727	54	2.3	437	9	DB379680	DB379680 DB379680	C 800	53	2.2	454	1	BY508242	BY508242 DKF2P686H
C 728	54	2.3	437	10	R35972	R35972 yh91b04.s1	C 801	53	2.2	458	4	BM508242	BM508242 HS-5336.B
C 729	54	2.3	440	5	CF137334	CF137334 UI-HF-BN0	C 802	53	2.2	464	11	AQ589864	AQ589864 HS-5336.B
C 730	54	2.3	441	3	BQ365388	BQ365388 IL5-GN003	C 803	53	2.2	476	5	CF709816	CF709816 CCADN72TF
C 731	54	2.3	442	2	BMS12395	BMS12395 iJ71G02.x	C 804	53	2.2	477	9	DB372844	DB372844 DB372844
C 732	54	2.3	446	11	AQ082745	AQ082745 RPT11-54	C 805	53	2.2	486	11	AQ138184	AQ138184 HS-3074.B
C 733	54	2.3	448	14	CR972883	CR972883 Homo sapi	C 806	53	2.2	496	5	CF143355	CF143355 UI-HF-BR0
C 734	54	2.3	449	11	AQ062661	AQ062661 CIT-HSP-2	C 807	53	2.2	498	11	AQ599623	AQ599623 HS-5361.A
C 735	54	2.3	450	10	N30585	N30585 yw66g01.s1	C 808	53	2.2	131	2	BE995364	BE995364 CM0-HT125
C 736	54	2.3	451	1	A1742771	A1742771 wg96a10.x	C 809	52	2.2	217	2	BF743890	BF743890 PM3-BT083
C 737	54	2.3	451	10	R82625	R82625 y119g12.s1	C 810	52	2.2	226	1	AA304782	AA304782 EST175771
C 738	54	2.3	455	10	W80462	W80462 zd82f07.s1	C 811	52	2.2	232	2	B1049324	B1049324 MRI-GN017
C 739	54	2.3	457	10	R34721	R34721 yG43f05.s1	C 812	52	2.2	270	11	AQ009958	AQ009958 CIT-HSP-2
C 740	54	2.3	458	2	BF869358	BF869358 IL5-ET011	C 813	52	2.2	299	11	AQ588919	AQ588919 CITBT-EI-
C 741	54	2.3	459	3	BU579746	BU579746 im90c01.x	C 814	52	2.2	303	14	AG025853	AG025853 Homo sapi
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C 743	54	2.3	465	1	AA1865870	AA1865870 zP74a05.s	C 816	52	2.2	312	4	BO330163	BO330163 QVO-ET003
C 744	54	2.3	466	4	BK109668	BK109668 BX109668	C 817	52	2.2	316	3	BO330163	BO330163 QVO-ET003
C 745	54	2.3	471	10	R71121	R71121 y153b05.r1	C 818	52	2.2	330	1	AA487995	AA487995 ab12a09.r
C 746	54	2.3	471	8	CR538207	CR538207 DKF2P459H	C 819	52	2.2	331	7	AA875935	AA875935 QV2-PT001
C 747	54	2.3	473	4	BK645847	BK645847 DKF2P781J	C 821	52	2.2	331	9	D57369	D57369 HMM298B07A
C 748	54	2.3	475	2	BF773306	BF773306 CM3-IT004	C 822	52	2.2	333	10	DM410653	DM410653 HHAGE0113

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C 824	52	2.2	336	11	AA632529	AA632529 np81f03.s	C 897	51	2.2	294	7	BE934616	BE934616 RCO-HT093
C 825	52	2.2	338	11	AA0552753	AA0552753 RPTC-11-4	C 898	51	2.2	294	10	DM422364	DM422364 HHAGE0220
C 826	52	2.2	345	10	DM467527	DM467527 HHAGE0087	C 899	51	2.2	299	10	DM420725	DM420725 HHAGE0204
C 827	52	2.2	350	10	AA259245	AA259245 nc34902.s	C 900	51	2.2	304	7	AA973802	AA973802 EST85903
C 828	52	2.2	353	10	DM466288	DM466288 HHAGE0075	C 901	51	2.2	304	10	DM418229	DM418229 HHAGE0189
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C 830	52	2.2	356	1	AA678443	AA678443 ah01e05.s	C 903	51	2.2	309	7	BE165312	BE165312 AGENCOURT
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C 834	52	2.2	376	1	AA474285	AA474285 av764285	C 907	51	2.2	316	11	B39802	B39802 HS-1050-B1
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C 836	52	2.2	386	10	TO3722	TO3722 1b795.1bFan	C 909	51	2.2	322	1	AL700837	AL700837 DKEFP686C
C 837	52	2.2	386	11	B31865	B31865 HS-1012-B1-	C 910	51	2.2	323	1	AA501722	AA501722 ng18e05.s
C 838	52	2.2	392	10	H74004	H74004 y813d08.r1	C 911	51	2.2	324	1	AA079515	AA079515 zmg97c01.s
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C 846	52	2.2	433	5	CD689013	CD689013 EST5535.h	C 919	51	2.2	339	10	DM409400	DM409400 HHAGE0101
C 847	52	2.2	437	3	BQ353303	BQ353303 RCO-HT093	C 920	51	2.2	340	10	DM409032	DM409032 HHAGE0097
C 848	52	2.2	448	10	R91994	R91994 yP96a02.B1	C 921	51	2.2	342	1	AA847984	AA847984 od72a12.s
C 849	52	2.2	449	11	AQ184635	AQ184635 HS_2212_A	C 922	51	2.2	342	1	AI367975	AI367975 qv93f10.x
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C 852	52	2.2	454	11	AQ016037	AQ016037 CIT-HSP-2	C 925	51	2.2	348	7	AW274349	AW274349 xw74g09.x
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C 855	52	2.2	479	9	DB214012	DB214012 DB214012	C 928	51	2.2	349	10	DM466972	DM466972 HHAGE0082
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C 857	52	2.2	491	4	CB856940	CB856940 NISC-na04	C 930	51	2.2	351	10	T06828	T06828 EST04717.Fe
C 858	52	2.2	500	3	BP397912	BP397912 BP397912	C 931	51	2.2	360	1	AT301700	AT301700 gnt36g08.x
C 859	52	2.2	106	7	BE748217	BE748217 601571432	C 932	51	2.2	362	8	CMB363902	CMB363902 170006003
C 860	51	2.2	117	3	BQ343448	BQ343448 IL3-NT010	C 933	51	2.2	362	11	AQ245201	AQ245201 HS_2057_B
C 861	51	2.2	123	7	BE157292	BE157292 RQ4-HT037	C 934	51	2.2	364	1	AA378623	AA378623 EST91342
C 862	51	2.2	160	2	BF874265	BF874265 MCI-ET014	C 935	51	2.2	364	1	AA533725	AA533725 nj92d04.s
C 863	51	2.2	188	10	DM453709	DM453709 HHAGE0504	C 936	51	2.2	364	11	AQ425900	AQ425900 CITRBI-E1-
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C 870	51	2.2	224	3	AA361344	AA361344 EST70608	C 942	51	2.2	378	5	CD559049	CD559049 AGENCOURT
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C 875	51	2.2	247	3	BQ352900	BQ352900 RCG-HT084	C 947	51	2.2	381	11	AQ096088	AQ096088 HS_3030_A
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C 878	51	2.2	257	3	BQ336826	BQ336826 CM3-MT011	C 950	51	2.2	383	11	AQ480855	AQ480855 RPTC-11-2
C 879	51	2.2	265	1	AA847952	AA847952 od72b02.s	C 951	51	2.2	384	11	AQ010095	AQ010095 HS_2263_A
C 880	51	2.2	267	10	DM431896	DM431896 HHAGE0306	C 952	51	2.2	384	11	B37215	B37215 HS-1043-A1-
C 881	51	2.2	268	1	AA279427	AA279427 z885e04.s	C 953	51	2.2	385	11	AQ0205724	AQ0205724 HS_3236_B
C 882	51	2.2	269	7	AM873325	AM873325 hm04d02.x	C 954	51	2.2	386	1	AL048616	AL048616 DKEFP654J
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C 886	51	2.2	276	11	DM428362	DM428362 HHAGE0280	C 958	51	2.2	393	11	AQ0240790	AQ0240790 CIT-HSP-2
C 887	51	2.2	276	10	DM428375	DM428375 HHAGE0281	C 959	51	2.2	394	1	AA401657	AA401657 zv65d11.s
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ALIGNMENTS

RESULT 1
LOCUS CN409877 400 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000418214393 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
ACCESSION CN409877
VERSION CN409877.1 GI:47397001
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowksi,J and Stanton,L.W.
TITLE Transcriptionome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 400 Std Error: 0.00.
Location/Qualifiers

FEATURES

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from embryoid body outgrowths derived from hbs cell lines
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conditions."

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Best Local Similarity 100.0%; Pred. No. 5.4e-171;
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ORIGIN

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RESULT 2
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 377)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsumura,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-QVO-BT0847-250

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VERSION AA214617.1 GI:1813254
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
REFERENCE 1 (bases 1 to 427)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-rt@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. Et from Amersham
High quality sequence stop: 412.
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1st strand cDNA was prepared from human tonsillar cells
enriched for germinal center B cells by flow sorting
(CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr.
David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA
synthesis was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAGAGGAGCGGCGCTCACTTTTCTTTT-3'
] Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 13.5%; Score 320; DB 1; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.6e-140;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
234 CCGCGTGAAGAACTGGGAGTCTTGAGGGACCCGACTCCAAGCGGAAACCCCGG 293
Db CCGCGTGAAGAACTGGGAGTCTTGAGGGACCCGACTCCAAGCGGAAACCCCGG 167
QY ATGGTGAAGACAGCAATGTGCAATCAACATGTCTGTACTACTGATGTGCTGTA 353
Db ATGGTGAAGACAGCAATGTGCAATCAACATGTCTGTACTACTGATGTGCTGTA 227
QY 168 ATGGTGAAGACAGCAATGTGCAATCAACATGTCTGTACTACTGATGTGCTGTA 227
Db 168 ATGGTGAAGACAGCAATGTGCAATCAACATGTCTGTACTACTGATGTGCTGTA 227
QY 354 ACCACCTCAAGATTCCAGCTTCGGAACAAGACCTGTGTTAGCCAAAGCATGTCTT 413
Db ACCACCTCAAGATTCCAGCTTCGGAACAAGACCTGTGTTAGCCAAAGCATGTCTT 287
QY 414 TTGAAGTATTAAGTCTGGTGGTGCACAAAGAATCTTATCATATAAGAGTCTTT 473
Db TTGAAGTATTAAGTCTGGTGGTGCACAAAGAATCTTATCATATAAGAGTCTTT 347
QY 288 TTGAAGTATTAAGTCTGGTGGTGCACAAAGAATCTTATCATATAAGAGTCTTT 347
Db 288 TTGAAGTATTAAGTCTGGTGGTGCACAAAGAATCTTATCATATAAGAGTCTTT 347
QY 474 TTTTATCTGGCCAGTATATATGACTAAGCATATATGATGAGAACAACATATT 533
Db TTTTATCTGGCCAGTATATATGACTAAGCATATATGATGAGAACAACATATT 407
QY 534 GTATATTGTCGAATGATCT 553
Db 408 GTATATTGTCGAATGATCT 427

RESULT 5
BX482386 300 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686H06230.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp686H06230.5', mRNA sequence.
ACCESSION BX482386
VERSION BX482386.1 GI:31942229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
REFERENCE 1 (bases 1 to 300)
AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amlid, C., Osanger, A.,
Fodor, G., Han, M. and Wiemann, S.
TITLE EST (Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amlid, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMWZ (Biomedical Research Center at the Heinrich-
Heine-University, Duesseldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No sl sequence available.
This clone (DKFZp686H06230) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..300
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686H06230"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1fb="686 (synonym: hlcc3)"
/note="Vector: pT73D-PacI; Site 1: SfiI; Site 2: SfiI;
cDNA-collection"

ORIGIN
Query Match 12.2%; Score 289; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 9.8e-126;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 613 CCATGATCTACAGGAATCTGTAGTACTCAATCAGCAGAAATCGAGTCAAGTACAT 672
Db CCATGATCTACAGGAATCTGTAGTACTCAATCAGCAGAAATCGAGTCAAGTACAT 71
QY 673 CTGTGAGTGAACAGAGTGTCACTTGAAGTGGAGATGATCAAAAGACCTTGTACAG 732
Db CTGTGAGTGAACAGAGTGTCACTTGAAGTGGAGATGATCAAAAGACCTTGTACAG 131
QY 72 CTGTGAGTGAACAGAGTGTCACTTGAAGTGGAGATGATCAAAAGACCTTGTACAG 131
Db 72 CTGTGAGTGAACAGAGTGTCACTTGAAGTGGAGATGATCAAAAGACCTTGTACAG 131
QY 733 AGCTTCAGGAAGAAACCTTCATCTCACTTTGTTTGAACATCTACCTCATCTA 792
Db AGCTTCAGGAAGAAACCTTCATCTCACTTTGTTTGAACATCTACCTCATCTA 191
QY 132 AGCTTCAGGAAGAAACCTTCATCTCACTTTGTTTGAACATCTACCTCATCTA 191
Db 132 AGCTTCAGGAAGAAACCTTCATCTCACTTTGTTTGAACATCTACCTCATCTA 191
QY 793 GAAAGAGCAATTAAGTGAAGACAGAAAGAAATTCAGATGAATTAATCTGTGAAGACAAA 852
Db GAAAGAGCAATTAAGTGAAGACAGAAAGAAATTCAGATGAATTAATCTGTGAAGACAAA 251
QY 192 GAAAGAGCAATTAAGTGAAGACAGAAAGAAATTCAGATGAATTAATCTGTGAAGACAAA 251
Db 192 GAAAGAGCAATTAAGTGAAGACAGAAAGAAATTCAGATGAATTAATCTGTGAAGACAAA 251
QY 853 GAAAGAGCAATTAAGTGAAGACAGAAAGAAATTCAGATGAATTAATCTGTGAAGACAAA 901
Db 853 GAAAGAGCAATTAAGTGAAGACAGAAAGAAATTCAGATGAATTAATCTGTGAAGACAAA 901
RESULT 6
AM070956 486 bp mRNA linear EST 20-OCT-2000
LOCUS AM070956
DEFINITION xai1h03.x1 NCI CGAP Br18 Homo sapiens cDNA clone IMAGE:2568437 3'

similar to gb:M92424 MDM2 PROTEIN (HUMAN); contains Alu repetitive element; contains element KER repetitive element ;, mRNA sequence.
AM070956
VERSION AM070956.1 GI:6025954
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 486)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmerit-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/biopr/image/image.html
Insert length: 2742 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 429.
Location/Qualifiers
1..486
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2568437"
/tissue_type="four pooled high-grade tumors, including two primary tumors and two metastatic to ovary"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Br18"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."
ORIGIN
Query Match 9.9%; Score 234; DB 7; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY CCCCCTGAAGAACTGGGAGTCTTGAAGGACCCCGACTCCAGCGGAAACCCCGG 293
Db CCCCCTGAAGAACTGGGAGTCTTGAAGGACCCCGACTCCAGCGGAAACCCCGG 186
QY 294 ATGTGAGGAGCAGCAATGTGCAATACCAACATGTCTGTACTGATGATGCTGTA 353
Db 187 ATGTGAGGAGCAGCAATGTGCAATACCAACATGTCTGTACTGATGATGCTGTA 246
QY 354 ACCACCTTCACGATTCGAGCTTCGGAACAAGACCTGTGTTAGCCAAAGCCATTGCTT 413
Db 247 ACCACCTTCACGATTCGAGCTTCGGAACAAGACCTGTGTTAGCCAAAGCCATTGCTT 306
QY 414 TTGAAGTTATTAAGTCTGTGTGTCACAAAAGACCTTATACATGAAAGAG 467
Db 307 TTGAAGTTATTAAGTCTGTGTGTCACAAAAGACCTTATACATGAAAGAG 360
RESULT 7
AL704062 393 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686N1428.r1.686 (synonym: hicc3) Homo sapiens cDNA clone
DEFINITION DKFZp686N1428.5', mRNA sequence.
ACCESSION AL704062
VERSION AL704062.1 GI:19687417
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 393)
AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Well, B. and Wiemann, S.
TITLE EST (Ottenwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Well, B. and Wiemann, S.)
JOURNAL Unpublished (2001)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No 5' sequence available.
This clone (DKFZp686N1428) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..393
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686N1428"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hicc3)"
/note="Vector: pTritex2; Site_1: SfiI; Site_2: SfiI; cDNA-collection"
ORIGIN
Query Match 9.7%; Score 231; DB 1; Length 393;
Best Local Similarity 99.4%; Pred. No. 4.1e-98;
Matches 331; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 305 CAGGCAATGTGCATATCAACATGTCTGTACTGATGATGCTGTACACCTGACA 364
Db 61 CAGGCAATGTGCATATCAACATGTCTGTACTGATGATGCTGTACACCTGACA 120
QY 365 GATTCACCTTCGGAACAAGACCTGTGTTAGCCAAAGCCATTGTTGAAGTTAT 424
Db 121 GATTCACCTTCGGAACAAGACCTGTGTTAGCCAAAGCCATTGTTGAAGTTAT 180
QY 425 AAAGTCTGTGTGTCACAAAAGACACTTATACATGAAAGAGTCTTTTATCTGG 484
Db 181 AAAGTCTGTGTGTCACAAAAGACACTTATACATGAAAGAGTCTTTTATCTGG 240
QY 485 CCAGTATATATGACTTAAGCATATATATGATGAGAGACAAACATATGATATGTC 544
Db 241 CCAGTATATATGACTTAAGCATATATATGATGAGAGACAAACATATGATATGTC 300
QY 545 AAATGATCTTTAGAGATTGTTGGGTCGCAAGCTTCTCTGTGAAGAGCAGAGAA 604
Db 301 AAATGATCTTTAGAGATTGTTGGGTCGCAAGCTTCTCTGTGAAGAGCAGAGAA 360
QY 605 AATATATACCAATGATCTTACAGAACTGTGTAGT 637
Db 361 AATATATACCAATGATCTTACAGAACTGTGTAGT 393
RESULT 8
BE676440 476 bp mRNA linear EST 08-SEP-2000
LOCUS BE676440
DEFINITION 7f29h02.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3296115.3', similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA sequence.
ACCESSION BE676440
VERSION BE676440.1 GI:10036981
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 476)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 436.
Location/Qualifiers
1..476
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:326115"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/clone_id="NCI-CCAP_CL11"
/note="Vector: pT7T3D-Pac1; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACCAATCTGAAGTGGAGCGCGCATGCTTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 9.2%; Score 219; DB 7; Length 476;
Best Local Similarity 99.4%; Pred. No. 2.1e-92;
Matches 319; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
234 CCCCCTAAGGAAGTGGAGTCTTGAGGGACCCCGACCTCGAAGCGGAAACCCCGG 293
|||
108 CCCCCTAAGGAAGTGGAGTCTTGAGGGACCCCGACCTCGAAGCGGAAACCCCGG 167
|||
294 ATGTGAGAGACAGCAAAATGTGCAATACCAATGCTGTACCTACTGATGTGTGTA 353
|||
168 ATGTGAGAGACAGCAAAATGTGCAATACCAATGCTGTACCTACTGATGTGTGTA 227
|||
354 ACCACCTCAGATTCAGCTTGGAGACAGACCTGTGTTAGCAAAAGCCATTGCTT 413
|||
228 ACCACCTCAGATTCAGCTTGGAGACAGACCTGTGTTAGCAAAAGCCATTGCTT 287
|||
414 TTGAAGTTAATGAAGTCTGTGGTGCACAAAAGACATTTATCTATGAAGAAGTTT 473
|||
288 TTGAAGTTAATGAAGTCTGTGGTGCACAAAAGACATTTATCTATGAAGAAGTTT 347
|||
474 TTATATCTGGCCAGTATATTATGACTAAAGATTTATGATGAGAACAACATTT 533
|||
348 TTATATCTGGCCAGTATATTATGACTAAAGATTTATGATGAGAACAACATTT 407
|||
534 GTATATTGTTCAATGATCTT 554
|||
408 GTATATTGTTCAATGATCTT 428
|||

RESULT 9
CT000980
LOCUS CT000980 265 bp mRNA linear EST 28-JUN-2005

DEFINITION CT000980 RZPD no.9016 Homo sapiens cDNA clone RZPDp9016H2223 5',
mRNA sequence.
ACCESSION CT000980
VERSION CT000980.1 GI:68294863
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 265)
Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
and Korn,B.
Human T-Lymphocytes library
JOURNAL Unpublished (2005)
COMMENT Contact: Inge Arltart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPDp9016H2223.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB No.9016
<http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016> Contact:
Inge Arltart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPDp9016H2223>
contact RZPD (product-support@rzpd.de) for further information.
Primer name: q93_4, Primer sequence: CGGATTAACATTACACAG.
Location/Qualifiers
1..265
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPDp9016H2223"
/tissue_type="T-Lymphocytes"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="RZPD no.9016"
/note="Vector: pQE80LSN_cloned; Site 1: SalI; Site 2:
NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned.pic.shtml
; 1st strand cDNA was prepared from mRNA obtained from
human T-Lymphocytes with a NotI - oligo(dT) primer [5',
GACTAGTCTAGATCGGACGCGCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
3'].
Double-stranded cDNA was ligated to SalI adaptors,
digested with NotI and cloned into the NotI and SalI sites
of the pQE80LSN_cloned vector"

ORIGIN
Query Match 8.9%; Score 211; DB 8; Length 265;
Best Local Similarity 100.0%; Pred. No. 1.4e-88;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
441 CAATAAGACCTTATCTATGAAGAAGTCTTTTATCTGGCCAGTATATTATGACT 500
|||
5 CAATAAGACCTTATCTATGAAGAAGTCTTTTATCTGGCCAGTATATTATGACT 64
|||
501 AAACGATTAATGATGAGAACAACAATATGTTATATGTTCAATGATCTTCTAGA 560
|||
65 AAACGATTAATGATGAGAACAACAATATGTTATATGTTCAATGATCTTCTAGA 124
|||
561 GATTGTTTGGCGTGCACAGCTTCTGTGTAAGAGACACAGAAATATATATCATGATC 620
|||
125 GATTGTTTGGCGTGCACAGCTTCTGTGTAAGAGACACAGAAATATATATCATGATC 184
|||
621 TACAGAACTTGATGATGATCAATCAGCAG 651
|||
185 TACAGAACTTGATGATGATCAATCAGCAG 215
|||

RESULT 10	
LOCUS	H79860
DEFINITION	H79860 399 bp mRNA linear EST 09-NOV-1995 yu78f12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:339951 5' similar to gb U87921 HUMALCD120 Human carcinoma cell-derived Alu RNA transcript, (tRNA); gb:M92424 MDM2 PROTEIN (HUMAN) ; mRNA sequence.
ACCESSION	H79860
VERSION	H79860.1 GI:1057949
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 399) Hillier,L., Clark,N., Dubugue,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williams,A., Woldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 332 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: M13RP1 High quality sequence stop: 332.
TITLE	
JOURNAL	
COMMENT	
FEATURES	
source	location/Qualifiers 1..399 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:3788904" /db_xref="taxon:9606" /clone="IMAGE:233951" /sex="male" /dev_stage="20 week post conception fetus" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares fetal liver spleen INFLS" /note="Organ: Liver and Spleen. Vector: pTR73 (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AATCGAAGAATTAAATTAAGACTTTTCTTTTTTTT 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTR73 vector. Library went through one round of normalization. library constructed by Bento Soares and M.Fatima Bernaldo."
ORIGIN	
Query Match	8.4%; Score 200; DB 10; Length 399;
Best Local Similarity	100.0%; Prid. No. 2,4e-83;
Matches 200, Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1800 TTAGAGATTATATATTTCTCACTATAATACCAGGAATTAGACAACCTGAATTTAT 1859 DB TTAGAGATTATATATTTCTCACTATAATACCAGGAATTAGACAACCTGAATTTAT 74
OY	1860 TCACATATATCAAAGTGAGAAAATGCCTCAATTGACATAGATTTCTCTTTAGTAA 1919 DB TCACATATATCAAAGTGAGAAAATGCCTCAATTGACATAGATTTCTCTTTAGTAA 134
OY	1920 TTGACCACTTTGGTAGGAATGTGAATCTTACTATATATTTGACTTGAAATGTAGC 1979 DB TTGACCACTTTGGTAGGAATGTGAATCTTACTATATATTTGACTTGAAATGTAGC 194

	DB	1980	TCATCCTTTACCAACTCC	1999
Db	195	TCATCCTTTACCAACTCC	214	
RESULT 11				
LOCUS	BFO89387	414 bp	mRNA	linear EST 19-OCT-2000
DEFINITION	PMO-HT0927-050900-003-cl2 HT0927 Homo sapiens cDNA,			mRNA sequence.
ACCESSION	BFO89387			
VERSION	BFO89387.1	GI:10895097		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 414) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.U. and Simpson,A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496	(2000)		
PUBLISHED	10737800			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01505-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICP Human Cancer Genome Project. This entry can be found in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l=cl2=PM2-HT0927-050 900-003-cl2&t3=2000-09-05&t4=1) Seq primer: puc 18 forward High quality sequence start: 19 High quality sequence stop: 414. Location/Qualifiers 1. .414 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_id="HT0927" /note="Organ: head-neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
FEATURES				
SOURCE				
ORIGIN				
Query Match	8.4%; Score 199;	DB 7;	Length 414;	
Best Local Similarity	100.0%;	Pred. No. 7.2e-83;		
Matches 199;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Db	235 CCGGTGAAGAACTGGGAGTCTTGAGGGACC	CGACTCCAAGCGGAAAACCCCGA	234	
Db	59 CCCTGAAGAACTGGGAGTCTTGAGGGACC	CGACTCCAAGCGGAAAACCCCGA	118	
Oy	295 TGTGAGGAGACAGCAATGTGAATAACAATGTCTGA	ACTTAAGTAGTGCTGTAA	354	
Db	119 TGTGAGGAGACAGCAATGTGAATAACAATGTCTGA	ACTTAAGTAGTGCTGTAA	178	
Oy	355 CGACCTTCACGATTCCAGTTCGGAAACAAGAACC	CTGTGATAGCCAAAGCCATTGCCTT	414	

Db	179	CCACCTACAGATTCCAGCTTCGGACAAGAGACCTTGTTAGACCAAGCATTGCTTT	238
QY	415	TGAAGTATTAAAGTCTGT	433
Db	239	TGAAGTATTAAAGTCTGT	257
RESULT 12			
BP350973			
LOCUS			
DEFINITION	OVI-HT0412-290400-178-d04 HT0412 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BP350973		
VERSION	BP350973.1	GI:11310047	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 221)		
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsumura,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
PUBMED	10737800		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?pl=QV1ct2-QV1-HT0412- 290400-178-d04&ct3=2000-04-29&ct4=1) Seq primer: puc 18 forward. Location/Qualifiers 1..221 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="HT0412" /note="Organ: head-neck; Vector: puc18; Site 1: Smal; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
ORIGIN			
Query Match	8.1%;	Score 193;	DB 7; Length 221;
Best Local Similarity	100.0%;	Pred. No. 5.3e-80;	
Matches 193;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1165	AGAGTGATGACATTCATTGTGAAGAAGATCCGAAATTTCTTACTGATGATTGGAAT	1224
Db	29	AGAGTGATGACATTCATTGTGAAGAAGATCCGAAATTTCTTACTGATGATTGGAAT	88
QY	1225	GCACCTCAGCATGCAATGAATGCCCTCCCTTCATCATCATTCGACAACAGATGTTGGGCC	1284
Db	89	GCACCTCAGCATGCAATGAATGCCCTCCCTTCATCATCATTCGACAACAGATGTTGGGCC	148
QY	1285	TTTCGTGAGATTTGGCTTCTCTGAAGATAAAGGAAAGATTAAGGGGAAATCTTGAGAAAG	1344

Dd		149	TTGCTGAAGATTGGCTTCCCTGAAGATAAAGGAAAGATTAAGGGAAATCTCGAGAAG	208
OY		1345	CCAAACTGGAAAA	1357
Dd		209	CCAAACTGGAAAA	221
RESULT 13				
H13638				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
OY				
Dd				
1773				
2				
ACTATATTCCTCCCTAGTTCAGCTGTCTCTATTAAGAGATTATATATTTCTTAACATATAAACC				
100.0%				
Pred.				
Mismatches				
Indels				
Gaps				
Score 167;				
DB 10;				
Length 319;				
Site 1:				
Not I - oligo(dT) primer [5'				
strand cDNA was primed with a Not I - oligo(dT) primer [5'				
double-stranded cDNA was ligated to Eco RI adaptors				
(Pharmacia), digested with Not I and cloned into the Not I				
and Eco RI sites of the modified pTV73 vector. Library				
went through one round of normalization. Library				
constructed by Bento Soares and W.Fatima Bernaldo.				
"				
/organism="Homo sapiens"				
/mol_type="mRNA"				
/db_xref="GDB:559774"				
/db_xref="taxon:9606"				
/clone="IMAGE:148052"				
/sex="Female"				
/dev_stage="placenta obtained at birth (full term)"				
/lab_host="DH10B (ampicillin resistant)"				
/clone_lib="Soares Placenta NB2HP"				
/note="Organ: placenta; Vector: pTV73D (Pharmacia) with a				
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st				
strand cDNA was primed with a Not I - oligo(dT) primer [5'				
AACGAGAAGATTGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'1,				
double-stranded cDNA was ligated to Eco RI adaptors				
(Pharmacia), digested with Not I and cloned into the Not I				
and Eco RI sites of the modified pTV73 vector. Library				
went through one round of normalization. Library				
constructed by Bento Soares and W.Fatima Bernaldo.				
"				
High quality sequence stops: 258				
Insert Length: 838				
Std Error: 0.00				
Seq primer: M13RPI				
High quality sequence stop: 258.				
Location/Qualifiers				
1..319				
Source: IMAGE Consortium, LML				
This clone is available royalty-free through LML ; contact the				
IMAGE Consortium (info@image.lml.gov) for further information.				
Unpublished (1995)				
Contact: Wilson RK				
Washington University School of Medicine				
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
Tel: 314 286 1800				
Fax: 314 286 1810				
Email: est@watson.wustl.edu				
Insert Size: 838				
High quality sequence stops: 258				
Source: IMAGE Consortium, LML				
This clone is available royalty-free through LML ; contact the				
IMAGE Consortium (info@image.lml.gov) for further information.				
Unpublished (1995)				
Contact: Wilson RK				
Washington University School of Medicine				
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
Tel: 314 286 1800				
Fax: 314 286 1810				
Email: est@watson.wustl.edu				
Insert Size: 838				
High quality sequence stops: 258				
Source: IMAGE Consortium, LML				
This clone is available royalty-free through LML ; contact the				
IMAGE Consortium (info@image.lml.gov) for further information.				
Unpublished (1995)				
Contact: Wilson RK				
Washington University School of Medicine				
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
Tel: 314 286 1800				
Fax: 314 286 1810				
Email: est@watson.wustl.edu				
Insert Size: 838				
High quality sequence stops: 258				
Source: IMAGE Consortium, LML				
This clone is available royalty-free through LML ; contact the				
IMAGE Consortium (info@image.lml.gov) for further information.				
Unpublished (1995)				
Contact: Wilson RK				
Washington University School of Medicine				
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
Tel: 314 286 1800				
Fax: 314 286 1810				
Email: est@watson.wustl.edu				

QY 1833 TAGGAATTAGACACCTGGAATTTATTCATATATCAAGTGAAGAAATGCTCAATT 1892
 DB 62 TAGGAATTAGACACCTGGAATTTATTCATATATCAAGTGAAGAAATGCTCAATT 121
 QY 1893 CACATAGATTTCTTCTCTTATGATATTAATGACCTACTTGGTAGTG 1939
 DB 122 CACATAGATTTCTTCTCTTATGATATTAATGACCTACTTGGTAGTG 168
 RESULT 14
 BE935243/c 469 bp mRNA linear EST 02-OCT-2000
 LOCUS M00-MT0124-250800-201-d08 MT0124 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE935243
 ACCESSION BE935243
 VERSION BE935243.1 GI:10461319
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 469)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
 TITLE Contact: Simpson A.J.G.
 JOURNAL Laboratory of Cancer Genetics
 PUBMED Ludwig Institute for Cancer Research
 COMMENT Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL.
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=MR0-MT0124-250
 800-201-d08&tc3=2000-08-25&tc4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 2
 High quality sequence stop: 469.
 Location/Qualifiers
 1..469
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="MT0124"
 /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 ORIGIN
 Query Match 7.0%; Score 167; DB 7; Length 469;
 Best Local Similarity 98.9%; Pred. No. 1.2e-67;
 Matches 367; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1518 ATTATTTATGACACCAAGAGATGTGAAGAGTTGAAAAGGAGAAACCAAGACAAA 1577
 DB 469 ATTATTTATGACACCAAGAGATGTGAAGAGTTGAAAAGGAGAAACCAAGACTAA 410
 QY 1578 GAAGAGAGTGTGGAATCTAGTTGCCCTTAATGCCATTTGAACCTGTGTGATTTGTCAA 1637

DB 409 GAAGAGAGTGTGGAATCTAGTTGCCCTTAATGCCATTTGAACCTGTGTGATTTGTCAA 350
 QY 1638 GGTGACCTTAAATGGTTGATTTGTCATGCGAAACAGACATCTTAGGCTGCTTT 1697
 DB 349 GGTGACCTTAAATGGTTGATTTGTCATGCGAAACAGACATCTTAGGCTGCTTT 290
 QY 1698 ACATGTGCAAGAAGCTTAAAGAAAGATTAAGCCCGCCAGATGTAGCAACCAATT 1757
 DB 289 ACATGTGCAAGAAGCTTAAAGAAAGATTAAGCCCGCCAGATGTAGCAACCAATT 230
 QY 1758 CAATGATGTGTCTACTTATTTCCCTAGTTGACCTGTCTATAGAGAAATTATATATT 1817
 DB 229 CAATGATGTGTCTACTTATTTCCCTAGTTGACCTGTCTATAGAGAAATTATATATT 170
 QY 1818 CTAACTATATPACCCTTAGAATTTAGACAACTGAAATTTATTCATATATCAAGTGA 1877
 DB 169 CTAACTATATPACCCTTAGAATTTAGACAACTGAAATTTATTCATATATCAAGTGA 110
 QY 1878 GAAATGCTTC 1888
 DB 109 GAAATGCTTC 99
 RESULT 15
 LOCUS A1281316/c 415 bp mRNA linear EST 28-JAN-1999
 DEFINITION g459d01.x1 NCI CGAP C08 Homo sapiens cDNA clone IMAGE:1873249 3'
 A1281316
 ACCESSION similar to gb:M92424 MDM2 PROTEIN (HUMAN)), mRNA sequence.
 VERSION A1281316
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 415)
 NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lemon, Ph.D.
 Cloned through the I.M.A.G.E. Consortium/LNL at:
 www-bio.lnl.gov/bdrip/image/image.html
 Insert Length: 1313 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 409.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:1873249"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP C08"
 /note="Organ: colon; Vector: pT73D-Pact; 1st strand cDNA
 was prepared from colon adenocarcinoma, and was then
 primed with a Not I oligo(dt) primer. Double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested
 with Not I and cloned into the Not I and Eco RI sites of
 the modified pT73 vector. Library is normalized. Library
 was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 7.0%; Score 166; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGT 710
|||||
DB 278 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGT 219
|||||

QY 711 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACTTTGGTT 770
|||||
DB 218 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACTTTGGTT 159
|||||

QY 771 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 816
|||||
DB 158 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 113
|||||

RESULT 16 421 bp mRNA linear EST 13-FEB-1999
A1336475/c
LOCUS go61d06.x1 NCI CGAP C08 Homo sapiens CDNA clone IMAGE:1913003 3'
DEFINITION similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA sequence.
ACCESSION A1336475
VERSION A1336475.1 GI:4073402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 421)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1356 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 396.
Location/Qualifiers
1. .421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1913003"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_11b="NCI CGAP C08"
/note="Organ: colon; Vector: pT73D-Pac1; 1st strand cDNA
was prepared from colon adenocarcinoma, and was then
primed with a Not I - oligo(dT) primer. Double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 7.0%; Score 166; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGT 710
|||||
DB 282 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGT 223
|||||

QY 711 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACTTTGGTT 770
|||||
DB 222 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACTTTGGTT 163
|||||

QY 771 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 816
|||||
DB 162 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 117
|||||

RESULT 17 423 bp mRNA linear EST 30-APR-1998
AA937920/c
LOCUS oF72e04.s1 NCI CGAP C08 Homo sapiens CDNA clone IMAGE:1435902 3'
DEFINITION similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA937920
VERSION AA937920.1 GI:3096031
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 423)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 396.
Location/Qualifiers
1. .423
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1435902"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_11b="NCI CGAP C08"
/note="Organ: colon; Vector: pT73D-Pac1; 1st strand cDNA
was prepared from colon adenocarcinoma, and was then
primed with a Not I - oligo(dT) primer. Double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 7.0%; Score 166; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGT 710
|||||
DB 278 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACAGGTGTCACTTGAAGTGGAGT 219
|||||

QY 711 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACTTTGGTT 770
|||||
DB 218 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACTTTGGTT 159
|||||

QY 771 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 816
|||||
DB 158 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 113
|||||

RESULT 18
AI346140/c 423 bp mRNA linear EST 30-DEC-1998
LOCUS
DEFINITION qp43e08.x1 NCI CGAP C08 Homo sapiens cDNA clone IMAGE:1925798 3'
similar to gb:M92424 MDM2 PROTEIN (HUMAN) ;, mRNA sequence.
AI346140
ACCESSION AI346140.1 GI:4083346
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
TITLE 1 (bases 1 to 423)
JOURNAL NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdrp/image/image.html
Seq primer: -40UP from GIBCO
High quality sequence stop: 407.
Location/Qualifiers
1. 423
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1925798"
/issue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_1b="NCI CGAP C08"
/note="Organ: colon; Vector: pT73D-Pact; 1st strand cDNA
was prepared from colon adenocarcinoma, and was then
primed with a Not I - oligo(dt) primer. Double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 7.0%; Score 166; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 651 GAATCATCGGACGAGTACATCTGTGAGGAGACGAGTCACTTGAAGGTGGAGT 710
DB 278 GAATCATCGGACGAGTACATCTGTGAGGAGACGAGTCACTTGAAGGTGGAGT 219
QY 711 GATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGAGAACTTCATCTTCACTTTGGTT 770
DB 218 GATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGAGAACTTCATCTTCACTTTGGTT 159
QY 771 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGTAGACAG 816
DB 158 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGTAGACAG 113

RESULT 19
AI274906/c 437 bp mRNA linear EST 29-JAN-1999
LOCUS
DEFINITION q149e03.x1 NCI CGAP C08 Homo sapiens cDNA clone IMAGE:1875628 3'
similar to gb:M92424 MDM2 PROTEIN (HUMAN) ;, mRNA sequence.
AI274906
ACCESSION

VERSION
KEYWORDS AI274906.1 GI:3897180
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
TITLE 1 (bases 1 to 437)
JOURNAL NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdrp/image/image.html
Insert Length: 1368 Std Error: 0.00
Seq primer: -40UP from GIBCO
High quality sequence stop: 405.
Location/Qualifiers
1. 437
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1875628"
/issue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_1b="NCI CGAP C08"
/note="Organ: colon; Vector: pT73D-Pact; 1st strand cDNA
was prepared from colon adenocarcinoma, and was then
primed with a Not I - oligo(dt) primer. Double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 7.0%; Score 166; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 651 GAATCATCGGACGAGTACATCTGTGAGGAGACGAGTCACTTGAAGGTGGAGT 710
DB 278 GAATCATCGGACGAGTACATCTGTGAGGAGACGAGTCACTTGAAGGTGGAGT 219
QY 711 GATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGAGAACTTCATCTTCACTTTGGTT 770
DB 218 GATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGAGAACTTCATCTTCACTTTGGTT 159
QY 771 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGTAGACAG 816
DB 158 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGTAGACAG 113

RESULT 20
AW999946/c 148 bp mRNA linear EST 05-JUN-2000
LOCUS
DEFINITION M90-BN0070-180400-014-C06 BN0070 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW999946
VERSION AW999946.1 GI:8260180
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
TITLE 1 (bases 1 to 148)

AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=fc2=MR0-BN0070-180
400-014-c06&ts=2000-04-18&rt=1)
Seq primer: puc 18 forward
High quality sequence stop: 148.

FEATURES
source
1. 148
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_11b="BN0070"
/note="Organ: breast normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 6.2%; Score 148; DB 7; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-58;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 849 CAAAGAAAGCGCAAAATCTGATGATATTCCTTCCTTGATGAAAGCCGTGGCTCG 908
DB 148 CAAAGAAAGCGCAAAATCTGATGATATTCCTTCCTTGATGAAAGCCGTGGCTCG 89
QY 909 TGTGTATTAAGGAGATATCTGTGAAAGAGCAGTAGCATCTACAGGAGGCCA 968
DB 88 TGTGTATTAAGGAGATATCTGTGAAAGAGCAGTAGCATCTACAGGAGGCCA 29
QY 969 TCGAATCCGATCTTGATGCTGGTGTA 996
DB 28 TCGAATCCGATCTTGATGCTGGTGTA 1

RESULT 21
A1339173 335 bp mRNA linear EST 29-DEC-1998
LOCUS A1339173
DEFINITION g999a02.x1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1946186 3', similar to gb:W92424 MDW2 PROTEIN (HUMAN), mRNA sequence.
ACCESSION A1339173
VERSION A1339173.1 GI:4076100
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 335)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
Tumor Gene Index
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

FEATURES
source
1. 335
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1946186"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_11b="NCI CGAP GC4"
/note="Vector: pTT3D-Pac1; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 5.9%; Score 140; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-55;
Matches 140; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 234 CCCCCTGAAGGAACCTGGGAGCTTGTAGGAGACCCCGACTCCAGCGGAAACCCCG 293
DB 108 CCCCCTGAAGGAACCTGGGAGCTTGTAGGAGACCCCGACTCCAGCGGAAACCCCG 167
QY 294 ATGTGAGGAGCAGCGCAATGTGCATATCAACATGTCTGTACTGTATGCTGCTGA 353
DB 168 ATGTGAGGAGCAGCGCAATGTGCATATCAACATGTCTGTACTGTATGCTGCTGA 227
QY 354 ACCACTCTCAAGATTCACG 373
DB 228 ACCACTCTCAAGATTCACG 247

RESULT 22
BF746144/c 233 bp mRNA linear EST 10-JAN-2001
LOCUS BF746144
DEFINITION RCL-BT0254-071100-118-c09 BT0254 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF746144
VERSION BF746144.1 GI:12072820
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 233)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED
COMMENT

10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RCl&t2=RCl-BT0254-
071100-118-c09&t3=2000-11-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 107
High quality sequence stop: 233.
Location/Qualifiers

FEATURES
source

1. 233
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="BT0254"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 5.8%; Score 138; DB 2; Length 233;
Best Local Similarity 100.0%; Pred.No. 8.4e-54;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1586 TGTGATCTAGTTGCCCCCTTATGCACTTGAACCTTGATTTGTCAGGTGACG 1645
DB 233 TGTGATCTAGTTGCCCCCTTATGCACTTGAACCTTGATTTGTCAGGTGACG 174
QY 1646 TAAAAATGTTGATTTGTCATGCAAAACAGACATCTTATGCGCTTTACATGTGC 1705
DB 173 TAAAAATGTTGATTTGTCATGCAAAACAGACATCTTATGCGCTTTACATGTGC 114
QY 1706 AAAAGAGCTAAAGAAAG 1723
DB 113 AAAAGAGCTAAAGAAAG 96

RESULT 23
LOCUS BF336925/c 253 bp mRNA linear EST 22-NOV-2000
DEFINITION CM2-CT5001-270900-403-b04 CT5001 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF336925
VERSION BF336925.1 GI:11307673
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 253)

REFERENCE
AUTHORS Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t2=CM2-CT5001-
270900-403-b04&t3=2000-09-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 253.
Location/Qualifiers

FEATURES
source

1. 253
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="CT5001"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORSTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 5.4%; Score 129; DB 7; Length 253;
Best Local Similarity 100.0%; Pred.No. 1.6e-49;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1651 ATGTTGATTTGTCATGCAAAACAGACATCTTATGCGCTTTACATGCAAGA 1710
DB 238 ATGTTGATTTGTCATGCAAAACAGACATCTTATGCGCTTTACATGCAAGA 179
QY 1711 AGCTAAAGAAAGAAATTAAGCCCTGCGCATGTATGACACCAATTCAAATGTTGC 1770
DB 178 AGCTAAAGAAAGAAATTAAGCCCTGCGCATGTATGACACCAATTCAAATGTTGC 119
QY 1771 TAACCTATT 1779
DB 118 TAACCTATT 110

RESULT 24
LOCUS BE765314 345 bp mRNA linear EST 19-SEP-2000
DEFINITION IL2-NT0102-280700-115-H11 NT0102 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE765314
VERSION BE765314.1 GI:10195238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 345)

REFERENCE
AUTHORS Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=PM1-AN0094-070
700-115-H11et3=2000-07-28&cl=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 344.
Location/Qualifiers
source
1. 345
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0102"
/note="Organ: nervous tumor; Vector: puc18; Site 1: Smal;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 5.3%; Score 125; DB 7; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.3e-47;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 470 TCTTTTTCCTGGCAGTATATATGACTAAAGATATATGATGAGAGAACAA 529
DB 170 TCTTTTTCCTGGCAGTATATATGACTAAAGATATATGATGAGAGAACAA 229
QY 530 TATTGATATGTTCAATGATCTTCTAGAGATTGTTGGCGTCCAAAGCTTCTGT 589
DB 230 TATTGATATGTTCTCAATGATCTTCTAGAGATTGTTGGCGTCCAAAGCTTCTGT 289
QY 590 GAAAGGACACAGAAATATATATCCATGATCTACAGAACTTGATGATCAATC 645
DB 290 GAAAGGACACAGAAATATATATCCATGATCTACAGAACTTGATGATCAATC 345
RESULT 25
BF081983 227 bp mRNA linear EST 18-OCT-2000
LOCUS PM1-AN0094-070900-003-c08 AN0094 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF081983
ACCESSION BF081983.1 GI:10875813
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 227)
Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Brines, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brumstein, A., deoliveira, P.S., Bucher, P., Jorgensen, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
JOURNAL Contact: Simpson A.J.G.
PUBMED Laboratory of Cancer Genetics
COMMENT Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=PM1-AN0094-070
900-003-c08&cl=3=2000-09-07&cl=4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 227.
Location/Qualifiers
source
1. 227
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="AN0094"
/note="Organ: amnion normal; Vector: puc18; Site 1: Smal;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 5.0%; Score 119; DB 7; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.4e-45;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1239 GAATGAATCCCCCTTCATCATGCAACAGATGTTGGCCCTTGTGAGATTGG 1298
DB 109 GAATGAATCCCCCTTCATCATGCAACAGATGTTGGCCCTTGTGAGATTGG 168
QY 1299 CTTCCTGAAGATTAAGGAAAGATTAAGGAAATCTCTGAAAGCCAAATGTGAAAA 1357
DB 169 CTTCCTGAAGATTAAGGAAAGATTAAGGAAATCTCTGAAAGCCAAATGTGAAAA 227
RESULT 26
AI246037 415 bp mRNA linear EST 28-JAN-1999
LOCUS qk44h12.x1 NCI_CGAP C08 Homo sapiens cDNA clone IMAGE:1871879 3'
DEFINITION similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI246037
VERSION AI246037.1 GI:3841434
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 415)
Email: cgapdb-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/HLN at:
www.bio.lnl.gov/bbrp/image/image.html
Insert Length: 1343 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 409.
Location/Qualifiers
source
1. 415
/organism="Homo sapiens"

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1871879"
/issue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_C08"
/note="Organ: Colon; Vector: pYT73D-PacI; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pYT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 4.8%; Score 115; DB 1; Length 415;
Best Local Similarity 99.4%; Pred. No. 7,4e-43;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 651 GAATCATCGAGCTCAGTACATCTGTAGTGAAGACAGTGCACCTTGAGGTGGAGT 710
DB 278 GAATCATCGAGCTCAGTACATCTGTAGTGAAGACAGTGCACCTTGAGGTGGAGT 219
QY 711 GATCAAGAGCAGCTTGTACAGAGCTTCAAGAGAACTTCATCTTCACTTTGGTT 770
DB 218 GATCTAAGAGCAGCTTGTACAGAGCTTCAAGAGAACTTCATCTTCACTTTGGTT 159
QY 771 TCTAGACCATCTACCTCATCTTGAAGAGAGCAATTAGTACAGAG 816
DB 158 TCTAGACCATCTACCTCATCTTGAAGAGAGCAATTAGTACAGAG 113

RESULT 27

LOCUS AA568852 366 bp mRNA linear EST 09-SEP-1997
DEFINITION nm27a12.s1 NCI CGAP Lip2 Homo sapiens cDNA clone IMAGE:1061374
similar to gb:M92424 MDM2 PROTEIN (HUMAN); contains Alu repetitive element, mRNA sequence.

ACCESSION AA568852
VERSION AA568852.1 GI:2341906
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 366)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmerit-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnlnl.gov/bhrp/image/image.html
Insert Length: 636 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 273.
Location/Qualifiers

FEATURES

source
1. 366
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1061374"
/issue_type="liposarcoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lip2"

ORIGIN

/note="Vector: pAMP10; mRNA made from liposarcoma, cDNA made by oligo-dT priming. Non-directionally cloned.
Size selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."

Query Match 4.6%; Score 108; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1947 AATCTACTAATTAATTTGACCTGAATATGATGCTCATCTTACACCACTCTAATTTT 2006
DB 37 AATCTACTAATTAATTTGACCTGAATATGATGCTCATCTTACACCACTCTAATTTT 96
QY 2007 AATTAATTTCTACTCTGTCTTAATGAGAAGTACTGTTTTTTTTTTT 2054
DB 97 AATTAATTTCTACTCTGTCTTAATGAGAAGTACTGTTTTTTTTTTT 144

RESULT 28

LOCUS R80235 456 bp mRNA linear EST 09-JUN-1995
DEFINITION Y196d02.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:147075 3' similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA sequence.

ACCESSION R80235
VERSION R80235.1 GI:856516
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 456)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, B., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Insert Size: 529
High quality sequence stops: 322
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnlnl.gov) for further information.
Insert Length: 529 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 322.
Location/Qualifiers

FEATURES

source
1. 456
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:558688"
/db_xref="taxon:9606"
/clone="IMAGE:147075"
/sex="Female"
/dev stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares Placenta Nb2HP"
/note="Organ: placenta; Vector: pYT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACGGAAGAATTCGCGCGAGAAATTTTATTTTATTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

Query Match 4.5%; Score 106; DB 10; Length 456;
 Best Local Similarity 99.4%; Pred. No. 1.4e-38;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

234 CCCCCTGAAGAAATGGGGAGTCTTTGAGGACCCCGACTCCAGCCGGAACCCCGG 293
 108 CCCCCTGAAGAAATGGGGAGTCTTTGAGGACCCCGACTCCAGCCGGAACCCCGG 167
 294 ATGGGAGAGACGAGCAATGTCATATCAATCATGTCTGACTACTGATGATGCTGTGA 353
 168 ATGGGAGAGACGAGCAATGTCATATCAATCATGTCTGACTACTGATGATGCTGTGA 227

354 ACCACCTCAGAGATTCCAGCTTGGAGACAGAGACCC 390
 228 ACCACCTCAGAGATTCCAGCTTGGAGACAGAGACCC 264

RESULT 29
 CC000590 489 bp DNA linear GSS 31-MAR-2003
 LOCUS UP 479-4N T7 RPl11 Human Male BAC library Homo sapiens genomic

DEFINITION clone 479-4N, genomic survey sequence.

ACCESSION CC000590
 VERSION CC000590.1 GI:29379150
 KEYWORDS GSS.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 489)
 Cheung,V.G., Dalrymple,H.L., Narasimhan,S., Watts,J., Schuler,G., Raap,A.K., Morley,M. and Bruzel,A.
 A resource of mapped human bacterial artificial chromosome clones
 Genome Res. 9 (10), 989-993 (1999)

TITLE Contact: Narasimhan SL, Morley M, Burdick J, Cheung VG
 PUBMED 10523527

COMMENT Department of Pediatrics
 University of Pennsylvania
 3516 Civic Center Blvd, ARC 516, Philadelphia, PA 19104, USA
 Tel: 215 590 2664
 Fax: 215 590 3709
 Email: mlennox@mail.med.upenn.edu
 Plate: 479 row: N column: 4
 Seq primer: T7
 Class: BAC ends.

FEATURES
 Location/Qualifiers

1..489
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="479-4N"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_1ib="RPl11 Human Male BAC library"
 /note="Vector: pBACe3.6; RPl11 Human Male BAC library"

ORIGIN

Query Match 4.1%; Score 98; DB 12; Length 489;
 Best Local Similarity 100.0%; Pred. No. 9.2e-35;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2260 TTTTGTAGAGACAGGCTTTCACCGTGTAGCCAGGATGCTCCGATCTCGACCTGCT 2319
 454 TTTTGTAGAGACAGGCTTTCACCGTGTAGCCAGGATGCTCCGATCTCGACCTGCT 395
 2320 GATCGCCCACTCGGCTCCCAAGTGTGGATTAC 2357

Db 394 GATCGCCCACTCGGCTCCCAAGTGTGGATTAC 357

RESULT 30

LOCUS N20967 385 bp mRNA linear EST 19-DEC-1995
 DEFINITION yk57c04.61 Soares melanocyte 2NbhM Homo sapiens cDNA clone
 IMAGE:265830 3' similar to contains Alu repetitive element; contains
 element 11 repetitive element ;, mRNA sequence.

ACCESSION N20967.1 GI:1126137
 VERSION N20967
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 385)
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaekis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

REFERENCE The Washu-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

High quality sequence stops: 313
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.lnl.gov) for further information.
 Insert Length: 2267 Std Error: 0.00
 Seq primer: ml3 -40 forward
 High quality sequence stop: 313.

FEATURES
 Location/Qualifiers

1..385
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3875472"
 /db_xref="taxon:9606"
 /clone="IMAGE:265830"
 /sex="Male"
 /tissue_type="melanocyte"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_1ib="Soares melanocyte 2NbhM"
 /note="Vector: pT73D (Pharmacia) with a modified
 polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5']
 TGTTCACATCTGAAAGTGGAGCGCGCGGACATTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo. RNA from normal foreskin melanocytes
 (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 4.0%; Score 94; DB 10; Length 385;
 Best Local Similarity 100.0%; Pred. No. 7.5e-33;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2274 GGGTTTACCGGTGTAGCCAGGATGCTTCGATCTCGACCTGTGATCGCCCACTGC 2333
 13 GGGTTTACCGGTGTAGCCAGGATGCTTCGATCTCGACCTGTGATCGCCCACTGC 72
 2334 GGGTTTCCAAAGTGTGGATTACAGGATGAGC 2367
 73 GGGTTTCCAAAGTGTGGATTACAGGATGAGC 106


```

RESULT 31
BE019522      437 bp      mRNA      linear      EST 06-JUN-2000
LOCUS         bb57c10.y1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3010770 5'
DEFINITION    similar to gb:92424 MDMA PROTEIN (HUMAN); gb:X58876 Murine mdm2
ACCESSION     BE019522
VERSION       BE019522.1 GI:8279598
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE     1 (bases 1 to 437)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LINL at:
              imgc.llnl.gov/image/html/resources.shtml
              Seq primer: -40RP from Gibco
              High quality sequence stop: 361.
              Location/Qualifiers
                1. 437
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3010770"
                  /cissue_type="rhabdomyosarcoma"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_1lb="NIH_MGC_17"
                  /note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
                  Site 2: XhoI; cDNA made by oligo-dT priming.
                  Directionally cloned into EcoRI/XhoI sites using the
                  following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
                  for average insert size 1.8kb. Library constructed by
                  Ling Hong in the laboratory of Gerald M. Rubin (University
                  of California, Berkeley) using ZAP-cDNA synthesis kit
                  (Stratagene) and Superscript II RT (Life Technologies)."
```

FEATURES

source

ORIGIN

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Query Match      4.0%; Score 94; DB 7; Length 437;
Best Local Similarity 100.0%; Pred. No. 7.4e-33;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 53 AGATGAGCAAGAACCGAGCGGGCGCGGACCCCTTGACCGAGATCTCTG 112
    |||
Db 1  AAGATGACCAAGAACCGAGCGGGCGCGGACCCCTTGACCGAGATCTCTG 60

Oy 113 TGCCTTGCAGCCAGGACGCTCCCTCCCGG 146
    |||
Db 61 TGCCTTGCAGCCAGGACGCTCCCTCCCGG 94

RESULT 32
BF949018      147 bp      mRNA      linear      EST 22-JAN-2001
LOCUS         MR3-NN0220-011100-009-b11 NN0220 Homo sapiens cDNA, mRNA sequence.
DEFINITION    BF949018
ACCESSION     BF949018.1 GI:12366293
VERSION       BF949018.1
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

```

REFERENCE     1 (bases 1 to 147)
AUTHORS      Dias Neto,F., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FADESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-NN0220-011100-009-b11&t3=2000-11-01&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 147.
              Location/Qualifiers
                1. 147
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /dev_stage="Adult"
                  /clone_1lb="NN0220"
                  /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
                  Site 2: SmaI; A mini-library was made by cloning products
                  derived from ORESTES PCR (U.S. Letters Patent application
                  No. 196,716 - Ludwig Institute for Cancer Research)
                  profiles into the puc 18 vector. Reverse transcription of
                  tissue mRNA and cDNA amplification were performed under
                  low stringency conditions."
```

FEATURES

source

ORIGIN

```

Query Match      3.9%; Score 92; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 7e-32;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1266 TGCACAGATGTGGGCGCTTGCTGAGATTGGCTTCGAGATTAAGGAAGTAA 1325
    |||
Db 56 TGCACAGATGTGGGCGCTTGCTGAGATTGGCTTCGAGATTAAGGAAGTAA 115

Oy 1326 GGGGAATCTCTGAGAAAGCCAACTGAAAA 1357
    |||
Db 116 GGGGAATCTCTGAGAAAGCCAACTGAAAA 147

RESULT 33
BF949413      147 bp      mRNA      linear      EST 22-JAN-2001
LOCUS         MR3-NN0220-031100-009-b11 NN0220 Homo sapiens cDNA, mRNA sequence.
DEFINITION    BF949413
ACCESSION     BF949413.1 GI:12366688
VERSION       BF949413.1
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE     1 (bases 1 to 147)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
```

Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&cl2=MR3-NN0220-
031100-009-b11&cl3=2000-11-03&cl4=1)
Seq primer: puc 18 forward
High quality sequence stop: 147.
Location/Qualifiers
1. 147
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN0220"
/note="Organ: nervous normal; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 3.9%; Score 92; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 7e-32;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1266 TGCAACAGATGTTGGCCCTTGTGAGATTGCTTCTGGAAGATTAAGGAGAAATATA 1325
DB 56 TGCAACAGATGTTGGCCCTTGTGAGATTGCTTCTGGAAGATTAAGGAGAAATATA 115
QY 1326 GGGGAAATCTCGAGAAAGCCAACTGGAAAA 1357
DB 116 GGGGAAATCTCGAGAAAGCCAACTGGAAAA 147
RESULT 34
F35659 151 bp mRNA linear EST 13-MAY-1999
LOCUS HSPD32490 HM3 Homo sapiens cDNA clone SHS-000005-0/C05, mRNA
DEFINITION F35659
ACCESSION F35659
VERSION F35659.1 GI:4821285
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
REFERENCE 1 (bases 1 to 151)
Lanfranchi,G., Muraro,T., Caldera,F., Pacchioni,B., Pallavicini,A.,
Pandofo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization
Genome Res. 6 (1), 35-42 (1996)
8681137
JOURNAL CONTACT: Valle G.
PUBMED CRIBI Biotechnology Centre
COMMENT University of Padua
Via Trieste 75, 35121 Padua, Italy

ABI Chromatograms and other information are available on WWW at
http://grp.bio.unipd.it.
Location/Qualifiers
1. 151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SHS-000005-0/C05"
/sex="female"
/tissue_type="Pectoral muscle (after mastectomy)"
/clone_lib="HM3"
/note="Vector: pCDNAII (Invitrogen); Site_1: BstXI;
Site_2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated
oligo-dT-NotI primer
(5'-biotin-AACCCGGCTCGAGCCCGCTTTTCTTTTCTTTT-3'). The
ds cDNA was sonicated and size-selected in the range
350-550 bp. The 3' specific fragments were selected by
streptavidin coated magnetic beads, ligated to
non-palindromic BstXI adapters, NotI digested and
directionally cloned into BstXI-NotI cut pCDNAII vector."
ORIGIN
Query Match 3.7%; Score 88; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 5.e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTACCGGTGTAGCCAGATGTTGCATCTCTGACCTGTATCCGCCACCTC 2333
DB 18 GGGTTTACCGGTGTAGCCAGATGTTGCATCTCTGACCTGTATCCGCCACCTC 77
QY 2334 GGGCTCCCAAGTGCTGGGATTACAGGC 2361
DB 78 GGGCTCCCAAGTGCTGGGATTACAGGC 105
RESULT 35
BG956827 298 bp mRNA linear EST 12-JUN-2001
LOCUS IL3-CT0674-210201-486-A08 CT0674 Homo sapiens cDNA, mRNA sequence.
DEFINITION BG956827
ACCESSION BG956827.1 GI:14374998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
REFERENCE 1 (bases 1 to 298)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&cl2=IL3-CT0674-
210201-486-A08&cl3=2001-02-21&cl4=1)
Seq primer: puc 18 forward

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo
1 (bases 1 to 454)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel.: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2234 row: L column: 2
Class: BAC ends
High quality sequence stop: 454.
Location/Qualifiers
1..454
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2234 Col=2 Row=L"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pbeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Query Match 3.7%; Score 88; DB 11; Length 454;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2274 GGGTTTCAACCGTTTACGAGATGCTCGATCTCTGACCTCGTATCCGCCACCTC 2333
|||||
DB 135 GGGTTTCAACCGTTTACGAGATGCTCGATCTCTGACCTCGTATCCGCCACCTC 194
|||||
OY 2334 GGCTCCCAAGTCTGGGATTACAGGC 2361
|||||
DB 195 GGCTCCCAAGTCTGGGATTACAGGC 222
|||||

RESULT 39
AL048925/c 474 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp434K1818.1 434 (synonym: htcs3) Homo sapiens cDNA clone
DEFINITION DKFZp434K1818.1 mRNA sequence.
ACCESSION AL048925
VERSION AL048925.2 GI:5866752
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 474)
Ostenweider,B., Ostermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Ostenweider, et al.)
Unpublished (1999)
On Apr 30, 1999 this sequence version replaced gi:4728234.
Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA

REFERENCE
JOURNAL
COMMENT

sequencing consortium of the German Genome Project. No si sequence available.
This clone (DKFZp434K1818) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434K1818"
/issue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htcs3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match 3.7%; Score 88; DB 1; Length 474;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2274 GGGTTTCAACCGTTTACGAGATGCTCGATCTCTGACCTCGTATCCGCCACCTC 2333
|||||
DB 285 GGGTTTCAACCGTTTACGAGATGCTCGATCTCTGACCTCGTATCCGCCACCTC 226
|||||
OY 2334 GGCTCCCAAGTCTGGGATTACAGGC 2361
|||||
DB 225 GGCTCCCAAGTCTGGGATTACAGGC 198
|||||

RESULT 40
B0351361/c 330 bp mRNA linear EST 20-MAY-2002
LOCUS QV0-HT0367-120600-261-e09 HT0367 Homo sapiens cDNA, mRNA sequence.
DEFINITION QV0-HT0367-120600-261-e09 HT0367 Homo sapiens cDNA, mRNA sequence.
ACCESSION B0351361
VERSION B0351361.1 GI:21015417
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 330)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S.C. Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV0&t2=QV0-HT0367-120600-261-e09&t3=2000-06-12&t4=1)
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High quality sequence stop: 330.
Location/Qualifiers
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FEATURES
source

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No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."
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ORIGIN

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Db 296 GGGTTTCAACCGTGTAGCCAGAGAGTCTCGATCTCTGACCTCGTATCGGCCACCTC 237  
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QY 2334 GGCTTCCCAAGTGTGGGATTACAG 2360  
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Search completed: August 4, 2006, 16:54:12
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